Claims:

1. An isolated polypeptide comprising a fibronectin type III tenth (^{10}Fn3) domain wherein the ^{10}Fn3 has a BC, DE and FG loop, and wherein the BC loop comprises SEQ ID NO:14, the DE comprises SEQ ID NO:25 and the FG loop comprises SEQ ID NO:37, and wherein the polypeptide binds proprotein convertase subtilisin kexin type (PCSK9).

2. The isolated polypeptide of claim 1, wherein the polypeptide binds PCSK9 with a K_D of less than 500 nM.

3. The isolated polypeptide of claim 1, further comprising one or more pharmacokinetic (PK) moieties selected from the group consisting of polyethylene glycol, sialic acid, Fc, Fc fragment, transferring, serum albumin, a serum albumin binding protein, and a serum immunoglobulin binding protein.

4. A pharmaceutically acceptable composition comprising the polypeptide of claim 1.

5. An isolated polypeptide comprising a ^{10}Fn3 domain wherein the isolated polypeptide comprises SEQ ID NO:82, and wherein the isolated polypeptide binds PCSK9.

6. The isolated polypeptide of claim 5, wherein the polypeptide binds PCSK9 with a K_D of less than 500 nM.

7. The isolated polypeptide of claim 5, further comprising one or more pharmacokinetic (PK) moieties selected from the group consisting of polyethylene glycol, sialic acid, Fc, Fc fragment, transferring, serum albumin, a serum albumin binding protein, and a serum immunoglobulin binding protein.

8. A pharmaceutically acceptable composition comprising the polypeptide of claim 5.

SEQUENCE LISTING

<110> BRISTOL-MYERS SQUIBB COMPANY

<120> FIBRONECTIN BASED SCAFFOLD DOMAIN PROTEINS THAT BIND PCSK9

<130> 11594 PCT

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<150> 61/330,731
<151> 2010-05-03

<150> 61/323,562
<151> 2010-04-13

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Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys Pro
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Glu Phe Thr Val Pro Pro Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
    50                  55                  60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro
65                  70                  75                  80

Tyr Lys His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
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Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
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Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr
65 70 75 80

Phe Lys His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

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atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatataca 240

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20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr
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Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
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35 40 45

Glu Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr
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Phe Lys His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
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Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
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Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr
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Phe Lys His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
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Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
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Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Gly Arg Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr
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Tyr Lys Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
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Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
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Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr
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atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacacg 240

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20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr
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acaggaggca atagccctgt ccaggagttc actgtgcctg ttggtgaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacacg 240

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20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr
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Tyr Glu Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
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acaggaggca atagccctgt ccaggagttc actgtgcctg ttggtgaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacacg 240

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Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Thr Pro Pro Pro Lys Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Ala
65 70 75 80

Tyr Asn Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Gly Ser Gly Ser His His His His His His
100 105

<210> 58
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 58
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggacgcctcc ccctaaaggg tatggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg ttggtgaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacgcg 240

tacaacggtg ccggttacta ccaccggcca atttccatta attaccgcac aggtagcggt 300

tcccaccatc accaccatca c 321

<210> 59
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 59
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Arg Pro Pro Ser His Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro
65 70 75 80

Trp Lys Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 60
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 60
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggcggccgcc atctcatgct tatggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttgggaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacccg 240

tggaaaggtt ctggttacta ccatcggcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 61
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 61
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Pro Pro Ser His Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro
65 70 75 80

Trp Lys Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Gly Ser Gly Ser His His His His His His
100 105

<210> 62
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 62
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacccgcc atctcatgct tatggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttgggaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacccg 240

tggaaaggtt ctggttacta ccatcggcca atttccatta attaccgcac aggtagcggt 300

tcccaccatc accaccatca c 321

<210> 63
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 63
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Pro Pro Ser His Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro
65 70 75 80

Trp Lys Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Gly Ser Gly Ser His His His His His His
100 105

<210> 64
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 64
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggaaccgcc atctcatgct tatggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttgggaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacccg 240

tggaaaggtt ctggttacta ccatcggcca atttccatta attaccgcac aggtagcggt 300

tcccaccatc accaccatca c 321

<210> 65
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 65
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Ser Pro Pro Ser His Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro
65 70 75 80

Trp Lys Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Gly Ser Gly Ser His His His His His His
100 105

<210> 66
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 66
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggagcccgcc atctcatgct tatggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttgggaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacccg 240

tggaaaggtt ctggttacta ccatcggcca atttccatta attaccgcac aggtagcggt 300

tcccaccatc accaccatca c 321

<210> 67
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 67
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Arg Pro Pro Ser Asn Gly His Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro
65 70 75 80

Phe Lys Trp Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 68
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 68
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggcggccccc ctctaatggt cacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg ttaatgaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcccc 240

ttcaagtggt cgggctacta ccatcgacca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 69
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 69
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Val Pro Pro Ser Asp Asp Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro
65 70 75 80

Trp Pro His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 70
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 70
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggtcccgcc ttcagatgat tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttggtaaagg aacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgagtttccg 240

tggccacatg ctggttacta tcatcggcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 71
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 71
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Val Pro Ser Ser His Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Ala
65 70 75 80

Phe Glu Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 72
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 72
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggttccgtc gtctcatgcc tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tgggggtagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacgct 240

ttcgaagggg ctggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 73
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 73
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Pro Ser Ser His Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Ala
65 70 75 80

Phe Glu Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 74
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 74
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacccgtc gtctcatgcc tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tgggggtagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacgct 240

ttcgaagggg ctggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 75
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 75
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Pro Ser Ser His Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Ala

65 70 75 80

Phe Glu Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 76
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 76
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggaaccgtc gtctcatgcc tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tgggggtagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacgct 240

ttcgaagggg ctggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 77
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 77
Gly Ser Gly Cys
1

<210> 78
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 78
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Val Pro Pro Ser Asp Asp Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro
65 70 75 80

Trp Pro His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Cys Gln
100

<210> 79
<211> 314
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 79
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggtcccgcc ttcagatgat tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttggtaaagg aacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgagtttccg 240

tggccacatg ctggttacta tcatcggcca atttccatta attaccgcac agaaattgac 300

aaaccatgcc agtg 314

<210> 80
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 80
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Val Pro Pro Ser Asp Asp Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro
65 70 75 80

Trp Pro His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Gly Ser Gly Cys
100

<210> 81
<211> 308
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 81
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggtcccgcc ttcagatgat tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttggtaaagg aacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgagtttccg 240

tggccacatg ctggttacta tcatcggcca atttccatta attaccgaac agaaggtagc 300

ggttgctg 308

<210> 82
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 82
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Val Pro Pro Ser Asp Asp Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro

65 70 75 80

Trp Pro His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Glu Lys Pro Cys Gln
100

<210> 83
<211> 314
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 83
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggtcccgcc ttcagatgat tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttggtaaagg aacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgagtttccg 240

tggccacatg ctggttacta tcatcggcca atttccatta attaccgcac agaaattgag 300

aaaccatgcc agtg 314

<210> 84
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 84
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Val Pro Pro Ser Asp Asp Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro
65 70 75 80

Trp Pro His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Gly Ser Gly Cys His His His His His His
100 105

<210> 85
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 85
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggtcccgcc ttcagatgat tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttggtaaagg aacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgagtttccg 240

tggccacatg ctggttacta tcatcggcca atttccatta attaccgcac aggtagcggt 300

tgccaccatc accaccatca c 321

<210> 86
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 86
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Pro Pro Pro Ser His Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Pro Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro
65 70 75 80

Tyr Lys His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Cys Gln His His His His His His
100 105 110

<210> 87
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 87
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggccgccgcc gtctcatggt tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccgc ctggtaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacccg 240

tacaaacatt ctggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatgcc agcaccatca ccaccaccac 330

<210> 88
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 88
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Arg Pro Pro Ile His Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr
65 70 75 80

Phe Lys His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Cys Gln His His His His His His
100 105 110

<210> 89
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 89
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggaggccgcc gattcatgct tacgggtatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttgttgaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatataca 240

tttaaacatt ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatgcc agcaccatca ccaccaccac 330

<210> 90
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 90
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Arg Pro Pro Ser Asn Gly His Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro
65 70 75 80

Phe Lys Trp Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Gly Ser Gly Cys His His His His His His
100 105

<210> 91
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 91
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggcggccccc ctctaatggt cacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg ttaatgaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcccc 240

ttcaagtggt cgggctacta ccatcgacca atttccatta attaccgcac aggtagcggt 300

tgccaccatc accaccatca c 321

<210> 92
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 92
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Val Pro Ser Ser His Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Ala
65 70 75 80

Phe Glu Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Gly Ser Gly Cys His His His His His His
100 105

<210> 93
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 93
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ctgatcagct gggttccgtc gtctcatgcc tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tgggggtagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacgct 240

ttcgaagggg ctggttacta ccatcgtcca atttccatta attaccgcac aggtagcggt 300

tgccaccatc accaccatca c 321

<210> 94
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 94
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Pro Ser Ser His Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Ala
65 70 75 80

Phe Glu Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Gly Ser Gly Cys His His His His His His
100 105

<210> 95
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 95
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ctgatcagct gggacccgtc gtctcatgcc tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tgggggtagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacgct 240

ttcgaagggg ctggttacta ccatcgtcca atttccatta attaccgcac agaaggtagc 300

ggttgccacc atcaccacca tcac 324

<210> 96
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 96
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Pro Ser Ser His Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Ala
65 70 75 80

Phe Glu Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Gly Ser Gly Cys His His His His His His
100 105

<210> 97
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 97
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ctgatcagct gggaaccgtc gtctcatgcc tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tgggggtagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacgct 240

ttcgaagggg ctggttacta ccatcgtcca atttccatta attaccgcac agaaggtagc 300

ggttgccacc atcaccacca tcac 324

<210> 98
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 98
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Thr Pro Pro Pro Lys Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr
65 70 75 80

Tyr Asn Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Gly Ser Gly Cys His His His His His His
100 105

<210> 99
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 99
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggacgcctcc ccctaaaggg tatggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg ttggtgaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacacg 240

tacaacggtg ccggttacta ccaccggcca atttccatta attaccgcac aggtagcggt 300

tgccaccatc accaccatca c 321

<210> 100
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 100
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Arg Pro Pro Ser His Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro
65 70 75 80

Trp Lys Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Gly Ser Gly Cys His His His His His His
100 105

<210> 101
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 101
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggcggccgcc atctcatgct tatggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttgggaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacccg 240

tggaaaggtt ctggttacta ccatcggcca atttccatta attaccgcac aggtagcggt 300

tgccaccatc accaccatca c 321

<210> 102
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 102
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Arg Pro Pro Ser His Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro
65 70 75 80

Trp Lys Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Cys Gln His His His His His His
100 105 110

<210> 103
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 103
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ctgatcagct ggcggccgcc atctcatgct tatggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttgggaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacccg 240

tggaaaggtt ctggttacta ccatcggcca atttccatta attaccgcac agaaattgac 300

aaaccatgcc agcaccacca ccaccaccac 330

<210> 104
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 104
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Pro Pro Ser His Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro
65 70 75 80

Trp Lys Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Gly Ser Gly Cys His His His His His His
100 105

<210> 105
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 105
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggaaccgcc atctcatgct tatggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttgggaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacccg 240

tggaaaggtt ctggttacta ccatcggcca atttccatta attaccgcac agaaggtagc 300

ggttgccacc atcaccacca tcac 324

<210> 106
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 106
Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly Gly Gly Glu
1 5 10

<210> 107
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 107
Ser Trp Asp Ala Pro Ala Asp Gly Gly Tyr Gly
1 5 10

<210> 108
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 108
Ser Trp Asp Ala Pro Ala Gly Asp Gly Tyr Gly
1 5 10

<210> 109
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 109
Ser Trp Ala Ala Pro Ala Gly Gly Gly Tyr Gly
1 5 10

<210> 110
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 110
Ser Trp Asp Ala Pro Ala Asp Ala Tyr Gly
1 5 10

<210> 111
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 111
Ser Trp Asp Ala Pro Ala Asp Gly Ala Tyr Gly
1 5 10

<210> 112
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 112
Ser Trp Asp Ala Pro Ala Glu Gly Tyr Gly
1 5 10

<210> 113
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 113
Ser Trp Asp Ala Pro Ala Asp Glu Ala Tyr Gly
1 5 10

<210> 114
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 114
Ser Trp Asp Ala Pro Ala Asp Gly Tyr Gly
1 5 10

<210> 115
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 115
Ser Trp Asp Ala Pro Ala Gly Gly Gly Tyr Gly
1 5 10

<210> 116
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 116
Ser Trp Asp Ala Pro Ala Ala Asp Ala Tyr Gly
1 5 10

<210> 117
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 117
Ser Trp Asp Ala Pro Ala Glu Ala Gly Lys His Tyr Gly
1 5 10

<210> 118
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 118
Ser Trp Asp Ala Pro Ala Glu Ala Tyr Gly
1 5 10

<210> 119
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 119
Ser Trp Asp Ala Pro Ala Ala Ala Tyr Gly
1 5 10

<210> 120
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 120
Ser Trp Asp Ala Pro Ala Gly Gly Tyr Gly
1 5 10

<210> 121
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 121
Ser Trp Asp Ala Pro Ala Ala Gly Gly Tyr Gly
1 5 10

<210> 122
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 122
Ser Trp Asp Ala Pro Ala Ala Gly Tyr Gly
1 5 10

<210> 123
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 123
Ser Trp Asp Ala Pro Ala Gly Ala Ala Ser Tyr Gly
1 5 10

<210> 124
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 124
Ser Trp Asp Ala Pro Ala Gly Ala Tyr Gly
1 5 10

<210> 125
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 125
Ser Trp Asp Pro Pro Ala Glu Gly Tyr Gly
1 5 10

<210> 126
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 126
Ser Trp Asn Pro Pro Asp Val Asn Tyr Gly
1 5 10

<210> 127
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 127
Ser Trp Asp Ala Pro Ala Glu Gly Gly Tyr Gly
1 5 10

<210> 128
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 128
Ser Trp Ser Glu Lys Leu Asp Gly Lys Ala Arg Arg Gly
1 5 10

<210> 129
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 129
Ser Trp Ser Pro Arg Asp Ser Thr Gly Leu Val Arg Arg Gly
1 5 10

<210> 130
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 130
Ser Trp Gly Asp Val Arg Thr Asn Glu Ala Arg Gln Gly
1 5 10

<210> 131
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 131
Ser Trp Asp Ala Pro Ala Glu Ala Glu Ala Tyr Gly
1 5 10

<210> 132
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 132
Ser Trp Asp Ala Pro Ala Glu Gly Ala Tyr Gly
1 5 10

<210> 133
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 133
Ser Trp Gln Pro Pro Ala Val Thr Tyr Gly
1 5 10

<210> 134
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 134
Ser Trp Asp Pro Pro Ala Gly Ala Tyr Gly
1 5 10

<210> 135
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 135
Ser Trp Ala Pro Pro Ser Asp Ala Tyr Gly
1 5 10

<210> 136
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 136
Pro Ser Ser Lys Gly Thr
1 5

<210> 137
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 137
Pro Val Ser Lys Ser Thr
1 5

<210> 138
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 138
Pro Val Ser Lys Gly Thr
1 5

<210> 139

<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 139
Pro Val Phe Lys Gly Thr
1 5

<210> 140
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 140
Pro Val Tyr Lys Gly Thr
1 5

<210> 141
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 141
Pro Gly Tyr Lys Gly Thr
1 5

<210> 142
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 142
Glu Tyr Pro Tyr Asp Tyr Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 143
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 143
Glu Tyr Pro Tyr Glu His Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 144
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 144
Glu Tyr Pro Tyr Pro His Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 145
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 145
Glu Tyr Thr Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro
1 5 10

<210> 146
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 146
Glu Tyr Pro Tyr Asp His Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 147
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 147
Glu Phe Pro Tyr Asp His Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 148
<211> 13

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 148
Glu Phe Pro Tyr Ala His Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 149
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 149
Glu Phe Thr Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro
1 5 10

<210> 150
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 150
Glu Tyr Pro Tyr Ala His Ser Gly Tyr Phe His Arg Pro
1 5 10

<210> 151
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 151
Glu Tyr Asp Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro
1 5 10

<210> 152
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 152
Glu Tyr Asp Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 153
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 153
Glu Phe Asp Tyr Pro Gly Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 154
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 154
Glu Tyr Ser Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro
1 5 10

<210> 155
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 155
Glu Phe Asp Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 156
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 156
Glu Phe Asp Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro
1 5 10

<210> 157
<211> 13
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 157
Glu Phe Pro Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 158
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 158
Glu Phe Asn Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro
1 5 10

<210> 159
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 159
Glu Phe Thr Tyr Pro Gly Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 160
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 160
Glu Phe Pro Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro
1 5 10

<210> 161
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 161

Glu Phe Asn Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 162
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 162
Glu Tyr Pro Tyr Ala His Ala Gly Tyr Tyr His Arg Pro
1 5 10

<210> 163
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 163
Glu Tyr Pro Tyr Pro Phe Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 164
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 164
Glu Tyr Asn Phe Ile Gly Ala Gly Tyr Tyr His Arg Pro
1 5 10

<210> 165
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 165
Glu Phe Pro Tyr Pro Phe Ala Gly Tyr Tyr His Arg Pro
1 5 10

<210> 166
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 166
Glu Tyr Thr Tyr Glu His Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 167
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 167
Glu Phe Asp Phe Val Gly Ala Gly Tyr Tyr His Arg Pro
1 5 10

<210> 168
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 168
Glu Tyr Asp Phe Ala Gly Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 169
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 169
Glu Phe Ala Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro
1 5 10

<210> 170
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 170
Glu Tyr Val Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro

1 5 10

<210> 171
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 171
Glu Tyr Pro Tyr Pro Phe Ala Gly Tyr Tyr His Arg Pro
1 5 10

<210> 172
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 172
Glu Tyr Pro Tyr Ser His Ala Gly Tyr Tyr His Arg Pro
1 5 10

<210> 173
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 173
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly
20 25 30

Gly Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser
35 40 45

Pro Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile
50 55 60

Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val
65 70 75 80

Glu Tyr Pro Tyr Asp Tyr Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile
85 90 95

Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His
100 105 110

His

<210> 174
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 174
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggagccgtt cagccggttg cccgggggcg gcgagtatta ccggatcact 120

tacggcgaaa caggaggcaa tagccctctg cagcagttca ctgtgcctgg ttctaaaggt 180

acagctacca tcagcggcct taaacctggc gttgattata ccatcactgt gtatgctgtc 240

gaatacccgt acgactattc tggttactac catcgcccca tttccattaa ttaccgcaca 300

gaaattgaca aaccatccca gcaccatcac caccaccac 339

<210> 175
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 175
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly
20 25 30

Gly Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser
35 40 45

Pro Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile
50 55 60

Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val
65 70 75 80

Glu Tyr Pro Tyr Glu His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile
85 90 95

Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His

100 105 110

His

<210> 176
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 176
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggagccgtt cagccggttg cccgggggcg gcgagtatta ccggatcact 120

tacggcgaaa caggaggcaa tagccctctg cagcagttca ctgtgcctgg ttctaaaggt 180

acagctacca tcagcggcct taaacctggc gttgattata ccatcactgt gtatgctgtc 240

gaatacccgt acgagcattc tgggtactat catcgtccga tttccattaa ttaccgcaca 300

gaaattgaca aaccatccca gcaccatcac caccaccac 339

<210> 177
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 177
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly
20 25 30

Gly Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser
35 40 45

Pro Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile
50 55 60

Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val
65 70 75 80

Glu Tyr Pro Tyr Pro His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile
85 90 95

Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His
100 105 110

His

<210> 178
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 178
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggagccgtt cagccggttg cccgggggcg gcgagtatta ccggatcact 120

tacggcgaaa caggaggcaa tagccctctg cagcagttca ctgtgcctgg ttctaaaggt 180

acagctacca tcagcggcct taaacctggc gttgattata ccatcactgt gtatgctgtc 240

gaatacccgt acccgcattc tggttactac catcgaccga tttccattaa ttaccgcaca 300

gaaattgaca aaccatccca gcaccatcac caccaccac 339

<210> 179
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 179
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr
65 70 75 80

Thr Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 180
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 180
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgatgga gggtacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctagttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtgtatgc tgtcgaatac 240

accttcccgg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 181
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 181
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly
20 25 30

Gly Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser
35 40 45

Pro Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile
50 55 60

Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val
65 70 75 80

Glu Tyr Pro Tyr Asp His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile
85 90 95

Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His
100 105 110

His

<210> 182
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 182
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggagccgtt cagccggttg cccgggggcg gcgagtatta ccggatcact 120

tacggcgaaa caggaggcaa tagccctctg cagcagttca ctgtgcctgg ttctaaaggt 180

acagctacca tcagcggcct taaacctggc gttgattata ccatcactgt gtatgctgtc 240

gaatacccgt acgaccattc tggttactac catcgtccca tttccattaa ttaccgcaca 300

gaaattgaca aaccatccca gcaccatcac caccaccac 339

<210> 183
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 183
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly
20 25 30

Gly Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser
35 40 45

Pro Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile
50 55 60

Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val
65 70 75 80

Glu Phe Pro Tyr Asp His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile
85 90 95

Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His
100 105 110

His

<210> 184

<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 184
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggagccgtt cagccggttg cccgggggcg gcgagtatta ccggatcact 120

tacggcgaaa caggaggcaa tagccctctg cagcagttca ctgtgcctgg ttctaaaggt 180

acagctacca tcagcggcct taaacctggc gttgattata ccatcactgt gtatgctgtc 240

gaattcccgt acgaccattc tggttactac catcggccca tttccattaa ttaccgcaca 300

gaaattgaca aaccatccca gcaccatcac caccaccac 339

<210> 185
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 185
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Ser Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr
65 70 75 80

Thr Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 186
<211> 333
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 186
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgacggg gggtacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa aagtacagct 180

accatcagcg gccttaaacc tggcgttgat tataccatca ctgtgtatgc tgtcgaatac 240

accttccccg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 187
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 187
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly
20 25 30

Gly Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser
35 40 45

Pro Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile
50 55 60

Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val
65 70 75 80

Glu Phe Pro Tyr Ala His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile
85 90 95

Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His
100 105 110

His

<210> 188
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 188
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggagccgtt cagccggttg cccgggggcg gcgagtatta ccggatcact 120

tacggcgaaa caggaggcaa tagccctctg cagcagttca ctgtgcctgg ttctaaaggt 180

acagctacca tcagcggcct taaacctggc gttgattata ccatcactgt gtatgctgtc 240

gaattcccgt acgcgcattc tgggtactac catcgtccga tttccattaa ttaccgcaca 300

gaaattgaca aaccatccca gcaccatcac caccaccac 339

<210> 189
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 189
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Asp Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe
65 70 75 80

Thr Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 190
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 190
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctggggac ggttacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ccgtttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtgtatgc tgtcgaattc 240

accttcccgg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 191
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 191
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly
20 25 30

Gly Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser
35 40 45

Pro Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile
50 55 60

Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val
65 70 75 80

Glu Tyr Pro Tyr Ala His Ser Gly Tyr Phe His Arg Pro Ile Ser Ile
85 90 95

Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His
100 105 110

His

<210> 192
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 192
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggagccgtt cagccggttg cccgggggcg gcgagtatta ccggatcact 120

tacggcgaaa caggaggcaa tagccctctg cagcagttca ctgtgcctgg ttctaaaggt 180

acagctacca tcagcggcct taaacctggc gttgattata ccatcactgt gtatgctgtc 240

gaatacccgt acgcgcattc tggttacttc catcgtccga tttccattaa ttaccgcaca 300

gaaattgaca aaccatccca gcaccatcac caccaccac 339

<210> 193
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 193
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Ala Ala Pro Ala Gly Gly Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr
65 70 75 80

Asp Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 194
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 194
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggccgctcc ggctggtggt ggctacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtgtatgc tgtcgaatac 240

gacttcccgg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 195
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 195
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asp
65 70 75 80

Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 196
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 196
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgataagct gggacgctcc ggctgacgcg tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta gttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacgac 240

ttccccggca gcggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 197
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 197
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Tyr Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 198
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 198
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgacgcg tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcgac 240

taccccggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 199
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 199
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Ala Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr
65 70 75 80

Ser Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 200
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 200
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgatggg gcatacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa gggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtgtatgc tgtcgaatac 240

tccttccccg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 201
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 201
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 202
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 202
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgagggt tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcgac 240

ttccccggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 203
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 203
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Glu Ala Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe
65 70 75 80

Asp Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 204
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 204
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgacgag gcgtacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa aggtacagct 180

accatcagcg gccttaaacc tggtgttgat ataccatca ctgtgtatgc tgtcgaattc 240

gacttccccg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 205
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 205
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe
65 70 75 80

Asp Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 206
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 206
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgatggt ggttacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtgtatgc tgtcgaattc 240

gacttcccgg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 207
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 207
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu

50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro
65 70 75 80

Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 208
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 208
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgatggc tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcccc 240

ttccccggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 209
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 209
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 210
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 210
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgaaggg tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcgac 240

ttccccggcg ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 211
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 211
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe
65 70 75 80

Asp Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 212
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 212
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctggcggg gggtacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtgtatgc tgtcgaattc 240

gacttcccgg gctccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 213
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 213
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Asp Ala Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe
65 70 75 80

Asn Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 214
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 214
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgccgat gcttacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtgtatgc tgtcgaattc 240

aacttcccgg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 215
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 215
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Ala Gly Lys
20 25 30

His Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser
35 40 45

Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile
50 55 60

Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val
65 70 75 80

Glu Phe Asp Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile
85 90 95

Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His
100 105 110

His

<210> 216

<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 216
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgaagca ggtaagcact acggttatta ccgcatcact 120

tacggcgaaa caggaggcaa tagccctgtc caggagttca ctgtgcctgt ttctaaaggt 180

acagctacca tcagcggcct taaacctggc gttgattata ccatcactgt gtatgctgtc 240

gaattcgact tcccgggcgc cggttactac catcgtccaa tttccattaa ttaccgcaca 300

gaaattgaca aaccatccca gcaccatcac caccaccac 339

<210> 217
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 217
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Thr
65 70 75 80

Tyr Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 218
<211> 330
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 218
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgaagca tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcacc 240

taccccggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 219
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 219
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asp
65 70 75 80

Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 220
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 220

atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgcagcc tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacgac 240

ttccccggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 221
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 221
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe
65 70 75 80

Asp Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 222
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 222
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctggtggg ggatacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctagttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat tataccatca ctgtgtatgc tgtcgaattc 240

gacttcccgg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 223
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 223
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 224
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 224
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgggggc tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcgac 240

ttccccggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 225
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 225
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Phe Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Tyr Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 226
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 226
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgatggt tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttttaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcgac 240

taccccggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 227
<211> 111

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 227
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Gly Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr
65 70 75 80

Asp Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 228
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 228
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgcgggg gggtacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctagttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtatatgc tgtcgaatac 240

gacttccccg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 229
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 229
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 230
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 230
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgatgct tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagcccagt ccaggagttc actgtgcctg gttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcgac 240

ttccccggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 231
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 231
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr

1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 232
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 232
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgcggct tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta gttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcgac 240

ttccccggct ccggttacta ccatcgccca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 233
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 233
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro
65 70 75 80

Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 234
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 234
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgcgggt tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcccc 240

ttccccggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 235
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 235
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Tyr Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 236
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 236
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctggggga tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta gttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcgac 240

taccccggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 237
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 237
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Ala Ala Ser
20 25 30

Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro
35 40 45

Val Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser
50 55 60

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu
65 70 75 80

Phe Pro Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn
85 90 95

Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 238
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 238
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctggggca gcgtcctacg gttattaccg catcacttac 120

ggcgaaacag gaggcaatag ccctgtccag gagttcactg tgcctgtttc taaaggtaca 180

gctaccatca gcggccttaa acctggcgtt gattatacca tcactgtgta tgctgtcgaa 240

ttccccttcc ccggcgccgg ttactaccat cgtccaattt ccattaatta ccgcacagaa 300

attgacaaac catcccagca ccatcaccac caccac 336

<210> 239
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 239
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg

85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 240
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 240
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctggcgcg tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcgac 240

ttccccggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 241
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 241
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Pro Pro Ala Glu Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asn
65 70 75 80

Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 242
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 242
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggaccctcc ggctgaaggt tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcaac 240

ttccccggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 243
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 243
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 244
<211> 330
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 244
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgggggc tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta gttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcgac 240

ttcccgggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 245
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 245
Met Gly Ile Thr Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asn Pro Pro Asp Val Asn Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Leu Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro
65 70 75 80

Tyr Ala His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 246
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 246
atgggtatca cggatgtgcc gcgagacttg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggaacccgcc ggatgtgaat tacggttatt atcgcatcac ttacggggaa 120

acaggaggca atagcccttt gcaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatatccg 240

tacgcgcacg ctggttacta ccatcgtccg atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 247
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 247
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Asp Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe
65 70 75 80

Asp Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 248
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 248
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctggggac gggtacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat tataccatca ctgtgtatgc tgtcgaattc 240

gacttccccg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 249
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 249
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe
65 70 75 80

Thr Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 250
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 250
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctggtggt ggatacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat tataccatca ctgtgtatgc tgtcgaattc 240

accttcccgg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 251
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 251
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Gly Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe
65 70 75 80

Asp Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 252
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 252
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgagggc ggctacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtgtatgc tgtcgaattc 240

gacttccccg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 253
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 253
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asp
65 70 75 80

Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 254
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 254
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgaggct tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacgac 240

ttccccggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 255
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 255
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly
20 25 30

Gly Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser
35 40 45

Pro Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile
50 55 60

Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val
65 70 75 80

Glu Tyr Pro Tyr Pro Phe Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile
85 90 95

Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His
100 105 110

His

<210> 256
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 256
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggagccgtt cagccggttg cccgggggcg gcgagtatta ccggatcact 120

tacggcgaaa caggaggcaa tagccctctg cagcagttca ctgtgcctgg ttctaaaggt 180

acagctacca tcagcggcct taaacctggc gttgattata ccatcactgt gtatgctgtc 240

gaatacccgt acccgttttc tggttactac catcgtccca tttccattaa ttaccgcaca 300

gaaattgaca aaccatccca gcaccatcac caccaccac 339

<210> 257
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 257
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr
65 70 75 80

Asp Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 258
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 258
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgacggc gggtacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctggttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtgtatgc tgtcgaatac 240

gacttcccgg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 259
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 259
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr
65 70 75 80

Asn Phe Ile Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 260
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 260
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgggggt ggatacggtt attaccgsat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtgtatgc tgtcgaatac 240

aacttcatcg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 261
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 261
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Ala Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe
65 70 75 80

Pro Tyr Pro Phe Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 262
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 262
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgacggt gcctacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtgtatgc tgtcgaattc 240

ccctacccct tcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 263
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 263
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Ser Glu Lys Leu Asp Gly Lys Ala
20 25 30

Arg Arg Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser

35 40 45

Pro Val Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile
50 55 60

Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val
65 70 75 80

Glu Phe Pro Tyr Asp His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile
85 90 95

Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His
100 105 110

His

<210> 264
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 264
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggtcggagaa gttggacggg aaggcgcgcc gcgggtatta ccgcatcaca 120

tacggcgaaa caggaggcaa tagccctgtc cagcagttca ctgtgcctgg ttctaaaggt 180

acagctacca tcagcggcct taaacctggc gttgattata ccatcactgt gtatgctgtc 240

gaattcccgt acgaccattc tggttactac catcgtccca tttccattaa ttaccgcaca 300

gaaattgaca aaccatccca gcaccatcac caccaccac 339

<210> 265
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 265
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Ser Pro Arg Asp Ser Thr Gly Leu
20 25 30

Val Arg Arg Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
35 40 45

Ser Pro Val Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr
50 55 60

Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala
65 70 75 80

Val Glu Tyr Pro Tyr Asp His Ser Gly Tyr Tyr His Arg Pro Ile Ser
85 90 95

Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His
100 105 110

His His

<210> 266
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 266
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggagcccgcg ggactccacc ggcttggtga ggcgggggta ttaccgcatc 120

acttacggcg aaacaggagg caatagccct gttcagcagt tcactgtgcc tggttctaaa 180

ggtacagcta ccatcagcgg ccttaaacct ggcgttgatt ataccatcac tgtgtatgct 240

gtcgaatacc cgtacgacca ttctggttac taccatcggc ccatttccat taattaccgc 300

acagaaattg acaaaccatc ccagcaccat caccaccacc ac 342

<210> 267
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 267
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Gly Asp Val Arg Thr Asn Glu Ala
20 25 30

Arg Gln Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser
35 40 45

Pro Leu Gln Gly Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile
50 55 60

Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val
65 70 75 80

Glu Tyr Thr Tyr Glu His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile
85 90 95

Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His
100 105 110

His

<210> 268
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 268
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggggcgacgt ccggacgaac gaggcgcggc agggctatta ccggatcact 120

tacggcgaaa caggaggcaa tagccctctc caggggttca ctgtgcctgg ttctaaaggt 180

acagctacca tcagcggcct taaacctggc gttgattata ccatcactgt gtatgctgtc 240

gagtatacgt acgagcattc tggttactac catcgtccga tttccattaa ttaccgcaca 300

gaaattgaca aaccatccca gcaccatcac caccaccac 339

<210> 269
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 269
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe
65 70 75 80

Asp Phe Val Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 270
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 270
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgggggg ggctacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtgtatgc tgtcgaattc 240

gacttcgtcg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 271
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 271
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asp

65 70 75 80

Phe Ala Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 272
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 272
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgcggcc tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacgac 240

ttcgcgggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 273
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 273
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Ala
65 70 75 80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 274
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 274
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgacgcg tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta gttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tatatgctgt cgaattcgcc 240

ttccccggcg ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 275
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 275
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asp
65 70 75 80

Phe Ala Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 276
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 276
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctggaggt tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacgac 240

ttcgcgggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 277
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 277
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Ala Glu Ala
20 25 30

Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro
35 40 45

Val Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser
50 55 60

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu
65 70 75 80

Tyr Val Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn
85 90 95

Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 278
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 278
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgaagca gaagcgtacg gttattaccg catcacttac 120

ggcgaaacag gaggcaatag ccctgtccag gagttcactg tgcctgtttc taaaggtaca 180

gctaccatca gcggccttaa acctggcgtt gattatacca tcactgtgta tgctgtcgaa 240

tacgtcttcc ccggcgccgg ttactaccat cgtccaattt ccattaatta ccgcacagaa 300

attgacaaac catcccagca ccatcaccac caccac 336

<210> 279
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 279
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Gly Ala Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr
65 70 75 80

Pro Tyr Pro Phe Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 280
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 280
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgagggc gcttacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtgtatgc tgtcgaatac 240

ccctacccct tcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacagaaatt 300

gacaaaccat cccagcacca tcaccaccac cac 333

<210> 281
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 281
Met Gly Val Thr Asp Val Pro Arg Asp Met Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Gln Pro Pro Ala Val Thr Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Thr Leu Gln
35 40 45

Gln Phe Thr Val Pro Val Tyr Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro
65 70 75 80

Tyr Asp His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 282
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 282
atgggtgtca ccgatgtgcc gcgcgacatg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct ggcagccgcc ggctgttact tacggttatt atcgcatcac ttacggcgaa 120

acaggaggca atagcactct ccagcagttc actgtgcctg tttataaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacccg 240

tacgaccatt ctgggtacta ccatcggccg atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 283
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 283
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Tyr Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 284
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 284
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgctgct tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcgac 240

taccccggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 285
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 285
Met Gly Ile Val Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Pro Pro Ala Gly Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Lys Gln
35 40 45

Gln Phe Thr Val Pro Gly Tyr Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro
65 70 75 80

Tyr Asp His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 286
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 286
atgggtatcg tggatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacccgcc ggctggtgct tacggttatt atcgcatcac ttacggcgaa 120

acaggaggca atagcccaaa gcagcagttc actgtgcctg gttataaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacccg 240

tacgaccatt ctggttacta ccatcggccg atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 287
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 287
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asp
65 70 75 80

Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 288
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 288
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgcgggg tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacgac 240

ttccccggct ccggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 289
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 289
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Ala Pro Pro Ser Asp Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro
65 70 75 80

Tyr Ser His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 290
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 290
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggcgccgcc ttctgatgcg tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttggtaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaatacccg 240

tattcacatg ctggttacta ccatcgtcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 291
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 291
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly
20 25 30

Gly Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser
35 40 45

Pro Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile
50 55 60

Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val
65 70 75 80

Glu Phe Pro Tyr Asp His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile
85 90 95

Asn Tyr Arg Thr Gly Ser Gly Cys His His His His His His
100 105 110

<210> 292
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 292
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggagccgtt cagccggttg cccgggggcg gcgagtatta ccggatcact 120

tacggcgaaa caggaggcaa tagccctctg cagcagttca ctgtgcctgg ttctaaaggt 180

acagctacca tcagcggcct taaacctggc gttgattata ccatcactgt gtatgctgtc 240

gaattcccgt acgaccattc tggttactac catcggccca tttccattaa ttaccgcaca 300

ggtagcggtt gccaccatca ccaccatcac 330

<210> 293
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 293
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Gly Ser Gly Cys His His His His His His
100 105

<210> 294
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 294
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgaaggg tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcgac 240

ttccccggcg ccggttacta ccatcgtcca atttccatta attaccgcac aggtagcggt 300

tgccaccatc accaccatca c 321

<210> 295
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 295
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val

35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe
65 70 75 80

Asp Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Gly Ser Gly Cys His His His His His His
100 105

<210> 296
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 296
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgatggt ggttacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtgtatgc tgtcgaattc 240

gacttcccgg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacaggtagc 300

ggttgccacc atcaccacca tcac 324

<210> 297
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 297
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Gly Gly Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe
65 70 75 80

Asp Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Gly Ser Gly Cys His His His His His His
100 105

<210> 298
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 298
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgagggc ggctacggtt attaccgcat cacttacggc 120

gaaacaggag gcaatagccc tgtccaggag ttcactgtgc ctgtttctaa aggtacagct 180

accatcagcg gccttaaacc tggcgttgat ataccatca ctgtgtatgc tgtcgaattc 240

gacttccccg gcgccggtta ctaccatcgt ccaatttcca ttaattaccg cacaggtagc 300

ggttgccacc atcaccacca tcac 324

<210> 299
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 299
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Tyr Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Gly Ser Gly Cys His His His His His His
100 105

<210> 300
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 300
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgctcc ggctgacgcg tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgcctg tttctaaagg tacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgaattcgac 240

taccccggct ccggttacta ccatcgtcca atttccatta attaccgcac aggtagcggt 300

tgccaccatc accaccatca c 321

<210> 301
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 301
Ser Trp Asp Pro Pro Ser Asp Asp Tyr Gly
1 5 10

<210> 302
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 302
Ser Trp Asp Ala Pro Ala Asp Asp Tyr Gly
1 5 10

<210> 303
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 303
Ser Trp Asp Ala Pro Ser Asp Asp Tyr Gly
1 5 10

<210> 304
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 304
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Pro Pro Ser Asp Asp Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro
65 70 75 80

Trp Pro His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 305
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 305
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacccgcc ttcggatgat tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttggtaaagg aacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgagtttccg 240

tggccacatg ctggttacta tcatcggcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 306
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 306
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Asp Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro
65 70 75 80

Trp Pro His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 307
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 307
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgcgcc tgcggatgat tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttggtaaagg aacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgagtttccg 240

tggccacatg ctggttacta tcatcggcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 308
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 308
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ser Asp Asp Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro
65 70 75 80

Trp Pro His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 309
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 309
atgggagttt ctgatgtgcc gcgcgacctg gaagtggttg ctgccacccc caccagcctg 60

ctgatcagct gggacgcgcc ttcggatgat tacggttatt accgcatcac ttacggcgaa 120

acaggaggca atagccctgt ccaggagttc actgtgccta ttggtaaagg aacagctacc 180

atcagcggcc ttaaacctgg cgttgattat accatcactg tgtatgctgt cgagtttccg 240

tggccacatg ctggttacta tcatcggcca atttccatta attaccgcac agaaattgac 300

aaaccatccc agcaccatca ccaccaccac 330

<210> 310
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 310
Ala Gly Gly Gly Gly Ser Gly
1 5

<210> 311
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 311
Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1 5 10

<210> 312
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 312
Gln Pro Asp Glu Pro Gly Gly Ser
1 5

<210> 313
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 313
Glu Leu Gln Leu Glu Glu Ser Ala Ala Glu Ala Gln Asp Gly Glu Leu
1 5 10 15

Asp

<210> 314
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 314
Thr Val Ala Ala Pro Ser
1 5

<210> 315
<211> 330
<212> PRT
<213> Homo sapiens

<400> 315
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

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

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

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

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 316
<211> 16
<212> PRT
<213> Homo sapiens

<400> 316
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

<210> 317
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 317
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser
20

<210> 318
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 318

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

Pro Glu Leu Leu Gly Gly Ser Ser
20

<210> 319
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 319
Glu Pro Lys Ser Ser Gly Ser Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Ser Ser
20

<210> 320
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 320
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser

<210> 321
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 321
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Ser Ser

<210> 322
<211> 350
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 322
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val
20 25 30

Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Val Pro Pro Ser Asp
35 40 45

Asp Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser
50 55 60

Pro Val Gln Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile
65 70 75 80

Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val
85 90 95

Glu Phe Pro Trp Pro His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile
100 105 110

Asn Tyr Arg Thr Glu Ile Glu Pro Lys Ser Ser Gly Ser Thr His Thr
115 120 125

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe
130 135 140

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
145 150 155 160

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
165 170 175

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
180 185 190

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
210 215 220

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
225 230 235 240

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
245 250 255

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
260 265 270

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
275 280 285

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
290 295 300

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
305 310 315 320

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
325 330 335

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
340 345 350

<210> 323
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> MOD_RES
<222> (3)..(11)
<223> Any amino acid and this region may encompass 6 to 9 residues

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="His"

<220>
<221> misc_feature
<222> (12)..(12)
<223> /note="Residue given in the sequence has no preference with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(13)
<223> /note="see specification as filed for detailed description of substitutions and preferred embodiments"

<400> 323
Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Gly
1 5 10

<210> 324
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> MOD_RES
<222> (2)..(4)
<223> Any amino acid

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (5)..(5)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(6)
<223> /note="see specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 324
Pro Xaa Xaa Xaa Gly Thr
1 5

<210> 325
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> VARIANT
<222> (2)..(2)
<223> /replace="Phe"

<220>
<221> misc_feature
<222> (2)..(2)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Any amino acid

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Phe" or "Trp"

<220>

<221> misc_feature
<222> (4)..(4)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotations for said position"

<220>
<221> MOD_RES
<222> (5)..(6)
<223> Any amino acid

<220>
<221> VARIANT
<222> (7)..(7)
<223> /replace="Ala"

<220>
<221> misc_feature
<222> (7)..(7)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> VARIANT
<222> (10)..(10)
<223> /replace="Phe"

<220>
<221> misc_feature
<222> (10)..(10)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(13)
<223> /note="see specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 325
Glu Tyr Xaa Tyr Xaa Xaa Ser Gly Tyr Tyr His Arg Pro
1 5 10

<210> 326
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 326
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly
20

<210> 327
<211> 86
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 327
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala
1 5 10 15

Pro Ala Val Thr Val Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser Lys Ser Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile
65 70 75 80

Ser Ile Asn Tyr Arg Thr
85

<210> 328
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> MOD_RES
<222> (7)..(21)
<223> Any amino acid and this region may encompass 1-15, 2-15, 1-10, 2-10, 1-8, 2-8, 1-5, 2-5, 1-4, 2-4, 1-3, 2-3 or 1-2 residues

<220>
<221> MOD_RES
<222> (26)..(45)
<223> Any amino acid and this region may encompass 2-20, 2-15, 2-10, 2-8, 5-20, 5-15, 5-10, 5-8, 6-20, 6-15, 6-10, 6-8, 2-7, 5-7 or 6-7 residues

<220>
<221> MOD_RES
<222> (54)..(73)
<223> Any amino acid and this region may encompass 2-20, 2-15, 2-10, 2-8, 5-20, 5-15, 5-10, 5-8, 6-20, 6-15, 6-10, 6-8, 2-7, 5-7 or 6-7 residues

<220>
<221> MOD_RES
<222> (79)..(98)
<223> Any amino acid and this region may encompass 2-20, 2-15, 2-10, 2-8, 5-20, 5-15, 5-10, 5-8, 6-20, 6-15, 6-10, 6-8, 2-7, 5-7 or 6-7 residues

<220>

<221> MOD_RES
<222> (102)..(121)
<223> Any amino acid and this region may encompass 2-20, 2-15, 2-10, 2-8, 5-20, 5-15, 5-10, 5-8, 6-20, 6-15, 6-10, 6-8, 2-7, 5-7 or 6-7 residues

<220>
<221> MOD_RES
<222> (131)..(150)
<223> Any amino acid and this region may encompass 2-20, 2-15, 2-10, 2-8, 5-20, 5-15, 5-10, 5-8, 6-20, 6-15, 6-10, 6-8, 2-7, 5-7 or 6-7 residues

<220>
<221> misc_feature
<222> (1)..(157)
<223> /note="see specification as filed for detailed description of substitutions and preferred embodiments"

<400> 328
Glu Val Val Ala Ala Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Ser Leu Leu Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Tyr Arg
35 40 45

Ile Thr Tyr Gly Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Glu Phe Thr Val Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Ala Thr Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Tyr Thr Ile Thr Val Tyr
115 120 125

Ala Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Ile Ser Ile Asn Tyr Arg Thr
145 150 155

<210> 329
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> MOD_RES
<222> (13)..(32)
<223> Any amino acid and this region may encompass 2-20, 2-15, 2-10, 2-8, 5-20, 5-15, 5-10, 5-8, 6-20, 6-15, 6-10, 6-8, 2-7, 5-7 or 6-7 residues

<220>
<221> MOD_RES
<222> (53)..(72)
<223> Any amino acid and this region may encompass 2-20, 2-15, 2-10, 2-8, 5-20, 5-15, 5-10, 5-8, 6-20, 6-15, 6-10, 6-8, 2-7, 5-7 or 6-7 residues

<220>
<221> MOD_RES
<222> (92)..(111)
<223> Any amino acid and this region may encompass 2-20, 2-15, 2-10, 2-8, 5-20, 5-15, 5-10, 5-8, 6-20, 6-15, 6-10, 6-8, 2-7, 5-7 or 6-7 residues

<220>
<221> misc_feature
<222> (1)..(118)
<223> /note="see specification as filed for detailed description of substitutions and preferred embodiments"

<400> 329
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Thr Ile Ser Gly Leu Lys Pro
65 70 75 80

Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile
100 105 110

Ser Ile Asn Tyr Arg Thr
115

<210> 330
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 330
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp His Ser
1 5 10 15

Tyr Tyr Glu Gln Asn Ser Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Tyr Ser Gln Thr Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Tyr Gly Ser Lys Tyr Tyr Tyr Pro Ile Ser Ile Asn Tyr
65 70 75 80

Arg Thr

<210> 331
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 331
His Ser Tyr Tyr Glu Gln Asn Ser
1 5

<210> 332
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 332
Tyr Ser Gln Thr
1

<210> 333
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 333
Tyr Gly Ser Lys Tyr Tyr Tyr
1 5

<210> 334
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 334
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Pro Lys
1 5 10 15

Tyr Asp Lys Thr Gly His Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Thr Arg Gln Thr Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Ser Lys Asp Asp Tyr Tyr Pro His Glu His Arg Pro Ile
65 70 75 80

Ser Ile Asn Tyr Arg Thr
85

<210> 335
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 335
Pro Lys Tyr Asp Lys Thr Gly His
1 5

<210> 336
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 336

Thr Arg Gln Thr
1

<210> 337
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 337
Ser Lys Asp Asp Tyr Tyr Pro His Glu His Arg
1 5 10

<210> 338
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 338
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ser Asn
1 5 10 15

Asp Gly Pro Gly Leu Ser Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Ser Gln Thr Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Ser Tyr Tyr Thr Lys Lys Ala Tyr Ser Ala Gly Pro Ile
65 70 75 80

Ser Ile Asn Tyr Arg Thr
85

<210> 339
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 339
Ser Asn Asp Gly Pro Gly Leu Ser
1 5

<210> 340
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 340
Ser Ser Gln Thr
1

<210> 341
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 341
Ser Tyr Tyr Thr Lys Lys Ala Tyr Ser Ala Gly
1 5 10

<210> 342
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 342
Glu Met Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Glu Asp
1 5 10 15

Asp Ser Tyr Tyr Ser Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Asp Leu Tyr Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Thr Tyr Asp Val Thr Asp Leu Ile Met His Glu Pro Ile
65 70 75 80

Ser Ile Asn Tyr Arg Thr
85

<210> 343
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 343
Glu Asp Asp Ser Tyr Tyr Ser Arg
1 5

<210> 344
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 344
Ser Asp Leu Tyr
1

<210> 345
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 345
Tyr Asp Val Thr Asp Leu Ile Met His Glu
1 5 10

<210> 346
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 346
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Glu Asp
1 5 10 15

Asp Ser Tyr Tyr Ser Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Asp Leu Tyr Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Thr Tyr Asp Val Thr Asp Leu Ile Met His Glu Pro Ile
65 70 75 80

Ser Ile Asn Tyr Arg Thr
85

<210> 347
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 347
Glu Asp Asp Ser Tyr Tyr Ser Arg
1 5

<210> 348
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 348
Ser Asp Leu Tyr
1

<210> 349
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 349
Tyr Asp Val Thr Asp Leu Ile Met His Glu
1 5 10

<210> 350
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 350
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Tyr Met
1 5 10 15

Asp Glu Tyr Asp Val Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
            20   25   30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Asn Tyr Tyr Asn Thr
        35   40   45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
    50   55   60

Tyr Ala Val Thr Arg Ile Lys Ala Asn Asn Tyr Met Tyr Gly Pro Ile
65   70   75   80

Ser Ile Asn Tyr Arg Thr
                85

<210> 351
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 351
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Asn His
1   5   10   15

Leu Glu His Val Ala Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
            20   25   30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Glu Tyr Pro Thr Thr
        35   40   45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
    50   55   60

Tyr Ala Val Thr Ile Thr Met Leu Lys Tyr Pro Thr Gln Ser Pro Ile
65   70   75   80

Ser Ile Asn Tyr Arg Thr
                85

<210> 352
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 352

Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Gly His
1 5 10 15

Tyr Arg Arg Ser Gly His Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Asp Pro Ser Ser Tyr Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Ser Lys Asp Asp Tyr Tyr Pro His Glu His Arg Pro Ile
65 70 75 80

Ser Ile Asn Tyr Arg Thr
85

<210> 353
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 353
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala
1 5 10 15

Ser His Tyr Glu Arg Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Arg Tyr His His Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Thr Gln Ala Gln Glu His Tyr Gln Pro Pro Ile Ser Ile
65 70 75 80

Asn Tyr Arg Thr

<210> 354
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 354
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Asn Ser
1 5 10 15

Tyr Tyr His Ser Ala Asp Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Tyr Pro Pro Thr Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Tyr Ser Ala Lys Ser Tyr Tyr Pro Ile Ser Ile Asn Tyr
65 70 75 80

Arg Thr

<210> 355
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 355
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ser Lys
1 5 10 15

Tyr Ser Lys His Gly His Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Gly Asn Ala Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Glu Asp Thr Asn Asp Tyr Pro His Thr His Arg Pro Ile
65 70 75 80

Ser Ile Asn Tyr Arg Thr
85

<210> 356
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 356
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp His Gly
1 5 10 15

Glu Pro Asp Gln Thr Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Pro Tyr Arg Arg Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Thr Ser Gly Tyr Thr Gly His Tyr Gln Pro Ile Ser Ile
65 70 75 80

Asn Tyr Arg Thr

<210> 357
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 357
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ser Lys
1 5 10 15

Tyr Ser Lys His Gly His Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Asp Pro Ser Ser Tyr Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Ser Lys Asp Asp Tyr Tyr Pro His Glu His Arg Pro Ile
65 70 75 80

Ser Ile Asn Tyr Arg Thr
85

<210> 358
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 358
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Tyr Glu
1 5 10 15

Pro Tyr Thr Pro Ile His Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Tyr Tyr Gly Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Tyr Gly Tyr Tyr Gln Tyr Thr Pro Ile Ser Ile Asn Tyr
65 70 75 80

Arg Thr

<210> 359
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 359
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ser Lys
1 5 10 15

Tyr Ser Lys His Gly His Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Gly Asn Ala Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Ser Asp Asp Asn Lys Tyr Tyr His Gln His Arg Pro Ile
65 70 75 80

Ser Ile Asn Tyr Arg Thr
85

<210> 360
<211> 86
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 360
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Gly His
1 5 10 15

Tyr Arg Arg Ser Gly His Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Asp Pro Ser Ser Tyr Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Ser Lys Asp Asp Tyr Tyr Pro His Glu His Arg Pro Ile
65 70 75 80

Ser Ile Asn Tyr Arg Thr
85

<210> 361
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 361
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ser Lys
1 5 10 15

Tyr Ser Lys His Gly His Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Gly Asn Ala Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Glu Asp Thr Asn Asp Tyr Pro His Thr His Arg Pro Ile
65 70 75 80

Ser Ile Asn Tyr Arg Thr
85

<210> 362

<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 362
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Tyr Glu
1 5 10 15

Pro Gly Ala Ser Val Tyr Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Tyr Tyr His Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Tyr Gly Tyr Tyr Glu Tyr Glu Pro Ile Ser Ile Asn Tyr
65 70 75 80

Arg Thr

<210> 363
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 363
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Gln Ser
1 5 10 15

Tyr Tyr Ala His Ser Asp Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Tyr Pro Pro Gln Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Tyr Ala Gly Ser Ser Tyr Tyr Pro Ile Ser Ile Asn Tyr
65 70 75 80

Arg Thr

<210> 364
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 364
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Gly His
1 5 10 15

Tyr Arg Arg Ser Gly His Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Asp Pro Ser Ser Tyr Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Ser Lys Asp Asp Tyr Tyr Pro His Glu His Arg Pro Ile
65 70 75 80

Ser Ile Asn Tyr Arg Thr
85

<210> 365
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 365
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Pro Glu
1 5 10 15

Pro Gly Thr Pro Val Tyr Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ala Tyr Tyr Gly Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Tyr Gly Tyr Tyr Asp Tyr Ser Pro Ile Ser Ile Asn Tyr
65 70 75 80

Arg Thr

<210> 366
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 366
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Tyr Arg
1 5 10 15

Tyr Glu Lys Thr Gln His Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Pro Glu Ser Gly Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Tyr Ala Gly Tyr Glu Tyr Pro His Thr His Arg Pro Ile
65 70 75 80

Ser Ile Asn Tyr Arg Thr
85

<210> 367
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 367
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Val Lys
1 5 10 15

Ser Glu Glu Tyr Tyr Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Tyr Tyr Val His Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Thr Glu Tyr Tyr Tyr Ala Gly Ala Val Val Ser Val Pro
65 70 75 80

Ile Ser Ile Asn Tyr Arg Thr
85

<210> 368
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 368
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Tyr Asp
1 5 10 15

Pro Tyr Thr Tyr Gly Ser Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Gly Pro Tyr Thr Thr Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Ser Tyr Tyr Tyr Ser Thr Gln Pro Ile Ser Ile Asn Tyr
65 70 75 80

Arg Thr

<210> 369
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 369
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Ser Asn
1 5 10 15

Asp Gly Pro Gly Leu Ser Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Ser Gln Thr Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Ser Tyr Tyr Thr Lys Lys Ala Tyr Ser Ala Gly Pro Ile

65 70 75 80

Ser Ile Asn Tyr Arg Thr
85

<210> 370
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 370
Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Pro Asp
1 5 10 15

Pro Tyr Tyr Lys Pro Asp Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly
20 25 30

Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Arg Asp Tyr Thr Thr
35 40 45

Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val
50 55 60

Tyr Ala Val Tyr Ser Tyr Tyr Gly Tyr Tyr Pro Ile Ser Ile Asn Tyr
65 70 75 80

Arg Thr

<210> 371
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 371
Met Gly Val Ser Asp Val Pro Arg Asp Leu
1 5 10

<210> 372
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 372

Gly Val Ser Asp Val Pro Arg Asp Leu
1 5

<210> 373
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 373
Val Ser Asp Val Pro Arg Asp Leu
1 5

<210> 374
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 374
Ser Asp Val Pro Arg Asp Leu
1 5

<210> 375
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 375
Asp Val Pro Arg Asp Leu
1 5

<210> 376
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 376
Val Pro Arg Asp Leu
1 5

<210> 377
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 377
Pro Arg Asp Leu
1

<210> 378
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 378
Arg Asp Leu
1

<210> 379
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 379
Asp Leu
1

<210> 380
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 380
Glu Ile Asp Lys Pro Ser Gln
1   5

<210> 381
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 381
Glu Ile Asp Lys Pro Ser

1 5

<210> 382
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 382
Glu Ile Asp Lys Pro Cys
1 5

<210> 383
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 383
Glu Ile Asp Lys Pro
1 5

<210> 384
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 384
Glu Ile Asp Lys
1

<210> 385
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 385
Glu Ile
1

<210> 386
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 386
Glu Ile Glu Lys Pro Ser Gln
1 5

<210> 387
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 387
Glu Ile Asp Lys Pro Ser Gln Leu Glu
1 5

<210> 388
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 388
Glu Ile Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
1 5 10

<210> 389
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 389
Glu Ile Glu Lys Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu
1 5 10 15

Asp

<210> 390
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 390
Glu Gly Ser Gly Ser
1 5

<210> 391
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 391
Glu Ile Asp Lys Pro Cys Gln
1 5

<210> 392
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 392
Glu Ile Glu Lys Pro Cys Gln
1 5

<210> 393
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 393
Gly Ser Gly Cys
1

<210> 394
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 394
Glu Gly Ser Gly Cys
1 5

<210> 395
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 395
Glu Ile Asp Lys Pro Cys Gln Leu Glu
1 5

<210> 396
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 396
Gly Gly Ser Gly Ser
1 5

<210> 397
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 397
Gly Gly Ser Gly Ser Gly Ser Gly Ser
1 5

<210> 398
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 398
Gly Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1 5 10

<210> 399
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 399
Gly Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1 5 10 15

<210> 400
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 400
Gly Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
1 5 10 15

<210> 401
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 401
Gly Ser Gly Ser
1

<210> 402
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 402
Gly Ser Gly Ser Gly Ser Gly Ser
1 5

<210> 403
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 403
Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1 5 10

<210> 404
<211> 13
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 404
Gly Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Gly Ser
1 5 10

<210> 405
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 405
Gly Ser Glu Gly Ser Glu Gly Ser Glu Gly Ser Glu Gly Ser Glu
1 5 10 15

<210> 406
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 406
Pro Ala Ser Pro Ala Ser Pro Ala Ser Pro Ala Ser Pro Ala Ser
1 5 10 15

<210> 407
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 407
Gly Ser Pro Gly Ser Pro Gly Ser Pro Gly Ser Pro Gly Ser Pro
1 5 10 15

<210> 408
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 408

Gly Ser Thr Val Ala Ala Pro Ser Thr Val Ala Ala Pro Ser
1 5 10

<210> 409
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 409
Gly Gly Ser Glu Gly Gly Ser Glu
1 5

<210> 410
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 410
Ser Thr Ser Thr Ser Thr Gly
1 5

<210> 411
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 411
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

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

Gly Gly Ser
35

<210> 412
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 412

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

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

<210> 413
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 413
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

<210> 414
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 414
Gly Pro Gly Pro Gly Pro Gly
1 5

<210> 415
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 415
Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly
1 5 10

<210> 416
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 416
Pro Ser Thr Ser Thr Ser Thr
1 5

<210> 417
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 417
Pro Ala Pro Ala Pro Ala
1 5

<210> 418
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 418
Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala
1 5 10

<210> 419
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 419
Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala
1 5 10 15

Pro Ala

<210> 420
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 420
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp His Ser Tyr Tyr Glu Gln Asn Ser
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr Gly Ser
65 70 75 80

Lys Tyr Tyr Tyr Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys
85 90 95

Pro Ser Gln His His His His His His
100 105

<210> 421
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 421
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp His Ser Tyr Tyr Glu Gln Asn Ser
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr Gly Ser
65 70 75 80

Lys Tyr Tyr Tyr Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Asp
85 90 95

Glu Asp Glu Asp Glu Asp Glu Asp
100

<210> 422
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 422
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp His Ser Tyr Tyr Glu Gln Asn Ser
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr Gly Ser
65 70 75 80

Lys Tyr Tyr Tyr Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Asp
85 90 95

Glu Asp Glu Asp Glu Asp Glu Asp His His His His His His
100 105 110

<210> 423
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 423
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Pro Lys Tyr Asp Lys Thr Gly His
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Ser Lys Asp
65 70 75 80

Asp Tyr Tyr Pro His Glu His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 424
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 424
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Ser Asn Asp Gly Pro Gly Leu Ser
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Ser Tyr Tyr
65 70 75 80

Thr Lys Lys Ala Tyr Ser Ala Gly Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 425
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 425
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Met Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Asp Asp Ser Tyr Tyr Ser Arg
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ser Asp Leu Tyr Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Tyr Asp

65 70 75 80

Val Thr Asp Leu Ile Met His Glu Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 426
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 426
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Glu Asp Asp Ser Tyr Tyr Ser Arg
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ser Asp Leu Tyr Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Tyr Asp
65 70 75 80

Val Thr Asp Leu Ile Met His Glu Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 427
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 427
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Tyr Met Asp Glu Tyr Asp Val Arg
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Arg Ile
65 70 75 80

Lys Ala Asn Asn Tyr Met Tyr Gly Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 428
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 428
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asn His Leu Glu His Val Ala Arg
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Glu Tyr Pro Thr Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ile Thr
65 70 75 80

Met Leu Lys Tyr Pro Thr Gln Ser Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 429
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 429
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Gly His Tyr Arg Arg Ser Gly His
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Asp Pro Ser Ser Tyr Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Ser Lys Asp
65 70 75 80

Asp Tyr Tyr Pro His Glu His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 430
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 430
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Ser His Tyr Glu Arg Arg
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Arg Tyr His His Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gln Ala
65 70 75 80

Gln Glu His Tyr Gln Pro Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile
85 90 95

Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 431
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 431
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Asn Ser Tyr Tyr His Ser Ala Asp
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Tyr Pro Pro Thr Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr Ser Ala
65 70 75 80

Lys Ser Tyr Tyr Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys
85 90 95

Pro Ser Gln His His His His His His
100 105

<210> 432
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 432
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Ser Lys Tyr Ser Lys His Gly His
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Asp Thr
65 70 75 80

Asn Asp Tyr Pro His Thr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 433
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 433
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp His Gly Glu Pro Asp Gln Thr Arg
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Pro Tyr Arg Arg Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Ser Gly
65 70 75 80

Tyr Thr Gly His Tyr Gln Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile
85 90 95

Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 434
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 434
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Ser Lys Tyr Ser Lys His Gly His
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Asp Pro Ser Ser Tyr Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Ser Lys Asp
65 70 75 80

Asp Tyr Tyr Pro His Glu His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 435
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 435
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Tyr Glu Pro Tyr Thr Pro Ile His
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Gly Tyr Tyr Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr Gly Tyr
65 70 75 80

Tyr Gln Tyr Thr Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys
85 90 95

Pro Ser Gln His His His His His His
100 105

<210> 436
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 436
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Ser Lys Tyr Ser Lys His Gly His
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Ser Asp Asp
65 70 75 80

Asn Lys Tyr Tyr His Gln His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 437
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 437
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Gly His Tyr Arg Arg Ser Gly His
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Asp Pro Ser Ser Tyr Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Ser Lys Asp
65 70 75 80

Asp Tyr Tyr Pro His Glu His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Pro Ser Gln His His His His His His

100 105

<210> 438
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 438
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Ser Lys Tyr Ser Lys His Gly His
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Asp Thr
65 70 75 80

Asn Asp Tyr Pro His Thr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 439
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 439
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Tyr Glu Pro Gly Ala Ser Val Tyr
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ser Tyr Tyr His Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr Gly Tyr
65 70 75 80

Tyr Glu Tyr Glu Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys
85 90 95

Pro Ser Gln His His His His His His
100 105

<210> 440
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 440
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Gln Ser Tyr Tyr Ala His Ser Asp
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr Ala Gly
65 70 75 80

Ser Ser Tyr Tyr Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys
85 90 95

Pro Ser Gln His His His His His His
100 105

<210> 441
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 441
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Gly His Tyr Arg Arg Ser Gly His

20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Asp Pro Ser Ser Tyr Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Ser Lys Asp
65 70 75 80

Asp Tyr Tyr Pro His Glu His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 442
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 442
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Pro Glu Pro Gly Thr Pro Val Tyr
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ala Tyr Tyr Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr Gly Tyr
65 70 75 80

Tyr Asp Tyr Ser Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys
85 90 95

Pro Ser Gln His His His His His His
100 105

<210> 443
<211> 109
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 443
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Tyr Arg Tyr Glu Lys Thr Gln His
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr Ala Gly
65 70 75 80

Tyr Glu Tyr Pro His Thr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 444
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 444
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Val Lys Ser Glu Glu Tyr Tyr Arg
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Tyr Tyr Val His Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Glu Tyr
65 70 75 80

Tyr Tyr Ala Gly Ala Val Val Ser Val Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105 110

<210> 445
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 445
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Tyr Asp Pro Tyr Thr Tyr Gly Ser
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Gly Pro Tyr Thr Thr Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Ser Tyr Tyr
65 70 75 80

Tyr Ser Thr Gln Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys
85 90 95

Pro Ser Gln His His His His His His
100 105

<210> 446
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 446
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Ser Asn Asp Gly Pro Gly Leu Ser
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Ser Tyr Tyr
65 70 75 80

Thr Lys Lys Ala Tyr Ser Ala Gly Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Pro Ser Gln His His His His His His
100 105

<210> 447
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 447
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Pro Asp Pro Tyr Tyr Lys Pro Asp
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

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

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr Ser Tyr
65 70 75 80

Tyr Gly Tyr Tyr Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys
85 90 95

Pro Ser Gln His His His His His His
100 105

<210> 448
<211> 208
<212> PRT
<213> Homo sapiens

<400> 448
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
1 5 10 15

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
20 25 30

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala

35 40 45

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
50 55 60

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
65 70 75 80

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
85 90 95

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
100 105 110

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
115 120 125

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
130 135 140

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

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
165 170 175

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
180 185 190

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 449
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> MOD_RES
<222> (1)..(9)
<223> Any amino acid and this region may encompass 6 to 9 residues

<220>
<221> VARIANT
<222> (10)..(10)
<223> /replace="His"

<220>
<221> misc_feature
<222> (10)..(10)
<223> /note="Residue given in the sequence has no preference

with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(11)
<223> /note="see specification as filed for detailed description of substitutions and preferred embodiments"

<400> 449
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Gly
1 5 10

<210> 450
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> MOD_RES
<222> (1)..(3)
<223> Any amino acid

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (4)..(4)
<223> /note="Residue given in the sequence has no preference with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(4)
<223> /note="see specification as filed for detailed description of substitutions and preferred embodiments"

<400> 450
Xaa Xaa Xaa Gly
1

<210> 451
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> VARIANT
<222> (2)..(2)
<223> /replace="Phe"

<220>

<221> misc_feature
<222> (2)..(2)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Any amino acid

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Phe" or "Trp"

<220>
<221> misc_feature
<222> (4)..(4)
<223> /note="Residue given in the sequence has no preference
with respect to those in the annotations for said position"

<220>
<221> MOD_RES
<222> (5)..(6)
<223> Any amino acid

<220>
<221> VARIANT
<222> (7)..(7)
<223> /replace="Ala"

<220>
<221> misc_feature
<222> (7)..(7)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> VARIANT
<222> (10)..(10)
<223> /replace="Phe"

<220>
<221> misc_feature
<222> (10)..(10)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(12)
<223> /note="see specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 451
Glu Tyr Xaa Tyr Xaa Xaa Ser Gly Tyr Tyr His Arg
1 5 10

<210> 452
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference

with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 452
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Pro Pro Pro Ser His Gly Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Pro Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

```
Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Tyr
65                  70                  75                  80

Lys His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 453
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 453
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Arg Pro Pro Ile His Ala Tyr Gly Tyr
20 25 30

```
Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Ile Val Glu Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr Phe
65                  70                  75                  80

Lys His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300
```

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 454
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>

<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 454
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ile His Ala Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Gly Ser Glu Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr Phe
65 70 75 80

Lys His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 455
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT

<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>

<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 455

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Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                  10                  15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala His Ala Tyr Gly Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr Phe
65                  70                  75                  80

Lys His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
```

225 230 235 240

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 456
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)

<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference

with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference with respect to the annotation for said position"

<400> 456
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr Phe
65 70 75 80

Lys His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 457
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 457

Gly	Val	Ser	Asp	Val	Pro	Arg	Asp	Leu	Glu	Val	Val	Ala	Ala	Thr	Pro
1				5				10						15	
Thr	Ser	Leu	Leu	Ile	Ser	Trp	Ser	Pro	Pro	Ala	Asn	Gly	Tyr	Gly	Tyr
			20					25					30		
Tyr	Arg	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly	Asn	Ser	Pro	Val	Gln	Glu
		35					40					45			
Phe	Thr	Val	Pro	Val	Gly	Arg	Gly	Thr	Ala	Thr	Ile	Ser	Gly	Leu	Lys
	50					55					60				
Pro	Gly	Val	Asp	Tyr	Thr	Ile	Thr	Val	Tyr	Ala	Val	Glu	Tyr	Thr	Tyr
65					70					75					80
Lys	Gly	Ser	Gly	Tyr	Tyr	His	Arg	Pro	Ile	Ser	Ile	Asn	Tyr	Arg	Thr
				85					90					95	
Glu	Ile	Asp	Lys	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro
			100					105					110		
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
		115					120					125			
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
	130					135					140				
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe
145					150					155					160

```
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 458
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT

<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT

<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 458
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Thr Pro Pro Pro Lys Gly Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Val Gly Glu Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr Tyr
65 70 75 80

Asn Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Lys
325 330

<210> 459
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)

<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)

<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 459
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Thr Pro Pro Pro Lys Gly Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Val Gly Glu Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr Tyr
65 70 75 80

Ile Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr

85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 460
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 460
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Thr Pro Pro Pro Lys Gly Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

```
Phe Thr Val Pro Val Gly Glu Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr Tyr
65                  70                  75                  80

Glu Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320
```

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 461
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>

<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 461
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

```
Thr Ser Leu Leu Ile Ser Trp Thr Pro Pro Pro Lys Gly Tyr Gly Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Val Gly Glu Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Ala Tyr
65                  70                  75                  80

Asn Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285
```

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 462
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT

<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>

<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 462

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Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                  10                  15

Thr Ser Leu Leu Ile Ser Trp Arg Pro Pro Ser His Ala Tyr Gly Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Trp
65                  70                  75                  80

Lys Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255
```

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 463
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)

<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)

<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference with respect to the annotation for said position"

<400> 463
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Pro Pro Ser His Ala Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Trp
65 70 75 80

Lys Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 464
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 464

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                  10                  15

Thr Ser Leu Leu Ile Ser Trp Glu Pro Pro Ser His Ala Tyr Gly Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Trp
65                  70                  75                  80

Lys Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175
```

```
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
```

<210> 465
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature

<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature

<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 465

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                  10                  15

Thr Ser Leu Leu Ile Ser Trp Ser Pro Pro Ser His Ala Tyr Gly Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Trp
65                  70                  75                  80

Lys Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140
```

```
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 466
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)

<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)

<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 466
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Arg Pro Pro Ser Asn Gly His Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

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

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro Phe
65 70 75 80

Lys Trp Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

```
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 467
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 467
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Val Pro Pro Ser Asp Asp Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro Trp

65 70 75 80

Pro His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 468

<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>

<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 468
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Val Pro Ser Ser His Ala Tyr Gly Tyr
20 25 30

```
Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Val Gly Val Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Ala Phe
65                  70                  75                  80

Glu Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300
```

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 469
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT

<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 469

```
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                  10                  15

Thr Ser Leu Leu Ile Ser Trp Asp Pro Ser Ser His Ala Tyr Gly Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Val Gly Val Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Ala Phe
65                  70                  75                  80

Glu Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270
```

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 470
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)

<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT

<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 470
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Glu Pro Ser Ser His Ala Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Val Gly Val Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Ala Phe
65 70 75 80

Glu Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 471
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> VARIANT
<222> (102)..(102)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace=" "

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (104)..(105)
<223> /replace=" "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (107)..(107)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (109)..(110)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (104)..(112)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="His"

<220>
<221> VARIANT
<222> (115)..(115)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (116)..(116)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (114)..(116)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (126)..(126)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (126)..(126)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (104)..(127)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (335)..(335)
<223> /replace=" "

<220>
<221> misc_feature
<222> (335)..(335)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 471
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly Gly
20 25 30

Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro
35 40 45

Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser
50 55 60

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu
65 70 75 80

Tyr Pro Tyr Asp Tyr Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn
85 90 95

Tyr Arg Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His
100 105 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
115 120 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
130 135 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145 150 155 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
165 170 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys

195 200 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
210 215 220

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
225 230 235 240

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

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
260 265 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
275 280 285

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
290 295 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305 310 315 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 472
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<222> (101)..(101)
<223> /replace=" "

<220>
<221> VARIANT
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<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace=" "

<220>
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<222> (100)..(103)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>

<221> misc_feature
<222> (100)..(103)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (104)..(105)
<223> /replace=" "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (107)..(107)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (109)..(110)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (104)..(112)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="His"

<220>
<221> VARIANT
<222> (115)..(115)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (116)..(116)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (114)..(116)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>

<221> VARIANT
<222> (126)..(126)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (126)..(126)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (104)..(127)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (335)..(335)
<223> /replace=" "

<220>
<221> misc_feature
<222> (335)..(335)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 472

Gly	Val	Ser	Asp	Val	Pro	Arg	Asp	Leu	Glu	Val	Val	Ala	Ala	Thr	Pro
1					5				10						15
Thr	Ser	Leu	Leu	Ile	Ser	Trp	Glu	Pro	Phe	Ser	Arg	Leu	Pro	Gly	Gly
			20					25					30		
Gly	Glu	Tyr	Tyr	Arg	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly	Asn	Ser	Pro
		35					40					45			
Leu	Gln	Gln	Phe	Thr	Val	Pro	Gly	Ser	Lys	Gly	Thr	Ala	Thr	Ile	Ser
	50					55					60				
Gly	Leu	Lys	Pro	Gly	Val	Asp	Tyr	Thr	Ile	Thr	Val	Tyr	Ala	Val	Glu
65					70					75					80
Tyr	Pro	Tyr	Glu	His	Ser	Gly	Tyr	Tyr	His	Arg	Pro	Ile	Ser	Ile	Asn
					85					90					95
Tyr	Arg	Thr	Glu	Ile	Asp	Lys	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His
			100					105					110		
Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val
		115					120					125			
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
	130					135					140				
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu
145					150					155					160

```
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                165                 170                 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
225                 230                 235                 240

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

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
        275                 280                 285

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
    290                 295                 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305                 310                 315                 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330                 335


<210> 473
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> VARIANT
<222> (102)..(102)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (103)..(103)
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<223> /replace=" "

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (104)..(105)
<223> /replace=" "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (107)..(107)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (109)..(110)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (104)..(112)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="His"

<220>
<221> VARIANT
<222> (115)..(115)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (116)..(116)

<223> /replace="Cys"

<220>
<221> misc_feature
<222> (114)..(116)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (126)..(126)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (126)..(126)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (104)..(127)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (335)..(335)
<223> /replace=" "

<220>
<221> misc_feature
<222> (335)..(335)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 473
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly Gly
20 25 30

Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro
35 40 45

Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser
50 55 60

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu
65 70 75 80

Tyr Pro Tyr Pro His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn
85 90 95

Tyr Arg Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His
100 105 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
115 120 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
130 135 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145 150 155 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
165 170 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
195 200 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
210 215 220

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
225 230 235 240

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

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
260 265 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
275 280 285

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
290 295 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305 310 315 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 474
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 474
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr
65 70 75 80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

```
Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
            100                 105                 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        115                 120                 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    130                 135                 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145                 150                 155                 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                165                 170                 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        195                 200                 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    210                 215                 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225                 230                 235                 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                245                 250                 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            260                 265                 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        275                 280                 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    290                 295                 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305                 310                 315                 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 475
<211> 335
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> VARIANT
<222> (102)..(102)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace=" "

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (104)..(105)
<223> /replace=" "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (107)..(107)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (109)..(110)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Lys" or "Ser"

<220>

<221> misc_feature
<222> (104)..(112)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="His"

<220>
<221> VARIANT
<222> (115)..(115)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (116)..(116)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (114)..(116)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (126)..(126)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (126)..(126)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (104)..(127)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (335)..(335)
<223> /replace=" "

<220>
<221> misc_feature
<222> (335)..(335)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 475
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly Gly
20 25 30

Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro
35 40 45

Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser

50 55 60

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu
65 70 75 80

Tyr Pro Tyr Asp His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn
85 90 95

Tyr Arg Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His
100 105 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
115 120 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
130 135 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145 150 155 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
165 170 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
195 200 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
210 215 220

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
225 230 235 240

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

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
260 265 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
275 280 285

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
290 295 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305 310 315 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

325 330 335

<210> 476
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (100)..(101)
<223> /replace=" "

<220>
<221> VARIANT
<222> (102)..(102)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace=" "

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (104)..(105)
<223> /replace=" "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (107)..(107)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (109)..(110)
<223> /replace="Ser" or " "

<220>
<221> VARIANT

<222> (111)..(111)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (104)..(112)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="His"

<220>
<221> VARIANT
<222> (115)..(115)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (116)..(116)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (114)..(116)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (126)..(126)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (126)..(126)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (104)..(127)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (335)..(335)
<223> /replace=" "

<220>
<221> misc_feature
<222> (335)..(335)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 476
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

```
Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly Gly
            20                  25                  30

Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro
        35                  40                  45

Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser
    50                  55                  60

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu
65                  70                  75                  80

Phe Pro Tyr Asp His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn
                85                  90                  95

Tyr Arg Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His
            100                 105                 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
        115                 120                 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
    130                 135                 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145                 150                 155                 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                165                 170                 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
225                 230                 235                 240

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

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
        275                 280                 285
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Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
290 295 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305 310 315 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 477
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
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<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
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<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)

<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature

<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 477
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr
65 70 75 80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
100 105 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
115 120 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
130 135 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145 150 155 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
165 170 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
195 200 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
210 215 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225 230 235 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
245 250 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
260 265 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
275 280 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
290 295 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305 310 315 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 478
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> VARIANT
<222> (102)..(102)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace=" "

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (104)..(105)
<223> /replace=" "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (107)..(107)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (109)..(110)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (104)..(112)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="His"

<220>
<221> VARIANT
<222> (115)..(115)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (116)..(116)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (114)..(116)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (126)..(126)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (126)..(126)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (104)..(127)
<223> /note="This region may encompass the sequences disclosed

as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (335)..(335)
<223> /replace=" "

<220>
<221> misc_feature
<222> (335)..(335)
<223> /note="Residue given in the sequence has no preference with respect to the annotation for said position"

<400> 478
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly Gly
20 25 30

Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro
35 40 45

Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser
50 55 60

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu
65 70 75 80

Phe Pro Tyr Ala His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn
85 90 95

Tyr Arg Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His
100 105 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
115 120 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
130 135 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145 150 155 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
165 170 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
195 200 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
210 215 220

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
225 230 235 240

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

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
260 265 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
275 280 285

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
290 295 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305 310 315 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 479
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>

<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 479

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Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Asp Gly Tyr Gly
            20                  25                  30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
        35                  40                  45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
    50                  55                  60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Thr
65                  70                  75                  80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
                85                  90                  95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
            100                 105                 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        115                 120                 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    130                 135                 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145                 150                 155                 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                165                 170                 175

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
```

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            180                 185                 190

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        195                 200                 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    210                 215                 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225                 230                 235                 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                245                 250                 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            260                 265                 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        275                 280                 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    290                 295                 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305                 310                 315                 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330


<210> 480
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> VARIANT
<222> (102)..(102)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace=" "

<220>
<221> misc_feature
<222> (100)..(103)
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (104)..(105)
<223> /replace=" "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (107)..(107)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (109)..(110)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (104)..(112)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="His"

<220>
<221> VARIANT
<222> (115)..(115)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (116)..(116)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (114)..(116)

<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (126)..(126)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (126)..(126)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (104)..(127)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (335)..(335)
<223> /replace=" "

<220>
<221> misc_feature
<222> (335)..(335)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 480
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly Gly
20 25 30

Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro
35 40 45

Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser
50 55 60

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu
65 70 75 80

Tyr Pro Tyr Ala His Ser Gly Tyr Phe His Arg Pro Ile Ser Ile Asn
85 90 95

Tyr Arg Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His
100 105 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
115 120 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
130 135 140

```
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145                 150                 155                 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                165                 170                 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
225                 230                 235                 240

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

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
        275                 280                 285

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
    290                 295                 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305                 310                 315                 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330                 335


<210> 481
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "
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<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 481
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Ala Ala Pro Ala Gly Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asp
65 70 75 80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
100 105 110

```
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        115                 120                 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    130                 135                 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145                 150                 155                 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                165                 170                 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        195                 200                 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    210                 215                 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225                 230                 235                 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                245                 250                 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            260                 265                 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        275                 280                 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    290                 295                 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305                 310                 315                 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 482
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 482
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Ala Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asp Phe
65 70 75 80

```
Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 483
<211> 332

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT

<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 483
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Ala Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu

35 40 45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp Tyr
65 70 75 80

Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 484
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)

<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 484

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Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                  10                  15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Ala Tyr Gly
            20                  25                  30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
        35                  40                  45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
    50                  55                  60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Ser
65                  70                  75                  80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
                85                  90                  95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
            100                 105                 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        115                 120                 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    130                 135                 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145                 150                 155                 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                165                 170                 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        195                 200                 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    210                 215                 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225                 230                 235                 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                245                 250                 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            260                 265                 270
```

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Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        275                 280                 285


Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    290                 295                 300


Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305                 310                 315                 320


His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330


<210> 485
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
      with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
      EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "
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<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)

<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 485
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Gly Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp Phe
65 70 75 80

Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 486
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference with respect to the annotation for said position"

<400> 486
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Glu Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
100 105 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
115 120 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
130 135 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145 150 155 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
165 170 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
195 200 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
210 215 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225 230 235 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
245 250 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
260 265 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
275 280 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
290 295 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305 310 315 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 487
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature

<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT

<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 487
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
100 105 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
115 120 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
130 135 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145 150 155 160

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

165 170 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
195 200 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
210 215 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225 230 235 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
245 250 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
260 265 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
275 280 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
290 295 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305 310 315 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 488
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 488
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro Phe
65 70 75 80

Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 489
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 489
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Gly Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp Phe
65 70 75 80

Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

```
Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 490
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature

<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 490
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

```
Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65                  70                  75                  80

Phe Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
                85                  90                  95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
            100                 105                 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        115                 120                 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    130                 135                 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145                 150                 155                 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                165                 170                 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        195                 200                 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    210                 215                 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225                 230                 235                 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                245                 250                 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            260                 265                 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        275                 280                 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    290                 295                 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305                 310                 315                 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 491
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)

<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 491
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Asp Ala Tyr Gly

20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asn
65 70 75 80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
100 105 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
115 120 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
130 135 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145 150 155 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
165 170 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
195 200 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
210 215 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225 230 235 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
245 250 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
260 265 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
275 280 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

290 295 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305 310 315 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 492
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> VARIANT
<222> (102)..(102)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace=" "

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (104)..(105)
<223> /replace=" "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (107)..(107)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (109)..(110)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (104)..(112)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="His"

<220>
<221> VARIANT
<222> (115)..(115)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (116)..(116)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (114)..(116)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (126)..(126)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (126)..(126)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (104)..(127)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (335)..(335)
<223> /replace=" "

<220>
<221> misc_feature
<222> (335)..(335)

<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 492
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Ala Gly Lys His
20 25 30

Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro
35 40 45

Val Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser
50 55 60

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu
65 70 75 80

Phe Asp Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn
85 90 95

Tyr Arg Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His
100 105 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
115 120 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
130 135 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145 150 155 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
165 170 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
195 200 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
210 215 220

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
225 230 235 240

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

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
260 265 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
275 280 285

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
290 295 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305 310 315 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 493
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 493
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Ala Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Thr Tyr
65 70 75 80

Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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


Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255


Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270


Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285


Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300


Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320


Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330


<210> 494
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
      with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
      EIDK, EIEK or is absent"

<220>
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<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature

<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 494
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Ala Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asp Phe
65 70 75 80

Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 495
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference

with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference

with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 495
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
100 105 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
115 120 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
130 135 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys

145 150 155 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
165 170 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
195 200 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
210 215 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225 230 235 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
245 250 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
260 265 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
275 280 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
290 295 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305 310 315 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 496
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 496
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp Phe
65 70 75 80

Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 497
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>

<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 497
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Val Phe Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp Tyr
65 70 75 80

```
Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 498
<211> 333
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)

<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 498
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

```
Glu Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
    50                  55                  60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asp
65                  70                  75                  80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
                85                  90                  95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
            100                 105                 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        115                 120                 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    130                 135                 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145                 150                 155                 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                165                 170                 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        195                 200                 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    210                 215                 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225                 230                 235                 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                245                 250                 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            260                 265                 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        275                 280                 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    290                 295                 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305                 310                 315                 320
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His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 499
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 499
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro

```
1               5                  10                  15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Ala Tyr Gly Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp Phe
65                  70                  75                  80

Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
```

275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 500
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 500
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Ala Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp Phe
65 70 75 80

Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 501
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>

<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>

<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference with respect to the annotation for said position"

<400> 501
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Gly Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro Phe
65 70 75 80

Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210   215   220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245   250   255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260   265   270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275   280   285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290   295   300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305   310   315   320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325   330

<210> 502
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
      with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)

<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)

<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 502
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp Tyr
65 70 75 80

Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

```
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 503
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 503
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
100 105 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
115 120 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

130 135 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145 150 155 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
165 170 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
195 200 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
210 215 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225 230 235 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
245 250 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
260 265 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
275 280 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
290 295 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305 310 315 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 504
<211> 334
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (99)..(100)
<223> /replace=" "

<220>

<221> VARIANT
<222> (101)..(101)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (102)..(102)
<223> /replace=" "

<220>
<221> misc_feature
<222> (99)..(102)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (99)..(102)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (103)..(104)
<223> /replace=" "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (107)..(107)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (108)..(109)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (103)..(111)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="His"

<220>

<221> VARIANT
<222> (114)..(114)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (115)..(115)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (113)..(115)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (125)..(125)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (125)..(125)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (103)..(126)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (334)..(334)
<223> /replace=" "

<220>
<221> misc_feature
<222> (334)..(334)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 504
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Ala Ala Ser Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe
65 70 75 80

Pro Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

```
Arg Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr
            100                 105                 110

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
        115                 120                 125

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    130                 135                 140

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
145                 150                 155                 160

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                165                 170                 175

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        195                 200                 205

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    210                 215                 220

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
225                 230                 235                 240

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                245                 250                 255

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            260                 265                 270

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        275                 280                 285

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    290                 295                 300

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
305                 310                 315                 320

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 505
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)

<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 505
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Ala Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

```
Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp Phe
65                  70                  75                  80

Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 506
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 506
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Pro Pro Ala Glu Gly Tyr Gly Tyr
20 25 30

```
Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asn Phe
65                  70                  75                  80

Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300
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Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 507
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference

with respect to the annotation for said position"

<400> 507

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Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                  10                  15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Tyr Gly Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp Phe
65                  70                  75                  80

Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
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260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 508
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
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<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
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<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
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<222> (101)..(102)
<223> /replace=" "

<220>
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<222> (103)..(103)
<223> /replace="Glu" or " "

<220>

<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
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<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 508

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Gly Ile Thr Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                  10                  15

Thr Ser Leu Leu Ile Ser Trp Asn Pro Pro Asp Val Asn Tyr Gly Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Leu Gln Glu
        35                  40                  45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Tyr
65                  70                  75                  80

Ala His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220
```

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 509
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
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<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
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<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)

<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 509
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Asp Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
100 105 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
115 120 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
130 135 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145 150 155 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
165 170 175

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

```
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        195                 200                 205


Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    210                 215                 220


Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225                 230                 235                 240


Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                245                 250                 255


Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            260                 265                 270


Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        275                 280                 285


Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    290                 295                 300


Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305                 310                 315                 320


His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330


<210> 510
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference
      with respect to those in the annotations for said positions"
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<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 510
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Thr
65 70 75 80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
100 105 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
115 120 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
130 135 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145 150 155 160

```
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                165                 170                 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        195                 200                 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    210                 215                 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225                 230                 235                 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                245                 250                 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            260                 265                 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        275                 280                 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    290                 295                 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305                 310                 315                 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330


<210> 511
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
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<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>

<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 511
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65 70 75 80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
100 105 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu

115 120 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
130 135 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145 150 155 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
165 170 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
195 200 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
210 215 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225 230 235 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
245 250 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
260 265 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
275 280 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
290 295 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305 310 315 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 512
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT

<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 512
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Ala Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asp Phe
65 70 75 80

```
Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 513
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> VARIANT
<222> (102)..(102)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace=" "

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (104)..(105)
<223> /replace=" "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (107)..(107)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (109)..(110)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (104)..(112)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="His"

<220>
<221> VARIANT
<222> (115)..(115)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (116)..(116)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (114)..(116)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (126)..(126)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (126)..(126)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (104)..(127)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (335)..(335)
<223> /replace=" "

<220>
<221> misc_feature
<222> (335)..(335)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 513
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Glu Pro Phe Ser Arg Leu Pro Gly Gly
20 25 30

Gly Glu Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro
35 40 45

```
Leu Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser
    50                  55                  60

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu
65                  70                  75                  80

Tyr Pro Tyr Pro Phe Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn
                85                  90                  95

Tyr Arg Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His
            100                 105                 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
        115                 120                 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
    130                 135                 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145                 150                 155                 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                165                 170                 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
225                 230                 235                 240

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

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
        275                 280                 285

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
    290                 295                 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305                 310                 315                 320
```

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 514
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 514
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

```
Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Gly Tyr Gly
            20                  25                  30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
        35                  40                  45

Glu Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
    50                  55                  60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asp
65                  70                  75                  80

Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
                85                  90                  95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
            100                 105                 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        115                 120                 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    130                 135                 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145                 150                 155                 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                165                 170                 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        195                 200                 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    210                 215                 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225                 230                 235                 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                245                 250                 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            260                 265                 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        275                 280                 285
```

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
290 295 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305 310 315 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 515
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>

<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 515
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asn
65 70 75 80

Phe Ile Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
100 105 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
115 120 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
130 135 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145 150 155 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
165 170 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
195 200 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
210 215 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225 230 235 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys

245 250 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
260 265 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
275 280 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
290 295 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305 310 315 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 516
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT

<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature

<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference with respect to the annotation for said position"

<400> 516
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Gly Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro
65 70 75 80

Tyr Pro Phe Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
100 105 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
115 120 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
130 135 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145 150 155 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
165 170 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
195 200 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
210 215 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225 230 235 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
245 250 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
260 265 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
275 280 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
290 295 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305 310 315 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 517
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> VARIANT
<222> (102)..(102)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace=" "

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="This region may encompass E, EI, EID,

EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (104)..(105)
<223> /replace=" "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (107)..(107)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (109)..(110)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (104)..(112)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="His"

<220>
<221> VARIANT
<222> (115)..(115)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (116)..(116)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (114)..(116)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (126)..(126)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (126)..(126)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (104)..(127)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (335)..(335)
<223> /replace=" "

<220>
<221> misc_feature
<222> (335)..(335)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 517
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Ser Glu Lys Leu Asp Gly Lys Ala Arg
20 25 30

Arg Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro
35 40 45

Val Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser
50 55 60

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu
65 70 75 80

Phe Pro Tyr Asp His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn
85 90 95

Tyr Arg Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His
100 105 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
115 120 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
130 135 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145 150 155 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
165 170 175

```
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
            180                 185                 190


Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205


Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220


Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
225                 230                 235                 240


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


Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270


Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
        275                 280                 285


Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
    290                 295                 300


Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305                 310                 315                 320


His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330                 335


<210> 518
<211> 336
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> VARIANT
<222> (102)..(102)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace=" "

<220>
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<221> misc_feature
<222> (100)..(103)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (104)..(105)
<223> /replace=" "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (107)..(107)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (109)..(110)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (104)..(112)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="His"

<220>
<221> VARIANT
<222> (115)..(115)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (116)..(116)
<223> /replace="Cys"

<220>

<221> misc_feature
<222> (114)..(116)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (126)..(126)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (126)..(126)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (104)..(127)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (336)..(336)
<223> /replace=" "

<220>
<221> misc_feature
<222> (336)..(336)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 518
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Ser Pro Arg Asp Ser Thr Gly Leu Val
20 25 30

Arg Arg Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser
35 40 45

Pro Val Gln Gln Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile
50 55 60

Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val
65 70 75 80

Glu Tyr Pro Tyr Asp His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile
85 90 95

Asn Tyr Arg Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr
100 105 110

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
115 120 125

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
130 135 140

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
145 150 155 160

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
165 170 175

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
195 200 205

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
210 215 220

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
225 230 235 240

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

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
260 265 270

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
275 280 285

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
290 295 300

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
305 310 315 320

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 519
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> VARIANT

<222> (102)..(102)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace=" "

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (100)..(103)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (104)..(105)
<223> /replace=" "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (107)..(107)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (109)..(110)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (104)..(112)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="His"

<220>
<221> VARIANT

<222> (115)..(115)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (116)..(116)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (114)..(116)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (126)..(126)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (126)..(126)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (104)..(127)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (335)..(335)
<223> /replace=" "

<220>
<221> misc_feature
<222> (335)..(335)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 519
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Gly Asp Val Arg Thr Asn Glu Ala Arg
20 25 30

Gln Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro
35 40 45

Leu Gln Gly Phe Thr Val Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser
50 55 60

Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu
65 70 75 80

Tyr Thr Tyr Glu His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn
85 90 95

Tyr Arg Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His

100 105 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
115 120 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
130 135 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145 150 155 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
165 170 175

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
195 200 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
210 215 220

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
225 230 235 240

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

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
260 265 270

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
275 280 285

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
290 295 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305 310 315 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 520
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference

with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 520
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Gly Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

```
Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp
65                  70                  75                  80

Phe Val Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
                85                  90                  95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
            100                 105                 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        115                 120                 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    130                 135                 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145                 150                 155                 160

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                165                 170                 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        195                 200                 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    210                 215                 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225                 230                 235                 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                245                 250                 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            260                 265                 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        275                 280                 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    290                 295                 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305                 310                 315                 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 521
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 521
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Ala Tyr Gly Tyr
20 25 30

```
Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asp Phe
65                  70                  75                  80

Ala Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300
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Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 522
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>

<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 522
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Ala Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Ser Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Ala Phe
65 70 75 80

Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 523
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT

<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>

<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 523

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Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                  10                  15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Gly Gly Tyr Gly Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asp Phe
65                  70                  75                  80

Ala Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
```

225 230 235 240

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 524
<211> 334
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (99)..(100)
<223> /replace=" "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (102)..(102)
<223> /replace=" "

<220>
<221> misc_feature
<222> (99)..(102)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (99)..(102)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (103)..(104)

<223> /replace=" "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (107)..(107)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (108)..(109)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (103)..(111)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="His"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (115)..(115)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (113)..(115)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (125)..(125)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (125)..(125)
<223> /note="Residue given in the sequence has no preference

with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (103)..(126)
<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (334)..(334)
<223> /replace=" "

<220>
<221> misc_feature
<222> (334)..(334)
<223> /note="Residue given in the sequence has no preference with respect to the annotation for said position"

<400> 524
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Ala Glu Ala Tyr
20 25 30

Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val
35 40 45

Gln Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly
50 55 60

Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr
65 70 75 80

Val Phe Pro Gly Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr
85 90 95

Arg Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr
100 105 110

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
115 120 125

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
130 135 140

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
145 150 155 160

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
165 170 175

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
195 200 205

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
210 215 220

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
225 230 235 240

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
245 250 255

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
260 265 270

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
275 280 285

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
290 295 300

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
305 310 315 320

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 525
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 525
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Glu Gly Ala Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro
65 70 75 80

Tyr Pro Phe Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
100 105 110

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
115 120 125

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
130 135 140

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
145 150 155 160

```
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                165                 170                 175

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        195                 200                 205

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    210                 215                 220

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
225                 230                 235                 240

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                245                 250                 255

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            260                 265                 270

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        275                 280                 285

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    290                 295                 300

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
305                 310                 315                 320

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330


<210> 526
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
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<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT

<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 526
Gly Val Thr Asp Val Pro Arg Asp Met Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Gln Pro Pro Ala Val Thr Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Thr Leu Gln Gln
35 40 45

Phe Thr Val Pro Val Tyr Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Tyr
65 70 75 80

Asp His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

```
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 527
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)

<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (99)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)

<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 527
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Ala Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp Tyr
65 70 75 80

Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr

85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 528
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 528
Gly Ile Val Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Pro Pro Ala Gly Ala Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Lys Gln Gln
35 40 45

```
Phe Thr Val Pro Gly Tyr Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Tyr
65                  70                  75                  80

Asp His Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320
```

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Lys
325 330

<210> 529
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>

<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 529
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

```
Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Ala Gly Tyr Gly Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Asp Phe
65                  70                  75                  80

Pro Gly Ser Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285
```

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 530
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT

<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>

<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 530
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Ala Pro Pro Ser Asp Ala Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Tyr
65 70 75 80

Ser His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 531
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)

<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)

<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference with respect to the annotation for said position"

<400> 531
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Pro Pro Ser Asp Asp Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro Trp
65 70 75 80

Pro His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145 150 155 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
165 170 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
180 185 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
195 200 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala

210 215 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
245 250 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
260 265 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
275 280 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
290 295 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305 310 315 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 532
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (97)..(98)
<223> /replace=" "

<220>
<221> VARIANT
<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace=" "

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (97)..(100)
<223> /note="This region may encompass E, EI, EID, EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (101)..(102)
<223> /replace=" "

<220>
<221> VARIANT
<222> (103)..(103)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (106)..(107)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (108)..(108)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (101)..(109)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (111)..(111)
<223> /replace="His"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (111)..(113)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (123)..(123)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (123)..(123)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (101)..(124)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (332)..(332)
<223> /replace=" "

<220>
<221> misc_feature
<222> (332)..(332)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 532

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Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1               5                   10                  15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Asp Asp Tyr Gly Tyr
            20                  25                  30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
        35                  40                  45

Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
    50                  55                  60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro Trp
65                  70                  75                  80

Pro His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
                85                  90                  95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            100                 105                 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        115                 120                 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    130                 135                 140

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175
```

```
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 533
<211> 333
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (98)..(99)
<223> /replace=" "

<220>
<221> VARIANT
<222> (100)..(100)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (101)..(101)
<223> /replace=" "

<220>
<221> misc_feature

<222> (98)..(101)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (98)..(101)
<223> /note="This region may encompass E, EI, EID,
EIDK, EIEK or is absent"

<220>
<221> VARIANT
<222> (102)..(103)
<223> /replace=" "

<220>
<221> VARIANT
<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (105)..(105)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (106)..(106)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (107)..(108)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (109)..(109)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (110)..(110)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (102)..(110)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (112)..(112)
<223> /replace="His"

<220>
<221> VARIANT
<222> (113)..(113)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (114)..(114)
<223> /replace="Cys"

<220>
<221> misc_feature

<222> (112)..(114)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (124)..(124)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (102)..(125)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (333)..(333)
<223> /replace=" "

<220>
<221> misc_feature
<222> (333)..(333)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<400> 533
Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro
1 5 10 15

Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ser Asp Asp Tyr Gly Tyr
20 25 30

Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu
35 40 45

Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys
50 55 60

Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro Trp
65 70 75 80

Pro His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr
85 90 95

Glu Ile Asp Lys Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
100 105 110

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
115 120 125

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
130 135 140

```
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
145                 150                 155                 160

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                165                 170                 175

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            180                 185                 190

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        195                 200                 205

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    210                 215                 220

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                245                 250                 255

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            260                 265                 270

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        275                 280                 285

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    290                 295                 300

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
305                 310                 315                 320

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Lys
                325                 330


<210> 534
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> VARIANT
<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
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<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)

<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT

<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<222> (350)..(350)

<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
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<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 534
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

```
    50                  55                  60

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Pro Pro Pro Ser His Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Pro Gly Lys
    290                 295                 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320

Thr Val Tyr Ala Val Glu Tyr Pro Tyr Lys His Ser Gly Tyr Tyr His
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325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 535
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT

<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>

<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 535

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

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

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

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

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

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

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

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

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

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

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

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

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205
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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 Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Arg Pro Pro Ile His Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ile Val Glu
    290                 295                 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320

Thr Val Tyr Ala Val Glu Tyr Thr Phe Lys His Ser Gly Tyr Tyr His
                325                 330                 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 536
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
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<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>

<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 536
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln

85 90 95

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ile His Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser Glu
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Thr Phe Lys His Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp

355 360

<210> 537
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

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<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)

<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

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<220>
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<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
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<222> (235)..(235)
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or "Asp"

<220>
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<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
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<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>

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<223> /replace="Gly" or " "

<220>
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<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
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<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
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<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
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<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
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<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference

with respect to those in the annotations for said positions"

<220>
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<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 380-395, 635 or is absent"

<400> 537
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

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Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255


Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270


Asp Ala Pro Ala His Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285


Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser Lys
    290                 295                 300


Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320


Thr Val Tyr Ala Val Glu Tyr Thr Phe Lys His Ser Gly Tyr Tyr His
                325                 330                 335


Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350


Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 538
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


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<220>
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<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "
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<220>
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<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
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<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<222> (242)..(242)
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<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)

<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<223> /replace="Gly" or " "

<220>
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<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Leu" or "Asp" or " "

<220>
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<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace=" "

<220>
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<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 538
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

115 120 125

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Val Thr Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser Lys
290 295 300

Ser Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Thr Phe Lys His Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 539
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<222> (1)..(2)
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<220>
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<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
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<223> /replace="His"

<220>
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<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="Ser"

<220>
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<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<220>
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or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
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<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
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or "Asp"

<220>
<221> VARIANT
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<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
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<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<220>
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<220>
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<222> (244)..(244)
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<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<220>
<221> VARIANT
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<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
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<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
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<222> (358)..(362)
<223> /replace=" "

<220>
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<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 539

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270
```

```
Ser Pro Pro Ala Asn Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285


Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Gly Arg
    290                 295                 300


Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320


Thr Val Tyr Ala Val Glu Tyr Thr Tyr Lys Gly Ser Gly Tyr Tyr His
                325                 330                 335


Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350


Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 540
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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      polypeptide"


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<220>
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<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
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<223> /replace="Lys" or "Ser"

<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"

or "Asp"

<220>
<221> VARIANT
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<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>

<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
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<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 540
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

145 150 155 160

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Thr Pro Pro Pro Lys Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Gly Glu
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Thr Tyr Asn Gly Ala Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 541
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)

<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
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<220>
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<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
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<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
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<220>

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<220>
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<220>
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<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
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<220>
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<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
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<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
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<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
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<222> (358)..(362)
<223> /replace=" "

<220>
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<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 541
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Thr Pro Pro Pro Lys Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Gly Glu
    290                 295                 300
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Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Thr Tyr Ile Gly Ala Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 542
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<220>
<221> VARIANT
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<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
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<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>

<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<220>
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<223> /replace="Gly" or " "

<220>
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<223> /note="Residues given in the sequence have no preference
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<220>
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as SEQ ID NOS 310-314 or 620-634"

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<220>
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<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

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<223> /replace="Asp" or "Gly" or "Cys" or " "

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<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Leu" or "Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace=" "

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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

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

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

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

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

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

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

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

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

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

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

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

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

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Thr Pro Pro Pro Lys Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Gly Glu
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Thr Tyr Glu Gly Ala Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 543
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
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<223> /replace="Ser" or " "

<220>
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<223> /replace="Asp" or "Gly"

<220>
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<222> (9)..(9)
<223> /replace="Lys" or "Ser"

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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

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<222> (11)..(11)
<223> /replace="His"

<220>
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<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

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<220>
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<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

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<223> /note="This region may encompass the sequences disclosed
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<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

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or "Pro" or "Val"

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or "Asp"

<220>
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<223> /replace="Ala" or "Gly" or " "

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<222> (240)..(240)
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<220>
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<223> /replace="Ser" or "Glu" or "Gly" or " "

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<220>
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<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

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<223> /note="Residues given in the sequence have no preference
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<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<220>
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<223> /replace="Gly" or "Ser" or " "

<220>
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<220>
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<223> /replace="Glu" or " "

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<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace=" "

<220>
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<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 543
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Thr Pro Pro Pro Lys Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Gly Glu
    290                 295                 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320

Thr Val Tyr Ala Val Glu Tyr Ala Tyr Asn Gly Ala Gly Tyr Tyr His
                325                 330                 335
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Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

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<220>
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<220>
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<220>
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<223> /replace="Ser" or " "

<220>
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<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<222> (11)..(11)
<223> /replace="His"

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<222> (12)..(12)
<223> /replace="Thr"

<220>
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<220>
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as SEQ ID NOS 317-321"

<220>
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<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
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<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
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<220>
<221> VARIANT
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<222> (237)..(237)
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<223> /replace="Ala" or "Gly" or " "

<220>
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<223> /replace="Ser" or "Glu" or "Gly" or " "

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<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

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<223> /replace="Glu" or " "

<220>
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<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<220>
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<220>
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<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
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<220>
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<223> /replace="Glu" or " "

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<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace=" "

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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as SEQ ID NOS 380-395, 635 or is absent"

<400> 544
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Arg Pro Pro Ser His Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ile Gly Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Pro Trp Lys Gly Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 545
<211> 362
<212> PRT
<213> Artificial Sequence

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<220>
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<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<223> /replace="Lys" or " "

<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<223> /replace="Asp" or "Gly"

<220>
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<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

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<223> /replace="His"

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<223> /replace="Thr"

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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

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<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

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<220>
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or "Ala" or "Gln" or "Thr"

<220>
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or "Pro" or "Val"

<220>
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<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
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<220>
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<220>
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<220>
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<220>
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<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Ser" or "Glu" or "Gly" or " "

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<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

<220>
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with respect to those in the annotations for said positions"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<220>
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<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Cys" or "Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
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<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace=" "

<220>
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<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 545
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Pro Pro Ser His Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ile Gly Lys
    290                 295                 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320

Thr Val Tyr Ala Val Glu Tyr Pro Trp Lys Gly Ser Gly Tyr Tyr His
                325                 330                 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360
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<210> 546
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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polypeptide"

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<220>
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<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<223> /replace="Gly" or " "

<220>
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<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<223> /replace="Cys" or "Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
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<222> (358)..(362)
<223> /replace=" "

<220>
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<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 380-395, 635 or is absent"

<400> 546

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg

245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Glu Pro Pro Ser His Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ile Gly Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Pro Trp Lys Gly Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 547
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>

<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<222> (9)..(9)
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<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

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<222> (13)..(13)
<223> /replace="Cys"

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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

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<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<222> (232)..(232)
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<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"

or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (239)..(239)
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<222> (240)..(240)
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<220>
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<220>
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<220>
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<220>
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<220>
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<222> (245)..(245)
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<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<223> /replace="Gly" or " "

<220>
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<223> /replace="Gly" or "Ser" or " "

<220>
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<220>
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<220>
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<220>
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<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Leu" or "Asp" or " "

<220>

<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
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<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
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<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<222> (358)..(362)
<223> /replace=" "

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 547
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Ser Pro Pro Ser His Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ile Gly Lys
    290                 295                 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320

Thr Val Tyr Ala Val Glu Tyr Pro Trp Lys Gly Ser Gly Tyr Tyr His
                325                 330                 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360
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<210> 548
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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<220>
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<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT

<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>

<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 548
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Arg Pro Pro Ser Asn Gly His Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu

275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Asn Glu
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Phe Pro Phe Lys Trp Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 549
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)

<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 549
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Val Pro Pro Ser Asp Asp Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ile Gly Lys
    290                 295                 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320

Thr Val Tyr Ala Val Glu Phe Pro Trp Pro His Ala Gly Tyr Tyr His
                325                 330                 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 550
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> VARIANT
<222> (1)..(2)
<223> /replace=" "
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<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)

<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 550
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

35 40 45

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Val Pro Ser Ser His Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Gly Val
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile

305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Ala Phe Glu Gly Ala Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 551
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>

<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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as SEQ ID NOS 317-321"

<220>
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<220>
<221> VARIANT
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<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
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or "Asp"

<220>
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<220>
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<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<223> /replace="Gly" or "Ser" or " "

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<220>
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<222> (240)..(240)
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<220>
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<222> (241)..(241)
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<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>

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<223> /note="Residues given in the sequence have no preference
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<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

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<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<220>
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<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
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<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
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<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT

<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
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<222> (358)..(362)
<223> /replace=" "

<220>
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<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 551
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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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 Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240


Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255


Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270


Asp Pro Ser Ser His Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285


Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Gly Val
    290                 295                 300


Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320


Thr Val Tyr Ala Val Glu Tyr Ala Phe Glu Gly Ala Gly Tyr Tyr His
                325                 330                 335


Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350


Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 552
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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      polypeptide"


<220>
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<220>
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<223> /replace="Glu" or " "

<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>

<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
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<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
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<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>

<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

<220>
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<222> (232)..(250)
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<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<223> /replace="Gly" or " "

<220>
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<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<220>
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<220>
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<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Leu" or "Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
<221> VARIANT
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<223> /replace=" "

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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as SEQ ID NOS 380-395, 635 or is absent"

<400> 552
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

65 70 75 80

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Glu Pro Ser Ser His Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Gly Val
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Ala Phe Glu Gly Ala Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln

340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 553
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
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<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

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<220>
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<222> (23)..(23)
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with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
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<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
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<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<222> (237)..(237)
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<220>
<221> VARIANT
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<220>

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<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<220>
<221> VARIANT
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<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)

<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Gly" or " "

<220>
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<222> (350)..(350)
<223> /replace="Gly" or "Ser" or " "

<220>
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<220>
<221> VARIANT
<222> (352)..(352)
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<220>
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<222> (353)..(353)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<222> (354)..(354)
<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
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<222> (356)..(356)
<223> /replace="Leu" or "Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<222> (359)..(359)
<223> /replace="Glu" or " "

<220>
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<220>
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<223> /replace=" "

<220>
<221> misc_feature
<222> (349)..(365)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (349)..(365)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 553
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

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Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240


Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255


Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270


Glu Pro Phe Ser Arg Leu Pro Gly Gly Gly Glu Tyr Tyr Arg Ile Thr
        275                 280                 285


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


Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
305                 310                 315                 320


Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Tyr Asp Tyr Ser Gly
                325                 330                 335


Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys
            340                 345                 350


Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360                 365


<210> 554
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
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<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "
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<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"

or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(359)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (360)..(360)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (361)..(365)
<223> /replace=" "

<220>
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<222> (349)..(365)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (349)..(365)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 554
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

100 105 110

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Glu Pro Phe Ser Arg Leu Pro Gly Gly Gly Glu Tyr Tyr Arg Ile Thr
275 280 285

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

Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
305 310 315 320

Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Tyr Glu His Ser Gly
325 330 335

Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys
340 345 350

Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360 365

<210> 555

<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature

<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(359)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (360)..(360)
<223> /replace="Asp" or " "

<220>
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<222> (361)..(365)
<223> /replace=" "

<220>
<221> misc_feature
<222> (349)..(365)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature

<222> (349)..(365)
<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 380-395, 635 or is absent"

<400> 555
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Glu Pro Phe Ser Arg Leu Pro Gly Gly Gly Glu Tyr Tyr Arg Ile Thr
275 280 285

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

Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
305 310 315 320

Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Tyr Pro His Ser Gly
325 330 335

Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys
340 345 350

Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360 365

<210> 556
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)

<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT

<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)

<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(363)
<223> /replace=" "

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 556
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr

130 135 140

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Asp Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
275 280 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Ser
290 295 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305 310 315 320

Ile Thr Val Tyr Ala Val Glu Tyr Thr Phe Pro Gly Ala Gly Tyr Tyr
325 330 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
340 345 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 557
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT

<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (351)..(351)

<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(359)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (360)..(360)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (361)..(365)
<223> /replace=" "

<220>
<221> misc_feature
<222> (349)..(365)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (349)..(365)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 557
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Glu Pro Phe Ser Arg Leu Pro Gly Gly Gly Glu Tyr Tyr Arg Ile Thr
        275                 280                 285
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Tyr Gly Glu Thr Gly Gly Asn Ser Pro Leu Gln Gln Phe Thr Val Pro
    290                 295                 300

Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
305                 310                 315                 320

Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Tyr Asp His Ser Gly
                325                 330                 335

Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys
            340                 345                 350

Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360                 365


<210> 558
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> VARIANT
<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT

<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>

<221> VARIANT
<222> (359)..(359)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (360)..(360)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (361)..(365)
<223> /replace=" "

<220>
<221> misc_feature
<222> (349)..(365)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (349)..(365)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 558
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

165 170 175

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Glu Pro Phe Ser Arg Leu Pro Gly Gly Gly Glu Tyr Tyr Arg Ile Thr
275 280 285

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

Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
305 310 315 320

Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro Tyr Asp His Ser Gly
325 330 335

Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys
340 345 350

Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360 365

<210> 559
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (1)..(2)
<223> /replace=" "

<220>

<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>

<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<223> /replace="Gly" or " "

<220>
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<222> (348)..(348)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (349)..(349)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>

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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<222> (352)..(352)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(363)
<223> /replace=" "

<220>
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<222> (347)..(363)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 559
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Asp Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
        275                 280                 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
    290                 295                 300

Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305                 310                 315                 320
```

Ile Thr Val Tyr Ala Val Glu Tyr Thr Phe Pro Gly Ala Gly Tyr Tyr
325 330 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
340 345 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 560
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)

<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)

<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (352)..(352)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Leu" or "Asp" or " "

<220>
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<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(359)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (360)..(360)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (361)..(365)
<223> /replace=" "

<220>
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<222> (349)..(365)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (349)..(365)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 560
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

195 200 205

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Glu Pro Phe Ser Arg Leu Pro Gly Gly Gly Glu Tyr Tyr Arg Ile Thr
275 280 285

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

Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
305 310 315 320

Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro Tyr Ala His Ser Gly
325 330 335

Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys
340 345 350

Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360 365

<210> 561
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)

<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<220>
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<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<222> (351)..(351)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(363)
<223> /replace=" "

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 561
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Gly Asp Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
        275                 280                 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
    290                 295                 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305                 310                 315                 320

Ile Thr Val Tyr Ala Val Glu Phe Thr Phe Pro Gly Ala Gly Tyr Tyr
                325                 330                 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
            340                 345                 350
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Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355   360

<210> 562
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<220>
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<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
      with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
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<222> (12)..(12)
<223> /replace="Thr"

<220>

<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)

<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(359)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (360)..(360)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (361)..(365)
<223> /replace=" "

<220>
<221> misc_feature

<222> (349)..(365)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (349)..(365)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 562
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala

225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Glu Pro Phe Ser Arg Leu Pro Gly Gly Gly Glu Tyr Tyr Arg Ile Thr
275 280 285

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

Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
305 310 315 320

Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Tyr Ala His Ser Gly
325 330 335

Tyr Phe His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys
340 345 350

Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360 365

<210> 563
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT

<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>

<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or " "

<220>
<221> VARIANT

<222> (354)..(354)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(363)
<223> /replace=" "

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 563
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Ala Ala Pro Ala Gly Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
        275                 280                 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
    290                 295                 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305                 310                 315                 320

Ile Thr Val Tyr Ala Val Glu Tyr Asp Phe Pro Gly Ala Gly Tyr Tyr
                325                 330                 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
            340                 345                 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360
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<210> 564
<211> 362
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference

with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>

<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT

<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed

as SEQ ID NOS 380-395, 635 or is absent"

<400> 564
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp

260 265 270

Asp Ala Pro Ala Asp Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Ser Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Asp Phe Pro Gly Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

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<211> 362
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<220>
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<220>
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<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<223> /replace="Lys" or " "

<220>
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<223> /replace="Ser" or " "

<220>
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<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<223> /replace="Cys"

<220>
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<223> /note="Residues given in the sequence have no preference
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<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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or "Ala" or "Gln" or "Thr"

<220>
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or "Pro" or "Val"

<220>
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<222> (235)..(235)
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or "Asp"

<220>
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<222> (237)..(237)
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<222> (238)..(238)
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<220>
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<222> (240)..(240)
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<220>
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<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<220>
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<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
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<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

<220>
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<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<220>
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<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<220>
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<223> /replace="Glu" or "Ser" or "Cys" or " "

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<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
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<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
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<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 565
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Asp Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys
    290                 295                 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320

Thr Val Tyr Ala Val Glu Phe Asp Tyr Pro Gly Ser Gly Tyr Tyr His
                325                 330                 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 566
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<220>
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<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<223> /note="Residues given in the sequence have no preference
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<220>
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<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<223> /note="Residues given in the sequence have no preference
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<223> /replace="Ser"

<220>

<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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as SEQ ID NOS 317-321"

<220>
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<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
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<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<220>
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<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

<220>
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<223> /note="Residues given in the sequence have no preference
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<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
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<220>
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<223> /replace="Gly" or "Ser" or " "

<220>
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<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

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<220>
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<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 566
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

```
            20                  25                  30

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Asp Gly Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
        275                 280                 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
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290 295 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305 310 315 320

Ile Thr Val Tyr Ala Val Glu Tyr Ser Phe Pro Gly Ala Gly Tyr Tyr
325 330 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
340 345 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 567
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<222> (8)..(8)
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<220>
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<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="His"

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<222> (12)..(12)
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<223> /replace="Cys"

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<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

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as SEQ ID NOS 317-321"

<220>
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or "Ala" or "Gln" or "Thr"

<220>
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or "Pro" or "Val"

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or "Asp"

<220>
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<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

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<223> /replace="Ala" or "Gly" or " "

<220>
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<220>
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<220>
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<220>
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<220>
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<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<220>
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<223> /replace="Gly" or "Ser" or " "

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<220>
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<220>
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<220>
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<220>
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<223> /replace="Glu" or " "

<220>
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<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 567
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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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 Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240


Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255


Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270


Asp Ala Pro Ala Glu Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285


Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys
    290                 295                 300


Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320


Thr Val Tyr Ala Val Glu Phe Asp Phe Pro Gly Ser Gly Tyr Tyr His
                325                 330                 335


Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350


Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 568
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<220>
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<220>
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<223> /replace="Lys" or " "

<220>
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<223> /replace="Ser" or " "

<220>
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<223> /replace="Asp" or "Gly"

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

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<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
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<220>
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<223> /note="Residue given in the sequence has no preference
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<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

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<220>
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<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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or "Asp"

<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
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<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

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<223> /note="Residues given in the sequence have no preference
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<223> /note="This region may encompass the sequences disclosed
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<220>
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<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<220>
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<223> /replace="Glu" or " "

<220>
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<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace=" "

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 568
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

```
    50                  55                  60

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Asp Glu Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
        275                 280                 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
    290                 295                 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305                 310                 315                 320

Ile Thr Val Tyr Ala Val Glu Phe Asp Phe Pro Gly Ala Gly Tyr Tyr
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325 330 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
340 345 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 569
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<220>
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<220>
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<223> /replace="His"

<220>
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<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="Ser"

<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
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<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
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<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
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<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

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<222> (240)..(240)
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<220>
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<220>
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<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
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<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

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<220>
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<223> /replace="Gly" or "Ser" or " "

<220>
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<220>
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<220>
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<223> /replace="Glu" or " "

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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>

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<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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as SEQ ID NOS 380-395, 635 or is absent"

<400> 569

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

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

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

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

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

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

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

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

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

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

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

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

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205
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```
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 Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Asp Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
        275                 280                 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
    290                 295                 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305                 310                 315                 320

Ile Thr Val Tyr Ala Val Glu Phe Asp Phe Pro Gly Ala Gly Tyr Tyr
                325                 330                 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
            340                 345                 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 570
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /replace="Glu" or " "

<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

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<220>
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<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<220>
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or "Ala" or "Gln" or "Thr"

<220>
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or "Pro" or "Val"

<220>
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or "Asp"

<220>
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<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<220>
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<222> (238)..(238)
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<220>
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<220>
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<222> (241)..(241)
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<220>
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<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
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<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

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as SEQ ID NOS 310-314 or 620-634"

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<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>

<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 570
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln

85 90 95

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Asp Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Phe Pro Phe Pro Gly Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp

355 360

<210> 571
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)

<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>

<221> VARIANT
<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference

with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 380-395, 635 or is absent"

<400> 571
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

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Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255


Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270


Asp Ala Pro Ala Glu Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285


Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys
    290                 295                 300


Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320


Thr Val Tyr Ala Val Glu Phe Asp Phe Pro Gly Ala Gly Tyr Tyr His
                325                 330                 335


Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350


Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 572
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "
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<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT

<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)

<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(363)
<223> /replace=" "

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 572
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

115 120 125

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Gly Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
275 280 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
290 295 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305 310 315 320

Ile Thr Val Tyr Ala Val Glu Phe Asp Phe Pro Gly Ser Gly Tyr Tyr
325 330 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
340 345 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 573
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)

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<223> /replace="Glu" or " "

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<223> /replace="Asp" or " "

<220>
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<220>
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as SEQ ID NOS 310-314 or 620-634"

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<223> /replace="Gly" or "Ser" or " "

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<223> /replace="Asp" or "Gly" or "Cys" or " "

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<223> /replace="Cys" or "Asp" or " "

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<223> /replace="Leu" or "Asp" or " "

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<223> /replace="Glu" or " "

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<223> /replace="Asp" or " "

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<223> /replace="Glu" or " "

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<223> /replace="Asp" or " "

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as SEQ ID NOS 380-395, 635 or is absent"

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Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
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Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270
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Asp Ala Pro Ala Ala Asp Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
275 280 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
290 295 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305 310 315 320

Ile Thr Val Tyr Ala Val Glu Phe Asn Phe Pro Gly Ala Gly Tyr Tyr
325 330 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
340 345 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 574
<211> 365
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<220>
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<223> /replace="Pro" or " "

<220>
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<223> /replace="Lys" or " "

<220>
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<223> /replace="Ser" or " "

<220>
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<223> /replace="Asp" or "Gly"

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

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<222> (11)..(11)
<223> /replace="His"

<220>
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<222> (12)..(12)
<223> /replace="Thr"

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<222> (13)..(13)
<223> /replace="Cys"

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<220>
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as SEQ ID NOS 317-321"

<220>
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or "Ala" or "Gln" or "Thr"

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or "Pro" or "Val"

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or "Asp"

<220>
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<223> /replace="Ser" or "Gly" or "Pro"

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<223> /replace="Gly" or "Ser" or " "

<220>
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<220>
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<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>

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<223> /replace="Gly" or " "

<220>
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<220>
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<220>
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<223> /replace="Asp" or " "

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<223> /note="Residues given in the sequence have no preference
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as SEQ ID NOS 380-395, 635 or is absent"

<400> 574
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

145 150 155 160

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Glu Ala Gly Lys His Tyr Gly Tyr Tyr Arg Ile Thr
275 280 285

Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro
290 295 300

Val Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
305 310 315 320

Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Asp Phe Pro Gly Ala Gly
325 330 335

Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys
340 345 350

Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360 365

<210> 575
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<222> (8)..(8)
<223> /replace="Asp" or "Gly"

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<223> /replace="Cys"

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<220>
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or "Ala" or "Gln" or "Thr"

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<223> /replace="Ala" or "Gly" or " "

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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
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<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<220>
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<220>
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<223> /replace="Asp" or " "

<220>
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<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
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<220>
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<223> /replace=" "

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 575
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Glu Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys
    290                 295                 300
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Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320


Thr Val Tyr Ala Val Glu Phe Thr Tyr Pro Gly Ser Gly Tyr Tyr His
                325                 330                 335


Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350


Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 576
<211> 362
<212> PRT
<213> Artificial Sequence

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<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<223> /replace="Lys" or " "

<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<223> /replace="Lys" or "Ser"

<220>
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<223> /note="Residues given in the sequence have no preference
      with respect to those in the annotations for said positions"
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<220>
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<222> (12)..(12)
<223> /replace="Thr"

<220>
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<223> /replace="Cys"

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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>

<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 576
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

180 185 190

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Ala Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Asp Phe Pro Gly Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 577
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (349)..(349)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(363)
<223> /replace=" "

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 577
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Gly Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
        275                 280                 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Ser
    290                 295                 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305                 310                 315                 320

Ile Thr Val Tyr Ala Val Glu Phe Asp Phe Pro Gly Ala Gly Tyr Tyr
                325                 330                 335
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His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
340 345 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 578
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT

<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>

<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)

<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 578
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Phe Asp Phe Pro Gly Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 579
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
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<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)

<223> /replace="Lys" or " "

<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<222> (9)..(9)
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<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<222> (232)..(232)
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<220>
<221> VARIANT

<222> (233)..(233)
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or "Ala" or "Gln" or "Thr"

<220>
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or "Pro" or "Val"

<220>
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<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
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<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (352)..(352)

<223> /replace="Glu" or " "

<220>
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<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
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<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
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<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 579
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Asp Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Phe Lys
    290                 295                 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320

Thr Val Tyr Ala Val Glu Phe Asp Tyr Pro Gly Ser Gly Tyr Tyr His
                325                 330                 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
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<210> 580
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<220>
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<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT

<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (347)..(347)

<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (349)..(349)
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<220>
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<220>
<221> VARIANT
<222> (351)..(351)
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<220>
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<222> (352)..(352)
<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (353)..(353)
<223> /replace="Glu" or " "

<220>
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<222> (354)..(354)
<223> /replace="Leu" or "Asp" or " "

<220>
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<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<222> (359)..(363)
<223> /replace=" "

<220>
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<222> (347)..(363)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 380-395, 635 or is absent"

<400> 580

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg

245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Ala Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
275 280 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Ser
290 295 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305 310 315 320

Ile Thr Val Tyr Ala Val Glu Tyr Asp Phe Pro Gly Ala Gly Tyr Tyr
325 330 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
340 345 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 581
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>

<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
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<223> /replace="Ser"

<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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as SEQ ID NOS 317-321"

<220>
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<222> (232)..(232)
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<220>
<221> VARIANT
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<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"

or "Pro" or "Val"

<220>
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<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
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<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<222> (237)..(237)
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<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<220>
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<220>
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<220>
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<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<220>
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Leu" or "Asp" or " "

<220>

<221> VARIANT
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<223> /replace="Glu" or " "

<220>
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<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
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<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
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<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 581
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Asp Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser Lys
    290                 295                 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320

Thr Val Tyr Ala Val Glu Phe Asp Phe Pro Gly Ser Gly Tyr Tyr His
                325                 330                 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 582
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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polypeptide"

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<223> /replace="Glu" or " "

<220>
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<222> (4)..(4)
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<220>
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<223> /replace="Lys" or " "

<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<220>
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<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
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or "Asp"

<220>
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<220>
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<222> (237)..(237)
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<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

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<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>

<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
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<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
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<222> (358)..(362)
<223> /replace=" "

<220>
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<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 582
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Ala Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu

275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Ser Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Phe Asp Phe Pro Gly Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 583
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
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<223> /replace="Glu" or " "

<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
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<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
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<220>
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<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
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<220>
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<222> (243)..(243)
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<220>
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<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)

<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<220>
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<223> /replace="Gly" or "Ser" or " "

<220>
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<220>
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<220>
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<222> (350)..(350)
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<220>
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<223> /replace="Cys" or "Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
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<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 583
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Ala Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys
    290                 295                 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320

Thr Val Tyr Ala Val Glu Phe Pro Phe Pro Gly Ser Gly Tyr Tyr His
                325                 330                 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 584
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
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<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<220>
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<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
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or "Pro" or "Val"

<220>
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or "Asp"

<220>
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<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
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<220>
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<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

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<223> /replace="Glu" or " "

<220>
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<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
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<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
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<222> (358)..(362)
<223> /replace=" "

<220>
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<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 584
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

35 40 45

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Ser Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile

305 310 315 320

Thr Val Tyr Ala Val Glu Phe Asp Tyr Pro Gly Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 585
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<220>
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<223> /replace="Glu" or " "

<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<220>
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<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

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<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
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<220>
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<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

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as SEQ ID NOS 317-321"

<220>
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<220>
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<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
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or "Asp"

<220>
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<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<222> (237)..(237)

<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>

<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
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<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (349)..(349)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<222> (352)..(352)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or " "

<220>
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<222> (354)..(354)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT

<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(363)
<223> /replace=" "

<220>
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<222> (347)..(363)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 585

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

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

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

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

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

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

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

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

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

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

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190
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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 Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Asp Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
        275                 280                 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
    290                 295                 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305                 310                 315                 320

Ile Thr Val Tyr Ala Val Glu Phe Asp Phe Pro Gly Ala Gly Tyr Tyr
                325                 330                 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
            340                 345                 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 586
<211> 364
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
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<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="Ser"

<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>

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<222> (232)..(232)
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<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
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<222> (235)..(235)
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or "Asp"

<220>
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<222> (236)..(236)
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<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

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<222> (238)..(238)
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>

<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<220>
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<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (351)..(351)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<223> /replace="Cys" or "Asp" or " "

<220>
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<220>
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<222> (357)..(357)
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as SEQ ID NOS 380-395, 635 or is absent"

<400> 586
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

65 70 75 80

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

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

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Gly Ala Ala Ser Tyr Gly Tyr Tyr Arg Ile Thr Tyr
275 280 285

Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val
290 295 300

Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr
305 310 315 320

Thr Ile Thr Val Tyr Ala Val Glu Phe Pro Phe Pro Gly Ala Gly Tyr
325 330 335

Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro

340 345 350

Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 587
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<220>
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<223> /replace="Glu" or " "

<220>
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<222> (4)..(4)
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<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

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<222> (11)..(11)
<223> /replace="His"

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<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
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<223> /note="Residues given in the sequence have no preference
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with respect to the annotation for said position"

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as SEQ ID NOS 317-321"

<220>
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<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<220>
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<222> (235)..(235)
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or "Asp"

<220>
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<220>
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<222> (237)..(237)
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<220>

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<223> /replace="Ala" or "Gly" or " "

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<220>
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<220>
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<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)

<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
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<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 587
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

```
Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240


Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255


Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270


Asp Ala Pro Ala Gly Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285


Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys
    290                 295                 300


Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320


Thr Val Tyr Ala Val Glu Phe Asp Phe Pro Gly Ser Gly Tyr Tyr His
                325                 330                 335


Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350


Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 588
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
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<222> (1)..(2)
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<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "
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<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"

or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 588
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala

100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Pro Pro Ala Glu Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Phe Asn Phe Pro Gly Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 589

<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature

<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature

<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 380-395, 635 or is absent"

<400> 589
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Ser Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Phe Asp Phe Pro Gly Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 590
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)

<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
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or "Asp"

<220>
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<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<222> (242)..(242)
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<220>
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<223> /replace="Ser" or "Gln" or "Gly" or " "

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<223> /replace="Asp" or "Ser" or "Gly" or " "

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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
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<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT

<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<222> (346)..(346)
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<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
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<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)

<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
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<222> (358)..(362)
<223> /replace=" "

<220>
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<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 590
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr

130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Ile Thr Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asn Pro Pro Asp Val Asn Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Leu Gln Glu Phe Thr Val Pro Val Ser Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Pro Tyr Ala His Ala Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 591
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
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<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT

<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<222> (347)..(347)
<223> /replace="Gly" or " "

<220>
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<222> (348)..(348)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (353)..(353)
<223> /replace="Glu" or " "

<220>
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<222> (354)..(354)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
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<223> /replace="Glu" or " "

<220>
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<222> (356)..(356)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
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<222> (359)..(363)
<223> /replace=" "

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 591
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Gly Asp Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
        275                 280                 285
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Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
290 295 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305 310 315 320

Ile Thr Val Tyr Ala Val Glu Phe Asp Phe Pro Gly Ala Gly Tyr Tyr
325 330 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
340 345 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 592
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<220>
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<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<222> (9)..(9)
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<220>

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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<223> /replace="Cys"

<220>
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with respect to those in the annotations for said positions"

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<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<222> (232)..(232)
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<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
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<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT

<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
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<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<220>
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<220>
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<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<222> (352)..(352)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or " "

<220>
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<222> (354)..(354)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Asp" or " "

<220>

<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
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<222> (359)..(363)
<223> /replace=" "

<220>
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<222> (347)..(363)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 592

Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala
1				5				10					15		
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
		20					25					30			
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
	35					40					45				
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
50					55					60					
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
65				70					75					80	
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
			85					90					95		
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
		100					105					110			
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
	115					120					125				
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr
130					135					140					
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
145				150					155					160	
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr

165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Gly Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
275 280 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
290 295 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305 310 315 320

Ile Thr Val Tyr Ala Val Glu Phe Thr Phe Pro Gly Ala Gly Tyr Tyr
325 330 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
340 345 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 593
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<222> (1)..(2)
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<220>

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<223> /replace="Glu" or " "

<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<222> (9)..(9)
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<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (11)..(11)
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<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
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<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>

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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<220>
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<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
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or "Asp"

<220>
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<222> (237)..(237)
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<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<223> /replace="Ser" or "Gln" or "Gly" or " "

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<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
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<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<222> (347)..(347)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Gly" or "Ser" or " "

<220>
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<220>
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<222> (350)..(350)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>

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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<222> (352)..(352)
<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (353)..(353)
<223> /replace="Glu" or " "

<220>
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<222> (354)..(354)
<223> /replace="Leu" or "Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(363)
<223> /replace=" "

<220>
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<222> (347)..(363)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (347)..(363)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 593
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

```
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Glu Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
        275                 280                 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
    290                 295                 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305                 310                 315                 320
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Ile Thr Val Tyr Ala Val Glu Phe Asp Phe Pro Gly Ala Gly Tyr Tyr
325 330 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
340 345 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 594
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)

<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
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<220>
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<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
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<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
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<223> /replace="Ser" or "Glu" or "Gly" or " "

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<220>
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<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

<220>
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<223> /note="Residues given in the sequence have no preference
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<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<220>
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<223> /replace="Gly" or "Ser" or " "

<220>
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<220>
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<220>
<221> VARIANT
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<222> (351)..(351)
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<220>
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<223> /replace="Glu" or " "

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<220>
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<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<220>
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<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 594
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Glu Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Asp Phe Pro Gly Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 595
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<220>
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<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
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<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

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<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
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<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
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<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

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<222> (242)..(242)
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<220>
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<220>
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<220>
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<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<223> /replace="Gly" or " "

<220>
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<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (351)..(351)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<220>
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<222> (354)..(354)
<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
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<222> (359)..(359)
<223> /replace="Glu" or " "

<220>
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<222> (360)..(360)
<223> /replace="Asp" or " "

<220>
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<222> (361)..(365)
<223> /replace=" "

<220>
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<222> (349)..(365)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (349)..(365)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 595
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

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Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Glu Pro Phe Ser Arg Leu Pro Gly Gly Gly Glu Tyr Tyr Arg Ile Thr
        275                 280                 285

Tyr Gly Glu Thr Gly Gly Asn Ser Pro Leu Gln Gln Phe Thr Val Pro
    290                 295                 300

Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
305                 310                 315                 320

Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Tyr Pro Phe Ser Gly
                325                 330                 335

Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys
            340                 345                 350
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Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360 365

<210> 596
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<223> /replace="Lys" or "Ser"

<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

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<222> (11)..(11)
<223> /replace="His"

<220>
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<222> (12)..(12)
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<220>

<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
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<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

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<222> (233)..(233)
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or "Ala" or "Gln" or "Thr"

<220>
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or "Pro" or "Val"

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or "Asp"

<220>
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<220>
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<222> (240)..(240)
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<223> /replace="Ser" or "Gln" or "Gly" or " "

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<223> /replace="Asp" or "Ser" or "Gly" or " "

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<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

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<223> /note="Residues given in the sequence have no preference
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<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

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<220>
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<223> /replace="Gly" or "Ser" or " "

<220>
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<220>
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<222> (352)..(352)
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<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Leu" or "Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace=" "

<220>
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<222> (347)..(363)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 596
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala

225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Asp Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
275 280 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser
290 295 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305 310 315 320

Ile Thr Val Tyr Ala Val Glu Tyr Asp Phe Pro Gly Ala Gly Tyr Tyr
325 330 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
340 345 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 597
<211> 363
<212> PRT
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<220>
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<220>
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<222> (4)..(4)
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<220>
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<222> (5)..(5)
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<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="His"

<220>
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<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<223> /note="Residues given in the sequence have no preference
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<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
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<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<222> (232)..(232)
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<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
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<222> (235)..(235)
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or "Asp"

<220>
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<220>
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<222> (237)..(237)
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<222> (238)..(238)
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

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<222> (240)..(240)
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<220>
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<220>
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<220>
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<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>

<221> VARIANT
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<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

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<220>
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<220>
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<220>
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<220>
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<220>
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<223> /replace="Leu" or "Asp" or " "

<220>
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<220>
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<223> /replace="Asp" or " "

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<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace=" "

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with respect to those in the annotations for said positions"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 597
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

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Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Gly Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
        275                 280                 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
    290                 295                 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305                 310                 315                 320

Ile Thr Val Tyr Ala Val Glu Tyr Asn Phe Ile Gly Ala Gly Tyr Tyr
                325                 330                 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
            340                 345                 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
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<210> 598
<211> 363
<212> PRT

<213> Artificial Sequence

<220>
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<220>
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<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="His"

<220>
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<222> (12)..(12)
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<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference

with respect to those in the annotations for said positions"

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<223> /replace="Ser"

<220>
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with respect to the annotation for said position"

<220>
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as SEQ ID NOS 317-321"

<220>
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or "Ala" or "Gln" or "Thr"

<220>
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or "Pro" or "Val"

<220>
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or "Asp"

<220>
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<220>
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<220>
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<222> (238)..(238)
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<220>
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<223> /replace="Ala" or "Gly" or " "

<220>
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<220>

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<220>
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<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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as SEQ ID NOS 310-314 or 620-634"

<220>
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<220>
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<222> (348)..(348)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (349)..(349)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(363)
<223> /replace=" "

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="This region may encompass the sequences disclosed

as SEQ ID NOS 380-395, 635 or is absent"

<400> 598
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp

260 265 270

Asp Ala Pro Ala Asp Gly Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
275 280 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
290 295 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305 310 315 320

Ile Thr Val Tyr Ala Val Glu Phe Pro Tyr Pro Phe Ala Gly Tyr Tyr
325 330 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
340 345 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 599
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT

<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(359)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (360)..(360)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (361)..(365)
<223> /replace=" "

<220>
<221> misc_feature
<222> (349)..(365)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (349)..(365)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 599
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

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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 Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Ser Glu Lys Leu Asp Gly Lys Ala Arg Arg Gly Tyr Tyr Arg Ile Thr
        275                 280                 285

Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Gln Phe Thr Val Pro
    290                 295                 300

Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
305                 310                 315                 320

Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro Tyr Asp His Ser Gly
                325                 330                 335

Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys
            340                 345                 350

Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360                 365


<210> 600
<211> 366
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>

<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (359)..(359)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (360)..(360)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (361)..(361)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (362)..(366)
<223> /replace=" "

<220>
<221> misc_feature
<222> (350)..(366)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (350)..(366)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 600
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro

20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Ser Pro Arg Asp Ser Thr Gly Leu Val Arg Arg Gly Tyr Tyr Arg Ile
275 280 285

Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Gln Phe Thr Val

290 295 300

Pro Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val
305 310 315 320

Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Pro Tyr Asp His Ser
325 330 335

Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu
340 345 350

Lys Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360 365

<210> 601
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)

<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
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<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
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<222> (250)..(250)
<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<222> (349)..(349)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (351)..(351)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (352)..(352)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
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<222> (353)..(353)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(359)

<223> /replace="Glu" or " "

<220>
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<222> (360)..(360)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (361)..(365)
<223> /replace=" "

<220>
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<222> (349)..(365)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (349)..(365)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 601
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

```
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190


Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205


Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220


Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240


Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255


Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270


Gly Asp Val Arg Thr Asn Glu Ala Arg Gln Gly Tyr Tyr Arg Ile Thr
        275                 280                 285


Tyr Gly Glu Thr Gly Gly Asn Ser Pro Leu Gln Gly Phe Thr Val Pro
    290                 295                 300


Gly Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp
305                 310                 315                 320


Tyr Thr Ile Thr Val Tyr Ala Val Glu Tyr Thr Tyr Glu His Ser Gly
                325                 330                 335


Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys
            340                 345                 350


Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360                 365


<210> 602
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
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<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)

<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT

<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (349)..(349)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (350)..(350)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)

<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (353)..(353)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (359)..(363)
<223> /replace=" "

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (347)..(363)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 602
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val

50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Gly Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
275 280 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
290 295 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305 310 315 320

Ile Thr Val Tyr Ala Val Glu Phe Asp Phe Val Gly Ala Gly Tyr Tyr

325 330 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
340 345 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 603
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT

<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>

<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 603

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Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                  10                  15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205
```

```
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Ala Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys
    290                 295                 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320

Thr Val Tyr Ala Val Glu Tyr Asp Phe Ala Gly Ser Gly Tyr Tyr His
                325                 330                 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 604
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<222> (232)..(232)
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<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
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<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
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<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
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<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>

<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 604
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln

85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Asp Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ser Ser Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Phe Ala Phe Pro Gly Ala Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp

355 360

<210> 605
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)

<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>

<221> VARIANT
<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference

with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 380-395, 635 or is absent"

<400> 605
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

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Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255


Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270


Asp Ala Pro Ala Gly Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285


Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys
    290                 295                 300


Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320


Thr Val Tyr Ala Val Glu Tyr Asp Phe Ala Gly Ser Gly Tyr Tyr His
                325                 330                 335


Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350


Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360


<210> 606
<211> 364
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
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<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "
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<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT

<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
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<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
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<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)

<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(358)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (359)..(359)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (360)..(364)
<223> /replace=" "

<220>
<221> misc_feature
<222> (348)..(364)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (348)..(364)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 606
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Glu Ala Glu Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr
275 280 285

Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val
290 295 300

Ser Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr
305 310 315 320

Thr Ile Thr Val Tyr Ala Val Glu Tyr Val Phe Pro Gly Ala Gly Tyr
325 330 335

Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro
340 345 350

Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 607
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> VARIANT
<222> (1)..(2)
<223> /replace=" "

<220>
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as SEQ ID NOS 317-321"

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or "Ala" or "Gln" or "Thr"

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<220>
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<220>
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<223> /replace="Gly" or " "

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<220>
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<223> /replace="Gly" or "Ser" or " "

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<223> /replace="Leu" or "Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace=" "

<220>
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<220>
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as SEQ ID NOS 380-395, 635 or is absent"

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Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
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Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270
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Asp Ala Pro Ala Glu Gly Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly
275 280 285

Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser
290 295 300

Lys Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
305 310 315 320

Ile Thr Val Tyr Ala Val Glu Tyr Pro Tyr Pro Phe Ala Gly Tyr Tyr
325 330 335

His Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser
340 345 350

Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 608
<211> 362
<212> PRT
<213> Artificial Sequence

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<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<223> /replace="Lys" or " "

<220>
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<223> /replace="Ser" or " "

<220>
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<223> /replace="Asp" or "Gly"

<220>
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<220>
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<222> (11)..(11)
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<222> (12)..(12)
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<223> /note="Residues given in the sequence have no preference
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<220>
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<220>
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<220>
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<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

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or "Asp"

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<223> /replace="Gly" or " "

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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
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<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

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<223> /replace="Gly" or " "

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<400> 608
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Thr Asp Val Pro Arg
245 250 255

Asp Met Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Gln Pro Pro Ala Val Thr Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Thr Leu Gln Gln Phe Thr Val Pro Val Tyr Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Pro Tyr Asp His Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 609
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<223> /replace="Glu" or " "

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<220>
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<220>
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<220>
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<220>
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<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<222> (358)..(362)
<223> /replace=" "

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 609
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

```
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Ala Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys
    290                 295                 300
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Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Phe Asp Tyr Pro Gly Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 610
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<223> /replace="Lys" or " "

<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<220>
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<222> (9)..(9)
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<220>
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<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

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<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
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<222> (13)..(13)
<223> /replace="Cys"

<220>
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<223> /note="Residues given in the sequence have no preference
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<220>
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<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

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<220>
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or "Ala" or "Gln" or "Thr"

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or "Pro" or "Val"

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<220>
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<220>
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<220>
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<222> (240)..(240)
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<220>
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<220>
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<223> /replace="Gly" or " "

<220>
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<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

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<223> /note="Residues given in the sequence have no preference
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<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

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<223> /replace="Gly" or " "

<220>
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<223> /replace="Gly" or "Ser" or " "

<220>
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<220>
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<220>
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<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Leu" or "Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<222> (358)..(362)
<223> /replace=" "

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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as SEQ ID NOS 380-395, 635 or is absent"

<400> 610
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Ile Val Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Pro Pro Ala Gly Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Lys Gln Gln Phe Thr Val Pro Gly Tyr Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Pro Tyr Asp His Ser Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 611
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /replace=" "

<220>
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<223> /replace="Glu" or " "

<220>
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<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
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<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
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<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
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<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (11)..(11)
<223> /replace="His"

<220>
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<223> /replace="Thr"

<220>
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<223> /replace="Cys"

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<220>
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with respect to the annotation for said position"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
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<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
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<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
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<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
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<220>
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<223> /replace="Ala" or "Gly" or " "

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<220>
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<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<220>
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<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<220>
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<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

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<220>
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<220>
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<223> /replace="Glu" or " "

<220>
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<220>
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<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace=" "

<220>
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<223> /note="Residues given in the sequence have no preference
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<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 611
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

```
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ala Ala Gly Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Val Ser Lys
    290                 295                 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320

Thr Val Tyr Ala Val Glu Tyr Asp Phe Pro Gly Ser Gly Tyr Tyr His
                325                 330                 335
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Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 612
<211> 362
<212> PRT
<213> Artificial Sequence

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<220>
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<220>
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<223> /replace="Lys" or " "

<220>
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<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
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<223> /replace="Asp" or "Gly"

<220>
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<223> /replace="Lys" or "Ser"

<220>
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<220>
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<222> (11)..(11)
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<220>
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<222> (12)..(12)
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<220>
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<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<223> /replace="Ser"

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with respect to the annotation for said position"

<220>
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as SEQ ID NOS 317-321"

<220>
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or "Ala" or "Gln" or "Thr"

<220>
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or "Pro" or "Val"

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or "Asp"

<220>
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<220>
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<220>
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<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
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<220>
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<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
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<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace="Gly" or " "

<220>
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<223> /replace=" "

<220>
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<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>

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<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
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<223> /replace="Gly" or " "

<220>
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<220>
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<220>
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<220>
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<220>
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<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)

<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 612
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys

210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Ala Pro Pro Ser Asp Ala Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ile Gly Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Tyr Pro Tyr Ser His Ala Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 613
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)

<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
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<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT

<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT

<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (346)..(346)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)

<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 613
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

```
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Pro Pro Ser Asp Asp Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ile Gly Lys
    290                 295                 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320

Thr Val Tyr Ala Val Glu Phe Pro Trp Pro His Ala Gly Tyr Tyr His
                325                 330                 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360
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<210> 614
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>
<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"
or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT

<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
<221> VARIANT
<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (249)..(249)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace=" "

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (232)..(250)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

<220>
<221> VARIANT
<222> (346)..(346)

<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (347)..(347)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (348)..(348)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (349)..(349)
<223> /replace="Asp" or "Gly" or "Cys" or " "

<220>
<221> VARIANT
<222> (350)..(350)
<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
<221> VARIANT
<222> (351)..(351)
<223> /replace="Cys" or "Asp" or " "

<220>
<221> VARIANT
<222> (352)..(352)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (353)..(353)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (354)..(354)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (355)..(355)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (356)..(356)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (357)..(357)
<223> /replace="Asp" or " "

<220>
<221> VARIANT
<222> (358)..(362)
<223> /replace=" "

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 380-395, 635 or is absent"

<400> 614

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225 230 235 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg

245 250 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
260 265 270

Asp Ala Pro Ala Asp Asp Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
275 280 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ile Gly Lys
290 295 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305 310 315 320

Thr Val Tyr Ala Val Glu Phe Pro Trp Pro His Ala Gly Tyr Tyr His
325 330 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
340 345 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
355 360

<210> 615
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> VARIANT
<222> (1)..(2)
<223> /replace=" "

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Glu" or " "

<220>
<221> VARIANT
<222> (4)..(4)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Lys" or " "

<220>
<221> VARIANT
<222> (6)..(7)
<223> /replace="Ser" or " "

<220>

<221> VARIANT
<222> (8)..(8)
<223> /replace="Asp" or "Gly"

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Lys" or "Ser"

<220>
<221> misc_feature
<222> (1)..(9)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="His"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Thr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Cys"

<220>
<221> misc_feature
<222> (11)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (23)..(23)
<223> /replace="Ser"

<220>
<221> misc_feature
<222> (23)..(23)
<223> /note="Residue given in the sequence has no preference
with respect to the annotation for said position"

<220>
<221> misc_feature
<222> (1)..(24)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 317-321"

<220>
<221> VARIANT
<222> (232)..(232)
<223> /replace="Ala" or "Gly" or "Gln" or "Glu" or "Thr"

<220>
<221> VARIANT
<222> (233)..(233)
<223> /replace="Gly" or "Ser" or "Pro" or "Leu" or "Val"
or "Ala" or "Gln" or "Thr"

<220>
<221> VARIANT
<222> (234)..(234)
<223> /replace="Gly" or "Asp" or "Gln" or "Ala" or "Ser"

or "Pro" or "Val"

<220>
<221> VARIANT
<222> (235)..(235)
<223> /replace="Gly" or "Ser" or "Glu" or "Leu" or "Ala"
or "Asp"

<220>
<221> VARIANT
<222> (236)..(236)
<223> /replace="Gly" or "Pro" or "Glu" or "Ser" or "Ala"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Ser" or "Gly" or "Pro"

<220>
<221> VARIANT
<222> (238)..(238)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (239)..(239)
<223> /replace="Ala" or "Gly" or " "

<220>
<221> VARIANT
<222> (240)..(240)
<223> /replace="Gly" or "Ser" or " "

<220>
<221> VARIANT
<222> (241)..(241)
<223> /replace="Ser" or "Glu" or "Gly" or " "

<220>
<221> VARIANT
<222> (242)..(242)
<223> /replace="Gly" or "Ala" or "Ser" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Ser" or "Gln" or "Gly" or " "

<220>
<221> VARIANT
<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
<221> VARIANT
<222> (245)..(245)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (246)..(246)
<223> /replace="Glu" or " "

<220>
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<222> (247)..(247)
<223> /replace="Leu" or " "

<220>
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<222> (248)..(248)
<223> /replace="Asp" or " "

<220>
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<220>
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<220>
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<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 310-314 or 620-634"

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<222> (347)..(347)
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<220>
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<220>
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<223> /replace="Glu" or " "

<220>
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<220>

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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (346)..(362)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395, 635 or is absent"

<400> 615

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Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125
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Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys Glu Leu Gln Leu Glu Glu Ser Ala
225                 230                 235                 240

Ala Glu Ala Gln Asp Gly Glu Leu Asp Gly Val Ser Asp Val Pro Arg
                245                 250                 255

Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp
            260                 265                 270

Asp Ala Pro Ser Asp Asp Tyr Gly Tyr Tyr Arg Ile Thr Tyr Gly Glu
        275                 280                 285

Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Ile Gly Lys
    290                 295                 300

Gly Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile
305                 310                 315                 320

Thr Val Tyr Ala Val Glu Phe Pro Trp Pro His Ala Gly Tyr Tyr His
                325                 330                 335

Arg Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys Pro Ser Gln
            340                 345                 350

Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp
        355                 360
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<210> 616
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (1)..(10)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 371-379 or is absent"

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<222> (98)..(98)
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<220>
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<223> /replace="Gly" or "Ser" or " "

<220>
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<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Cys" or "Gly" or " "

<220>
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (104)..(104)
<223> /replace="Glu" or " "

<220>
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<222> (105)..(105)
<223> /replace="Leu" or "Asp" or " "

<220>
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<222> (106)..(106)
<223> /replace="Glu" or " "

<220>
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<222> (107)..(107)
<223> /replace="Asp" or " "

<220>
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<222> (108)..(108)
<223> /replace="Glu" or " "

<220>
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<222> (109)..(109)
<223> /replace="Asp" or " "

<220>
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<222> (110)..(114)
<223> /replace=" "

<220>
<221> misc_feature
<222> (98)..(114)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395 or is absent"

<220>
<221> VARIANT
<222> (115)..(115)
<223> /replace="Pro" or "Ser"

<220>
<221> VARIANT
<222> (116)..(116)
<223> /replace="Ser" or "Ala" or "Thr" or "Pro"

<220>
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<222> (117)..(117)
<223> /replace="Ser" or "Ala" or "Glu" or "Pro" or "Thr"

<220>
<221> VARIANT
<222> (118)..(118)
<223> /replace="Ser" or "Ala" or "Pro" or "Val" or "Glu"
or "Thr"

<220>
<221> VARIANT
<222> (119)..(119)
<223> /replace="Gly" or "Ala" or "Thr" or "Pro" or " "

<220>
<221> VARIANT
<222> (120)..(120)
<223> /replace="Ser" or "Ala" or "Glu" or "Pro" or "Thr"
or " "

<220>
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<222> (121)..(121)
<223> /replace="Ser" or "Ala" or "Pro" or "Thr" or " "

<220>
<221> VARIANT
<222> (122)..(122)
<223> /replace="Ser" or "Ala" or "Glu" or "Pro" or " "

<220>
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<222> (123)..(123)
<223> /replace="Ser" or "Gly" or "Ala" or "Glu" or "Pro"
or "Thr" or " "

<220>
<221> VARIANT
<222> (124)..(124)
<223> /replace="Gly" or "Ala" or "Pro" or "Val" or " "

<220>
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<222> (125)..(125)
<223> /replace="Ser" or "Ala" or "Pro" or " "

<220>
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<222> (126)..(126)
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<220>
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<222> (127)..(127)
<223> /replace="Ser" or "Pro" or " "

<220>
<221> VARIANT
<222> (128)..(128)
<223> /replace="Ser" or "Ala" or " "

<220>
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<222> (129)..(129)
<223> /replace="Glu" or "Pro" or " "

<220>
<221> VARIANT
<222> (130)..(130)
<223> /replace="Ala" or " "

<220>
<221> VARIANT
<222> (131)..(131)
<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (132)..(132)
<223> /replace="Ala" or " "

<220>
<221> VARIANT
<222> (133)..(149)
<223> /replace=" "

<220>
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<222> (115)..(149)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 396-419"

<220>
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<222> (150)..(159)
<223> /replace=" "

<220>
<221> misc_feature
<222> (150)..(159)

<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 371-379 or is absent"

<220>
<221> misc_feature
<222> (98)..(159)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
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<222> (242)..(242)
<223> /replace="Gly" or " "

<220>
<221> VARIANT
<222> (243)..(243)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (244)..(244)
<223> /replace="Asp" or "Ser" or "Gly" or " "

<220>
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<223> /replace="Asp" or "Cys" or "Gly" or " "

<220>
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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (248)..(248)
<223> /replace="Glu" or " "

<220>
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<222> (249)..(249)
<223> /replace="Leu" or "Asp" or " "

<220>
<221> VARIANT
<222> (250)..(250)
<223> /replace="Glu" or " "

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<222> (251)..(251)
<223> /replace="Asp" or " "

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<222> (252)..(252)
<223> /replace="Glu" or " "

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<222> (253)..(253)
<223> /replace="Asp" or " "

<220>
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<222> (254)..(258)
<223> /replace=" "

<220>
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<222> (242)..(258)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (242)..(258)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395 or is not present"

<400> 616
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp Val Pro Pro Ser Asp Asp Tyr Gly
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro
65 70 75 80

Trp Pro His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
85 90 95

Thr Glu Ile Glu Lys Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp
100 105 110

Glu Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Gly Gly Gly Gly Ser Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu
145 150 155 160

Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp His Ser Tyr
165 170 175

Tyr Glu Gln Asn Ser Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
180 185 190

Asn Ser Pro Val Gln Glu Phe Thr Val Pro Tyr Ser Gln Thr Thr Ala

195 200 205

Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr
210 215 220

Ala Val Tyr Gly Ser Lys Tyr Tyr Tyr Pro Ile Ser Ile Asn Tyr Arg
225 230 235 240

Thr Glu Ile Glu Lys Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp
245 250 255

Glu Asp

<210> 617
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /replace=" "

<220>
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<222> (1)..(10)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
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<222> (1)..(10)
<223> /note="This region may encompass the sequences disclosed as SEQ ID NOS 371-379 or is absent"

<220>
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<222> (93)..(93)
<223> /replace="Gly" or " "

<220>
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<222> (94)..(94)
<223> /replace="Gly" or "Ser" or " "

<220>
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<222> (95)..(95)
<223> /replace="Asp" or "Ser" or "Gly" or " "

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<223> /replace="Asp" or "Cys" or "Gly" or " "

<220>

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<223> /replace="Glu" or "Ser" or "Cys" or " "

<220>
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<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (99)..(99)
<223> /replace="Glu" or " "

<220>
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<222> (100)..(100)
<223> /replace="Leu" or "Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<223> /replace="Glu" or " "

<220>
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<220>
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<223> /replace=" "

<220>
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<222> (93)..(109)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395 or is absent"

<220>
<221> VARIANT
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<220>
<221> VARIANT
<222> (111)..(111)
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<220>
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<222> (112)..(112)
<223> /replace="Ser" or "Ala" or "Glu" or "Pro" or "Thr"

<220>
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<222> (113)..(113)

<223> /replace="Ser" or "Ala" or "Pro" or "Val" or "Glu"
or "Thr"

<220>
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<222> (114)..(114)
<223> /replace="Gly" or "Ala" or "Thr" or "Pro" or " "

<220>
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<223> /replace="Ser" or "Ala" or "Glu" or "Pro" or "Thr"
or " "

<220>
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<223> /replace="Ser" or "Ala" or "Pro" or "Thr" or " "

<220>
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or "Thr" or " "

<220>
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<223> /replace="Gly" or "Ala" or "Pro" or "Val" or " "

<220>
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<222> (120)..(120)
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<220>
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<223> /replace="Ser" or "Glu" or "Pro" or "Ala" or " "

<220>
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<222> (122)..(122)
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<220>
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<223> /replace="Glu" or "Pro" or " "

<220>
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<222> (125)..(125)
<223> /replace="Ala" or " "

<220>
<221> VARIANT
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<223> /replace="Pro" or " "

<220>
<221> VARIANT
<222> (127)..(127)
<223> /replace="Ala" or " "

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<222> (128)..(144)
<223> /replace=" "

<220>
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<223> /replace=" "

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<222> (145)..(154)
<223> /note="This region may encompass the sequences disclosed
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with respect to those in the annotations for said positions"

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<223> /replace="Gly" or "Ser" or " "

<220>
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<220>
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<220>
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<222> (247)..(247)
<223> /replace="Cys" or "Asp" or " "

<220>
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<222> (248)..(248)
<223> /replace="Glu" or " "

<220>
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<220>
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<223> /replace="Glu" or " "

<220>
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<223> /replace="Asp" or " "

<220>
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<222> (252)..(252)
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<220>
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<220>
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<223> /replace=" "

<220>
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<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> misc_feature
<222> (242)..(258)
<223> /note="This region may encompass the sequences disclosed
as SEQ ID NOS 380-395 or is absent"

<400> 617
Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
1 5 10 15

Pro Thr Ser Leu Leu Ile Ser Trp His Ser Tyr Tyr Glu Gln Asn Ser
20 25 30

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
35 40 45

Glu Phe Thr Val Pro Tyr Ser Gln Thr Thr Ala Thr Ile Ser Gly Leu
50 55 60

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Tyr Gly Ser
65 70 75 80

Lys Tyr Tyr Tyr Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Glu Lys
85 90 95

Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp Glu Asp Gly Gly Gly
100 105 110

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Met Gly Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr
145 150 155 160

Pro Thr Ser Leu Leu Ile Ser Trp Val Pro Pro Ser Asp Asp Tyr Gly
165 170 175

Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln
180 185 190

Glu Phe Thr Val Pro Ile Gly Lys Gly Thr Ala Thr Ile Ser Gly Leu
195 200 205

Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Glu Phe Pro
210 215 220

Trp Pro His Ala Gly Tyr Tyr His Arg Pro Ile Ser Ile Asn Tyr Arg
225 230 235 240

Thr Glu Ile Glu Lys Pro Ser Gln Glu Asp Glu Asp Glu Asp Glu Asp
245 250 255

Glu Asp

<210> 618

<400> 618
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<210> 619

<400> 619
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<210> 620
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 620
Lys Ala Gly Gly Gly Gly Ser Gly
1 5

<210> 621
<211> 13

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 621
Lys Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1 5 10

<210> 622
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 622
Lys Gln Pro Asp Glu Pro Gly Gly Ser
1 5

<210> 623
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 623
Lys Glu Leu Gln Leu Glu Glu Ser Ala Ala Glu Ala Gln Asp Gly Glu
1 5 10 15

Leu Asp

<210> 624
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 624
Lys Thr Val Ala Ala Pro Ser
1 5

<210> 625
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 625
Lys Ala Gly Gly Gly Gly Ser Gly Gly
1 5

<210> 626
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 626
Lys Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
1 5 10

<210> 627
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 627
Lys Gln Pro Asp Glu Pro Gly Gly Ser Gly
1 5 10

<210> 628
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 628
Lys Glu Leu Gln Leu Glu Glu Ser Ala Ala Glu Ala Gln Asp Gly Glu
1 5 10 15

Leu Asp Gly

<210> 629
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 629
Lys Thr Val Ala Ala Pro Ser Gly
1 5

<210> 630
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<220>
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<400> 630
Ala Gly Gly Gly Gly Ser Gly Gly
1 5

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<400> 632
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Asp Gly

<210> 634
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Thr Val Ala Ala Pro Ser Gly
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<210> 635
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Glu Ile Glu Lys
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<210> 636
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Ile Asn Tyr Arg Thr
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<400> 637
His His His His His His
1 5

<210> 638
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<400> 638
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<210> 639
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<400> 639
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<400> 640
Tyr Gly Ser Lys Tyr Tyr Tyr
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<210> 641
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<400> 641
Ser Trp His Ser Tyr Tyr Glu Gln Asn Ser
1 5 10

<210> 642
<211> 6
<212> PRT
<213> Artificial Sequence

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<400> 642
Pro Tyr Ser Gln Thr Thr
1 5

<210> 643
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<400> 643
Tyr Gly Ser Lys Tyr Tyr Tyr Pro
1 5