

SEQUENCE LISTING

<110> INTREXON CORPORATION

<120> EXPRESSION OF NOVEL CELL TAGS

<130> 50471-708.601

<140>

<141>

<150> 62/516,639

<151> 2017-06-07

<160> 240

<170> PatentIn version 3.5

<210> 1

<211> 66

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown:
GMCSFR alpha signal sequence

<400> 1

atgcttctcc tggtgacaag ccttctgctc tgtgagttac cacacccagc attcctcctg 60

atccca 66

<210> 2

<211> 22

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
GMCSFR alpha signal sequence

<400> 2

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro
20

<210> 3

<211> 60

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown:
Ig Kappa signal sequence

<400> 3

atgaggctcc ctgctcagct cctggggctg ctaatgctct gggtcccagg atccagtggg 60

<210> 4

<211> 20

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Ig Kappa signal sequence

<400> 4

Met	Arg	Leu	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Met	Leu	Trp	Val	Pro
1				5				10					15		

Gly	Ser	Ser	Gly
			20

<210> 5

<211> 54

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown:
Immunoglobulin E signal sequence

<400> 5

atggattgga cctggattct gtttctggtg gccgctgcca caagagtgca cagc 54

<210> 6

<211> 18

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Immunoglobulin E signal sequence

<400> 6

Met	Asp	Trp	Thr	Trp	Ile	Leu	Phe	Leu	Val	Ala	Ala	Ala	Thr	Arg	Val
1				5				10					15		

His Ser

<210> 7
<211> 63
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
CD8-alpha signal sequence

<400> 7
atggcgctgc ccgtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
ccg 63

<210> 8
<211> 21
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
CD8-alpha signal sequence

<400> 8
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro
20

<210> 9
<211> 63
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
TVB2(T21A) signal sequence

<400> 9
atggggcacca gcctcctctg ctggatggcc ctgtgtctcc tgggggcaga tcacgcagat 60
gct 63

<210> 10

<211> 21
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
TVB2(T21A) signal sequence

<400> 10

Met	Gly	Thr	Ser	Leu	Leu	Cys	Trp	Met	Ala	Leu	Cys	Leu	Leu	Gly	Ala
1				5				10					15		

Asp	His	Ala	Asp	Ala
			20	

<210> 11

<211> 72

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown:
CD52 signal sequence

<400> 11

atgaagcgcct	tcctcttcct	cctactcacc	atcagcctcc	tggttatggt	acagatacaa	60
-------------	------------	------------	------------	------------	------------	----

actggactct	ca	72
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<210> 12

<211> 24

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
CD52 signal sequence

<400> 12

Met	Lys	Arg	Phe	Leu	Phe	Leu	Leu	Leu	Thr	Ile	Ser	Leu	Leu	Val	Met
1				5				10					15		

Val	Gln	Ile	Gln	Thr	Gly	Leu	Ser
			20				

<210> 13

<211> 84

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown:

Low-affinity nerve growth factor receptor
(LNGFR, TNFRSF16) signal sequence

<400> 13

atgggggcag gtgccaccgg ccgcgccatg gacgggccgc gcctgctgct gttgctgctt 60

ctgggggtgt cccttgagg tgcc 84

<210> 14

<211> 28

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

Low-affinity nerve growth factor receptor
(LNGFR, TNFRSF16) signal sequence

<400> 14

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

Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala
20 25

<210> 15

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 15

ggaagcgga 9

<210> 16

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 16

Gly Ser Gly
1

<210> 17
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 17
agtggcagcg gc

12

<210> 18
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 18
Ser Gly Ser Gly
1

<210> 19
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 19
ggcggaggcg gaagcggagg cggaggctcc ggcggaggcg gaagc

45

<210> 20
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 20

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

<210> 21
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 21
ggtggcggtg gctcgggcgg tggtaggtcg ggtggcggcg gatctggtgg cggtggctcg 60

<210> 22
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 22
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 23
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 23
ggcagcacct ccggcagcgg caagcctggc agcggcgagg gcagcaccaa gggc 54

<210> 24
<211> 18
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 24

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15

Lys Gly

<210> 25

<211> 78

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown:
Glycophorin A (E91-R116) sequence

<400> 25

gagataacac tcattatattt tggggtgatg gctggtgtta ttggaacgat cctcttaatt 60

tcttacggta ttcgccga 78

<210> 26

<211> 26

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Glycophorin A (E91-R116) sequence

<400> 26

Glu Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile Gly Thr
1 5 10 15

Ile Leu Leu Ile Ser Tyr Gly Ile Arg Arg
20 25

<210> 27

<211> 69

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown:
Glycophorin A (I92-I114) sequence

<400> 27
ataacactca ttatTTTTGG ggtgatggct ggtgttattg gaacgacCCT cTTaatttct 60
tacggtatt 69

<210> 28
<211> 23
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Glycophorin A (I92-I114) sequence

<400> 28
Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile Gly Thr Ile
1 5 10 15

Leu Leu Ile Ser Tyr Gly Ile
20

<210> 29
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 29
ataacactca ttatTTTTGG ggtgatggct ggtgttattg gaacgacCCT cTtagccctg 60
ctcatctgg 69

<210> 30
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 30
Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile Gly Thr Ile
1 5 10 15

Leu Leu Ala Leu Leu Ile Trp

<210> 31
 <211> 63
 <212> DNA
 <213> Unknown

<220>

<223> Description of Unknown:
 CD3 zeta (CD247) transmembrane domain sequence

<400> 31
 ctctgctacc tgctggatgg aatcctcttc atctatggtg tcattctcac tgccttgttc 60
 ctg 63

<210> 32
 <211> 21
 <212> PRT
 <213> Unknown

<220>

<223> Description of Unknown:
 CD3 zeta (CD247) transmembrane domain sequence

<400> 32
 Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu
 1 5 10 15

Thr Ala Leu Phe Leu
 20

<210> 33
 <211> 84
 <212> DNA
 <213> Unknown

<220>

<223> Description of Unknown:
 CD8-alpha transmembrane domain sequence

<400> 33
 atctacatct gggcccctct ggccggcacc tgtggcgtgc tgctgctgag cctggtcac 60
 accctgtact gcaaccaccg gaat 84

<210> 34
 <211> 28
 <212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
CD8-alpha transmembrane domain sequence

<400> 34

Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu
1				5				10					15		

Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Asn	His	Arg	Asn
			20					25			

<210> 35

<211> 81

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown:
CD28 transmembrane domain sequence

<400> 35

ttttgggtgc tgggtggtggt tgggtggagtc ctggcttgct atagcttgct agtaacagtg 60

gcctttatta ttttctgggt g 81

<210> 36

<211> 27

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
CD28 transmembrane domain sequence

<400> 36

Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu
1				5				10					15		

Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val
			20					25		

<210> 37

<211> 63

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown:
Cytotoxic T-lymphocyte protein 4 transmembrane domain sequence

<400> 37
ttcctcctct ggatccttgc agcagttagt tcggggttgt ttttttatag ctttctcctc 60

aca 63

<210> 38
<211> 21
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cytotoxic T-lymphocyte protein 4 transmembrane domain sequence

<400> 38
Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe Tyr
1 5 10 15

Ser Phe Leu Leu Thr
20

<210> 39
<211> 66
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
Low-affinity nerve growth factor receptor
(LNGFR, TNFRSF16) transmembrane domain sequence

<400> 39
ctcatccctg tctattgctc catcctggct gctgtggttg tgggccttgt ggcctacata 60

gccttc 66

<210> 40
<211> 22
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Low-affinity nerve growth factor receptor
(LNGFR, TNFRSF16) transmembrane domain sequence

<400> 40

Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu
1 5 10 15

Val Ala Tyr Ile Ala Phe
20

<210> 41
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 41
gcaacgaact tctctctcct aaaacaggct ggtgatgtgg aggagaatcc tgggtcca 57

<210> 42
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 42
Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1 5 10 15

Pro Gly Pro

<210> 43
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 43
cagtgtacta attatgctct cttgaaattg gctggagatg ttgagagcaa ccctggacct 60

<210> 44
<211> 20

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 44
Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1 5 10 15

Asn Pro Gly Pro
20

<210> 45
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 45
gagggcagag gaagtctgct aacatgcggt gacgtcgagg agaatcctgg acct 54

<210> 46
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 46
Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1 5 10 15

Gly Pro

<210> 47
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide

<400> 47

gtcaaacaga ccctaaactt tgatctgcta aaactggccg gggatgtgga aagtaatccc 60

ggcccc 66

<210> 48

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 48

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
1 5 10 15

Glu Ser Asn Pro Gly Pro
20

<210> 49

<211> 570

<212> DNA

<213> Encephalomyocarditis virus

<400> 49

ccccctctcc ctccccccc cctaacttta ctggccgaag cgccttgga taaggccggt 60

gtgcgtttgt ctatatgtta ttttccacca tattgccgtc ttttggcaat gtgagggccc 120

ggaaacctgg ccctgtcttc ttgacgagca ttcctagggg tctttcccct ctcgccaaag 180

gaatgcaagg tctgttgaat gtcgtgaagg aagcagttcc tctggaagct tcttgaagac 240

aaacaacgtc tgtagcgacc ctttgcaggc agcggaaccc cccacctggc gacaggtgcc 300

tctgcggcca aaagccacgt gtataagata cacctgcaaa ggcggcaciaa cccagtgcc 360

acgttgtgag ttggatagtt gtggaaagag tcaaatggct ctctcaagc gtattcaaca 420

aggggctgaa ggatgccag aaggtacccc attgtatggg atctgatctg gggcctcggt 480

gcacatgctt tacatgtgtt tagtcgaggt taaaaaacgt ctaggcccc cgaaccacgg 540

ggacgtgggtt ttcctttgaa aaacacgatc 570

<210> 50

<211> 1210
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
Epidermal growth factor receptor (EGFR) isoform a
precursor sequence

<400> 50

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

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65 70 75 80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210 215 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
245 250 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305 310 315 320

Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
325 330 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
340 345 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450 455 460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625 630 635 640

Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
645 650 655

Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
660 665 670

Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
675 680 685

Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
690 695 700

Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
705 710 715 720

Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
725 730 735

Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
740 745 750

Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
755 760 765

Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
770 775 780

Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
785 790 795 800

Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
805 810 815

Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
820 825 830

Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
835 840 845

Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
850 855 860

Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
865 870 875 880

Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
885 890 895

Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
900 905 910

Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
915 920 925

Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
930 935 940

Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
945 950 955 960

Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
965 970 975

Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
980 985 990

Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp
995 1000 1005

Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe
1010 1015 1020

Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu
1025 1030 1035

Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn
1040 1045 1050

Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg
1055 1060 1065

Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp
1070 1075 1080

Asp Thr Phe Leu Pro Val Pro Glu Tyr Ile Asn Gln Ser Val Pro
1085 1090 1095

Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln
1100 1105 1110

Pro Leu Asn Pro Ala Pro Ser Arg Asp Pro His Tyr Gln Asp Pro
1115 1120 1125

His Ser Thr Ala Val Gly Asn Pro Glu Tyr Leu Asn Thr Val Gln
1130 1135 1140

Pro Thr Cys Val Asn Ser Thr Phe Asp Ser Pro Ala His Trp Ala
1145 1150 1155

Gln Lys Gly Ser His Gln Ile Ser Leu Asp Asn Pro Asp Tyr Gln
1160 1165 1170

Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn Gly Ile Phe Lys
1175 1180 1185

Gly Ser Thr Ala Glu Asn Ala Glu Tyr Leu Arg Val Ala Pro Gln
1190 1195 1200

Ser Ser Glu Phe Ile Gly Ala
1205 1210

<210> 51

<211> 1255

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

Receptor tyrosine-protein kinase ErbB2 (HER2) isoform a precursor sequence

<400> 51

Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
1 5 10 15

Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
20 25 30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
35 40 45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
50 55 60

Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
65 70 75 80

Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
85 90 95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
100 105 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
115 120 125

Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
130 135 140

Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
145 150 155 160

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
165 170 175

Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
180 185 190

His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser

195

200

205

Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
 210 215 220

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
 225 230 235 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
 245 250 255

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

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
 275 280 285

Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
 290 295 300

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
 305 310 315 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
 325 330 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
 340 345 350

Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
 355 360 365

Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
 370 375 380

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
 385 390 395 400

Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
 405 410 415

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
420 425 430

Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
435 440 445

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
450 455 460

Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
465 470 475 480

Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
485 490 495

Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
500 505 510

Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
515 520 525

Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
530 535 540

Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
545 550 555 560

Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
565 570 575

Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
580 585 590

Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
595 600 605

Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
610 615 620

Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys

625		630		635		640									
Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser	Pro	Leu	Thr	Ser	Ile	Ile	Ser
				645					650					655	
Ala	Val	Val	Gly	Ile	Leu	Leu	Val	Val	Val	Leu	Gly	Val	Val	Phe	Gly
			660					665					670		
Ile	Leu	Ile	Lys	Arg	Arg	Gln	Gln	Lys	Ile	Arg	Lys	Tyr	Thr	Met	Arg
		675					680					685			
Arg	Leu	Leu	Gln	Glu	Thr	Glu	Leu	Val	Glu	Pro	Leu	Thr	Pro	Ser	Gly
	690						695					700			
Ala	Met	Pro	Asn	Gln	Ala	Gln	Met	Arg	Ile	Leu	Lys	Glu	Thr	Glu	Leu
705					710					715					720
Arg	Lys	Val	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys
				725					730					735	
Gly	Ile	Trp	Ile	Pro	Asp	Gly	Glu	Asn	Val	Lys	Ile	Pro	Val	Ala	Ile
			740					745					750		
Lys	Val	Leu	Arg	Glu	Asn	Thr	Ser	Pro	Lys	Ala	Asn	Lys	Glu	Ile	Leu
		755					760					765			
Asp	Glu	Ala	Tyr	Val	Met	Ala	Gly	Val	Gly	Ser	Pro	Tyr	Val	Ser	Arg
	770					775					780				
Leu	Leu	Gly	Ile	Cys	Leu	Thr	Ser	Thr	Val	Gln	Leu	Val	Thr	Gln	Leu
785					790					795					800
Met	Pro	Tyr	Gly	Cys	Leu	Leu	Asp	His	Val	Arg	Glu	Asn	Arg	Gly	Arg
				805					810					815	
Leu	Gly	Ser	Gln	Asp	Leu	Leu	Asn	Trp	Cys	Met	Gln	Ile	Ala	Lys	Gly
			820					825					830		
Met	Ser	Tyr	Leu	Glu	Asp	Val	Arg	Leu	Val	His	Arg	Asp	Leu	Ala	Ala
		835					840					845			

Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe
850 855 860

Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp
865 870 875 880

Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg
885 890 895

Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
900 905 910

Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala
915 920 925

Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro
930 935 940

Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
945 950 955 960

Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe
965 970 975

Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu
980 985 990

Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu
995 1000 1005

Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr
1010 1015 1020

Leu Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly
1025 1030 1035

Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg
1040 1045 1050

Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu

1055					1060					1065				
Glu	Ala	Pro	Arg	Ser	Pro	Leu	Ala	Pro	Ser	Glu	Gly	Ala	Gly	Ser
1070					1075					1080				
Asp	Val	Phe	Asp	Gly	Asp	Leu	Gly	Met	Gly	Ala	Ala	Lys	Gly	Leu
1085					1090					1095				
Gln	Ser	Leu	Pro	Thr	His	Asp	Pro	Ser	Pro	Leu	Gln	Arg	Tyr	Ser
1100					1105					1110				
Glu	Asp	Pro	Thr	Val	Pro	Leu	Pro	Ser	Glu	Thr	Asp	Gly	Tyr	Val
1115					1120					1125				
Ala	Pro	Leu	Thr	Cys	Ser	Pro	Gln	Pro	Glu	Tyr	Val	Asn	Gln	Pro
1130					1135					1140				
Asp	Val	Arg	Pro	Gln	Pro	Pro	Ser	Pro	Arg	Glu	Gly	Pro	Leu	Pro
1145					1150					1155				
Ala	Ala	Arg	Pro	Ala	Gly	Ala	Thr	Leu	Glu	Arg	Pro	Lys	Thr	Leu
1160					1165					1170				
Ser	Pro	Gly	Lys	Asn	Gly	Val	Val	Lys	Asp	Val	Phe	Ala	Phe	Gly
1175					1180					1185				
Gly	Ala	Val	Glu	Asn	Pro	Glu	Tyr	Leu	Thr	Pro	Gln	Gly	Gly	Ala
1190					1195					1200				
Ala	Pro	Gln	Pro	His	Pro	Pro	Pro	Ala	Phe	Ser	Pro	Ala	Phe	Asp
1205					1210					1215				
Asn	Leu	Tyr	Tyr	Trp	Asp	Gln	Asp	Pro	Pro	Glu	Arg	Gly	Ala	Pro
1220					1225					1230				
Pro	Ser	Thr	Phe	Lys	Gly	Thr	Pro	Thr	Ala	Glu	Asn	Pro	Glu	Tyr
1235					1240					1245				
Leu	Gly	Leu	Asp	Val	Pro	Val								
1250					1255									

<210> 52
<211> 1342
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
Receptor tyrosine-protein kinase ErbB3 (HER3) isoform 1
precursor sequence

<400> 52

Met Arg Ala Asn Asp Ala Leu Gln Val Leu Gly Leu Leu Phe Ser Leu
1 5 10 15

Ala Arg Gly Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr
20 25 30

Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
35 40 45

Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
50 55 60

Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
65 70 75 80

Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
85 90 95

Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
100 105 110

Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
115 120 125

His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
130 135 140

Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
145 150 155 160

Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
165 170 175

Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
180 185 190

Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
195 200 205

Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
210 215 220

Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp
225 230 235 240

Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val
245 250 255

Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
260 265 270

Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala
275 280 285

Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala
290 295 300

Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys
305 310 315 320

Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser
325 330 335

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

Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu
355 360 365

Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu
370 375 380

Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln
385 390 395 400

Ser Trp Pro Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr
405 410 415

Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile
420 425 430

Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu
435 440 445

Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr
450 455 460

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

Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu
485 490 495

Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro
500 505 510

Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val
515 520 525

Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala
530 535 540

His Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu
545 550 555 560

Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys
565 570 575

Ala His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly
580 585 590

Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn
595 600 605

Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro
610 615 620

Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr
625 630 635 640

His Leu Thr Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe
645 650 655

Met Met Leu Gly Gly Thr Phe Leu Tyr Trp Arg Gly Arg Arg Ile Gln
660 665 670

Asn Lys Arg Ala Met Arg Arg Tyr Leu Glu Arg Gly Glu Ser Ile Glu
675 680 685

Pro Leu Asp Pro Ser Glu Lys Ala Asn Lys Val Leu Ala Arg Ile Phe
690 695 700

Lys Glu Thr Glu Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe
705 710 715 720

Gly Thr Val His Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys
725 730 735

Ile Pro Val Cys Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser
740 745 750

Phe Gln Ala Val Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His
755 760 765

Ala His Ile Val Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln
770 775 780

Leu Val Thr Gln Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg
785 790 795 800

Gln His Arg Gly Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val
805 810 815

Gln Ile Ala Lys Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His
820 825 830

Arg Asn Leu Ala Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val
835 840 845

Gln Val Ala Asp Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys
850 855 860

Gln Leu Leu Tyr Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu
865 870 875 880

Glu Ser Ile His Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser
885 890 895

Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr
900 905 910

Ala Gly Leu Arg Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu
915 920 925

Arg Leu Ala Gln Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met
930 935 940

Val Lys Cys Trp Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu
945 950 955 960

Leu Ala Asn Glu Phe Thr Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu
965 970 975

Val Ile Lys Arg Glu Ser Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro
980 985 990

His Gly Leu Thr Asn Lys Lys Leu Glu Glu Val Glu Leu Glu Pro Glu
995 1000 1005

Leu Asp Leu Asp Leu Asp Leu Glu Ala Glu Glu Asp Asn Leu Ala
1010 1015 1020

Thr Thr Thr Leu Gly Ser Ala Leu Ser Leu Pro Val Gly Thr Leu
1025 1030 1035

Asn Arg Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro Ser Ser Gly
1040 1045 1050

Tyr Met Pro Met Asn Gln Gly Asn Leu Gly Glu Ser Cys Gln Glu
1055 1060 1065

Ser Ala Val Ser Gly Ser Ser Glu Arg Cys Pro Arg Pro Val Ser
1070 1075 1080

Leu His Pro Met Pro Arg Gly Cys Leu Ala Ser Glu Ser Ser Glu
1085 1090 1095

Gly His Val Thr Gly Ser Glu Ala Glu Leu Gln Glu Lys Val Ser
1100 1105 1110

Met Cys Arg Ser Arg Ser Arg Ser Arg Ser Pro Arg Pro Arg Gly
1115 1120 1125

Asp Ser Ala Tyr His Ser Gln Arg His Ser Leu Leu Thr Pro Val
1130 1135 1140

Thr Pro Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp Val Asn Gly
1145 1150 1155

Tyr Val Met Pro Asp Thr His Leu Lys Gly Thr Pro Ser Ser Arg
1160 1165 1170

Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser Val Leu Gly Thr
1175 1180 1185

Glu Glu Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg Arg
1190 1195 1200

Arg Arg His Ser Pro Pro His Pro Pro Arg Pro Ser Ser Leu Glu
1205 1210 1215

Glu Leu Gly Tyr Glu Tyr Met Asp Val Gly Ser Asp Leu Ser Ala
1220 1225 1230

Ser Leu Gly Ser Thr Gln Ser Cys Pro Leu His Pro Val Pro Ile
1235 1240 1245

Met Pro Thr Ala Gly Thr Thr Pro Asp Glu Asp Tyr Glu Tyr Met
1250 1255 1260

Asn Arg Gln Arg Asp Gly Gly Gly Pro Gly Gly Asp Tyr Ala Ala
1265 1270 1275

Met Gly Ala Cys Pro Ala Ser Glu Gln Gly Tyr Glu Glu Met Arg
1280 1285 1290

Ala Phe Gln Gly Pro Gly His Gln Ala Pro His Val His Tyr Ala
1295 1300 1305

Arg Leu Lys Thr Leu Arg Ser Leu Glu Ala Thr Asp Ser Ala Phe
1310 1315 1320

Asp Asn Pro Asp Tyr Trp His Ser Arg Leu Phe Pro Lys Ala Asn
1325 1330 1335

Ala Gln Arg Thr
1340

<210> 53

<211> 1308

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

Receptor tyrosine-protein kinase ErbB4 (HER4) isoform
JM-a/CVT-1 precursor sequence

<400> 53

Met Lys Pro Ala Thr Gly Leu Trp Val Trp Val Ser Leu Leu Val Ala
1 5 10 15

Ala Gly Thr Val Gln Pro Ser Asp Ser Gln Ser Val Cys Ala Gly Thr
20 25 30

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

Leu Arg Lys Tyr Tyr Glu Asn Cys Glu Val Val Met Gly Asn Leu Glu
50 55 60

Ile Thr Ser Ile Glu His Asn Arg Asp Leu Ser Phe Leu Arg Ser Val
65 70 75 80

Arg Glu Val Thr Gly Tyr Val Leu Val Ala Leu Asn Gln Phe Arg Tyr
85 90 95

Leu Pro Leu Glu Asn Leu Arg Ile Ile Arg Gly Thr Lys Leu Tyr Glu
100 105 110

Asp Arg Tyr Ala Leu Ala Ile Phe Leu Asn Tyr Arg Lys Asp Gly Asn
115 120 125

Phe Gly Leu Gln Glu Leu Gly Leu Lys Asn Leu Thr Glu Ile Leu Asn
130 135 140

Gly Gly Val Tyr Val Asp Gln Asn Lys Phe Leu Cys Tyr Ala Asp Thr
145 150 155 160

Ile His Trp Gln Asp Ile Val Arg Asn Pro Trp Pro Ser Asn Leu Thr
165 170 175

Leu Val Ser Thr Asn Gly Ser Ser Gly Cys Gly Arg Cys His Lys Ser
180 185 190

Cys Thr Gly Arg Cys Trp Gly Pro Thr Glu Asn His Cys Gln Thr Leu
195 200 205

Thr Arg Thr Val Cys Ala Glu Gln Cys Asp Gly Arg Cys Tyr Gly Pro
210 215 220

Tyr Val Ser Asp Cys Cys His Arg Glu Cys Ala Gly Gly Cys Ser Gly
225 230 235 240

Pro Lys Asp Thr Asp Cys Phe Ala Cys Met Asn Phe Asn Asp Ser Gly
245 250 255

Ala Cys Val Thr Gln Cys Pro Gln Thr Phe Val Tyr Asn Pro Thr Thr

260

265

270

Phe Gln Leu Glu His Asn Phe Asn Ala Lys Tyr Thr Tyr Gly Ala Phe
 275 280 285

Cys Val Lys Lys Cys Pro His Asn Phe Val Val Asp Ser Ser Ser Cys
 290 295 300

Val Arg Ala Cys Pro Ser Ser Lys Met Glu Val Glu Glu Asn Gly Ile
 305 310 315 320

Lys Met Cys Lys Pro Cys Thr Asp Ile Cys Pro Lys Ala Cys Asp Gly
 325 330 335

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

Ile Asp Lys Phe Ile Asn Cys Thr Lys Ile Asn Gly Asn Leu Ile Phe
 355 360 365

Leu Val Thr Gly Ile His Gly Asp Pro Tyr Asn Ala Ile Glu Ala Ile
 370 375 380

Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly
 385 390 395 400

Phe Leu Asn Ile Gln Ser Trp Pro Pro Asn Met Thr Asp Phe Ser Val
 405 410 415

Phe Ser Asn Leu Val Thr Ile Gly Gly Arg Val Leu Tyr Ser Gly Leu
 420 425 430

Ser Leu Leu Ile Leu Lys Gln Gln Gly Ile Thr Ser Leu Gln Phe Gln
 435 440 445

Ser Leu Lys Glu Ile Ser Ala Gly Asn Ile Tyr Ile Thr Asp Asn Ser
 450 455 460

Asn Leu Cys Tyr Tyr His Thr Ile Asn Trp Thr Thr Leu Phe Ser Thr
 465 470 475 480

Ile Asn Gln Arg Ile Val Ile Arg Asp Asn Arg Lys Ala Glu Asn Cys
485 490 495

Thr Ala Glu Gly Met Val Cys Asn His Leu Cys Ser Ser Asp Gly Cys
500 505 510

Trp Gly Pro Gly Pro Asp Gln Cys Leu Ser Cys Arg Arg Phe Ser Arg
515 520 525

Gly Arg Ile Cys Ile Glu Ser Cys Asn Leu Tyr Asp Gly Glu Phe Arg
530 535 540

Glu Phe Glu Asn Gly Ser Ile Cys Val Glu Cys Asp Pro Gln Cys Glu
545 550 555 560

Lys Met Glu Asp Gly Leu Leu Thr Cys His Gly Pro Gly Pro Asp Asn
565 570 575

Cys Thr Lys Cys Ser His Phe Lys Asp Gly Pro Asn Cys Val Glu Lys
580 585 590

Cys Pro Asp Gly Leu Gln Gly Ala Asn Ser Phe Ile Phe Lys Tyr Ala
595 600 605

Asp Pro Asp Arg Glu Cys His Pro Cys His Pro Asn Cys Thr Gln Gly
610 615 620

Cys Asn Gly Pro Thr Ser His Asp Cys Ile Tyr Tyr Pro Trp Thr Gly
625 630 635 640

His Ser Thr Leu Pro Gln His Ala Arg Thr Pro Leu Ile Ala Ala Gly
645 650 655

Val Ile Gly Gly Leu Phe Ile Leu Val Ile Val Gly Leu Thr Phe Ala
660 665 670

Val Tyr Val Arg Arg Lys Ser Ile Lys Lys Lys Arg Ala Leu Arg Arg
675 680 685

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

690

695

700

Pro Asn Gln Ala Gln Leu Arg Ile Leu Lys Glu Thr Glu Leu Lys Arg
 705 710 715 720

Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly Ile
 725 730 735

Trp Val Pro Glu Gly Glu Thr Val Lys Ile Pro Val Ala Ile Lys Ile
 740 745 750

Leu Asn Glu Thr Thr Gly Pro Lys Ala Asn Val Glu Phe Met Asp Glu
 755 760 765

Ala Leu Ile Met Ala Ser Met Asp His Pro His Leu Val Arg Leu Leu
 770 775 780

Gly Val Cys Leu Ser Pro Thr Ile Gln Leu Val Thr Gln Leu Met Pro
 785 790 795 800

His Gly Cys Leu Leu Glu Tyr Val His Glu His Lys Asp Asn Ile Gly
 805 810 815

Ser Gln Leu Leu Leu Asn Trp Cys Val Gln Ile Ala Lys Gly Met Met
 820 825 830

Tyr Leu Glu Glu Arg Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn
 835 840 845

Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe Gly Leu
 850 855 860

Ala Arg Leu Leu Glu Gly Asp Glu Lys Glu Tyr Asn Ala Asp Gly Gly
 865 870 875 880

Lys Met Pro Ile Lys Trp Met Ala Leu Glu Cys Ile His Tyr Arg Lys
 885 890 895

Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Ile Trp Glu
 900 905 910

Leu Met Thr Phe Gly Gly Lys Pro Tyr Asp Gly Ile Pro Thr Arg Glu
915 920 925

Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile
930 935 940

Cys Thr Ile Asp Val Tyr Met Val Met Val Lys Cys Trp Met Ile Asp
945 950 955 960

Ala Asp Ser Arg Pro Lys Phe Lys Glu Leu Ala Ala Glu Phe Ser Arg
965 970 975

Met Ala Arg Asp Pro Gln Arg Tyr Leu Val Ile Gln Gly Asp Asp Arg
980 985 990

Met Lys Leu Pro Ser Pro Asn Asp Ser Lys Phe Phe Gln Asn Leu Leu
995 1000 1005

Asp Glu Glu Asp Leu Glu Asp Met Met Asp Ala Glu Glu Tyr Leu
1010 1015 1020

Val Pro Gln Ala Phe Asn Ile Pro Pro Pro Ile Tyr Thr Ser Arg
1025 1030 1035

Ala Arg Ile Asp Ser Asn Arg Ser Glu Ile Gly His Ser Pro Pro
1040 1045 1050

Pro Ala Tyr Thr Pro Met Ser Gly Asn Gln Phe Val Tyr Arg Asp
1055 1060 1065

Gly Gly Phe Ala Ala Glu Gln Gly Val Ser Val Pro Tyr Arg Ala
1070 1075 1080

Pro Thr Ser Thr Ile Pro Glu Ala Pro Val Ala Gln Gly Ala Thr
1085 1090 1095

Ala Glu Ile Phe Asp Asp Ser Cys Cys Asn Gly Thr Leu Arg Lys
1100 1105 1110

Pro Val Ala Pro His Val Gln Glu Asp Ser Ser Thr Gln Arg Tyr

1115

1120

1125

Ser Ala Asp Pro Thr Val Phe Ala Pro Glu Arg Ser Pro Arg Gly
 1130 1135 1140

Glu Leu Asp Glu Glu Gly Tyr Met Thr Pro Met Arg Asp Lys Pro
 1145 1150 1155

Lys Gln Glu Tyr Leu Asn Pro Val Glu Glu Asn Pro Phe Val Ser
 1160 1165 1170

Arg Arg Lys Asn Gly Asp Leu Gln Ala Leu Asp Asn Pro Glu Tyr
 1175 1180 1185

His Asn Ala Ser Asn Gly Pro Pro Lys Ala Glu Asp Glu Tyr Val
 1190 1195 1200

Asn Glu Pro Leu Tyr Leu Asn Thr Phe Ala Asn Thr Leu Gly Lys
 1205 1210 1215

Ala Glu Tyr Leu Lys Asn Asn Ile Leu Ser Met Pro Glu Lys Ala
 1220 1225 1230

Lys Lys Ala Phe Asp Asn Pro Asp Tyr Trp Asn His Ser Leu Pro
 1235 1240 1245

Pro Arg Ser Thr Leu Gln His Pro Asp Tyr Leu Gln Glu Tyr Ser
 1250 1255 1260

Thr Lys Tyr Phe Tyr Lys Gln Asn Gly Arg Ile Arg Pro Ile Val
 1265 1270 1275

Ala Glu Asn Pro Glu Tyr Leu Ser Glu Phe Ser Leu Lys Pro Gly
 1280 1285 1290

Thr Val Leu Pro Pro Pro Pro Tyr Arg His Arg Asn Thr Val Val
 1295 1300 1305

<210> 54

<211> 1298

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

Receptor tyrosine-protein kinase ErbB4 (HER4) isoform JM-b
(isoform X7) precursor sequence

<400> 54

Met Lys Pro Ala Thr Gly Leu Trp Val Trp Val Ser Leu Leu Val Ala
1 5 10 15

Ala Gly Thr Val Gln Pro Ser Asp Ser Gln Ser Val Cys Ala Gly Thr
20 25 30

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

Leu Arg Lys Tyr Tyr Glu Asn Cys Glu Val Val Met Gly Asn Leu Glu
50 55 60

Ile Thr Ser Ile Glu His Asn Arg Asp Leu Ser Phe Leu Arg Ser Val
65 70 75 80

Arg Glu Val Thr Gly Tyr Val Leu Val Ala Leu Asn Gln Phe Arg Tyr
85 90 95

Leu Pro Leu Glu Asn Leu Arg Ile Ile Arg Gly Thr Lys Leu Tyr Glu
100 105 110

Asp Arg Tyr Ala Leu Ala Ile Phe Leu Asn Tyr Arg Lys Asp Gly Asn
115 120 125

Phe Gly Leu Gln Glu Leu Gly Leu Lys Asn Leu Thr Glu Ile Leu Asn
130 135 140

Gly Gly Val Tyr Val Asp Gln Asn Lys Phe Leu Cys Tyr Ala Asp Thr
145 150 155 160

Ile His Trp Gln Asp Ile Val Arg Asn Pro Trp Pro Ser Asn Leu Thr
165 170 175

Leu Val Ser Thr Asn Gly Ser Ser Gly Cys Gly Arg Cys His Lys Ser
180 185 190

Cys Thr Gly Arg Cys Trp Gly Pro Thr Glu Asn His Cys Gln Thr Leu
195 200 205

Thr Arg Thr Val Cys Ala Glu Gln Cys Asp Gly Arg Cys Tyr Gly Pro
210 215 220

Tyr Val Ser Asp Cys Cys His Arg Glu Cys Ala Gly Gly Cys Ser Gly
225 230 235 240

Pro Lys Asp Thr Asp Cys Phe Ala Cys Met Asn Phe Asn Asp Ser Gly
245 250 255

Ala Cys Val Thr Gln Cys Pro Gln Thr Phe Val Tyr Asn Pro Thr Thr
260 265 270

Phe Gln Leu Glu His Asn Phe Asn Ala Lys Tyr Thr Tyr Gly Ala Phe
275 280 285

Cys Val Lys Lys Cys Pro His Asn Phe Val Val Asp Ser Ser Ser Cys
290 295 300

Val Arg Ala Cys Pro Ser Ser Lys Met Glu Val Glu Glu Asn Gly Ile
305 310 315 320

Lys Met Cys Lys Pro Cys Thr Asp Ile Cys Pro Lys Ala Cys Asp Gly
325 330 335

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

Ile Asp Lys Phe Ile Asn Cys Thr Lys Ile Asn Gly Asn Leu Ile Phe
355 360 365

Leu Val Thr Gly Ile His Gly Asp Pro Tyr Asn Ala Ile Glu Ala Ile
370 375 380

Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly
385 390 395 400

Phe Leu Asn Ile Gln Ser Trp Pro Pro Asn Met Thr Asp Phe Ser Val
405 410 415

Phe Ser Asn Leu Val Thr Ile Gly Gly Arg Val Leu Tyr Ser Gly Leu
420 425 430

Ser Leu Leu Ile Leu Lys Gln Gln Gly Ile Thr Ser Leu Gln Phe Gln
435 440 445

Ser Leu Lys Glu Ile Ser Ala Gly Asn Ile Tyr Ile Thr Asp Asn Ser
450 455 460

Asn Leu Cys Tyr Tyr His Thr Ile Asn Trp Thr Thr Leu Phe Ser Thr
465 470 475 480

Ile Asn Gln Arg Ile Val Ile Arg Asp Asn Arg Lys Ala Glu Asn Cys
485 490 495

Thr Ala Glu Gly Met Val Cys Asn His Leu Cys Ser Ser Asp Gly Cys
500 505 510

Trp Gly Pro Gly Pro Asp Gln Cys Leu Ser Cys Arg Arg Phe Ser Arg
515 520 525

Gly Arg Ile Cys Ile Glu Ser Cys Asn Leu Tyr Asp Gly Glu Phe Arg
530 535 540

Glu Phe Glu Asn Gly Ser Ile Cys Val Glu Cys Asp Pro Gln Cys Glu
545 550 555 560

Lys Met Glu Asp Gly Leu Leu Thr Cys His Gly Pro Gly Pro Asp Asn
565 570 575

Cys Thr Lys Cys Ser His Phe Lys Asp Gly Pro Asn Cys Val Glu Lys
580 585 590

Cys Pro Asp Gly Leu Gln Gly Ala Asn Ser Phe Ile Phe Lys Tyr Ala
595 600 605

Asp Pro Asp Arg Glu Cys His Pro Cys His Pro Asn Cys Thr Gln Gly
610 615 620

Cys Ile Gly Ser Ser Ile Glu Asp Cys Ile Gly Leu Met Asp Arg Thr
625 630 635 640

Pro Leu Ile Ala Ala Gly Val Ile Gly Gly Leu Phe Ile Leu Val Ile
645 650 655

Val Gly Leu Thr Phe Ala Val Tyr Val Arg Arg Lys Ser Ile Lys Lys
660 665 670

Lys Arg Ala Leu Arg Arg Phe Leu Glu Thr Glu Leu Val Glu Pro Leu
675 680 685

Thr Pro Ser Gly Thr Ala Pro Asn Gln Ala Gln Leu Arg Ile Leu Lys
690 695 700

Glu Thr Glu Leu Lys Arg Val Lys Val Leu Gly Ser Gly Ala Phe Gly
705 710 715 720

Thr Val Tyr Lys Gly Ile Trp Val Pro Glu Gly Glu Thr Val Lys Ile
725 730 735

Pro Val Ala Ile Lys Ile Leu Asn Glu Thr Thr Gly Pro Lys Ala Asn
740 745 750

Val Glu Phe Met Asp Glu Ala Leu Ile Met Ala Ser Met Asp His Pro
755 760 765

His Leu Val Arg Leu Leu Gly Val Cys Leu Ser Pro Thr Ile Gln Leu
770 775 780

Val Thr Gln Leu Met Pro His Gly Cys Leu Leu Glu Tyr Val His Glu
785 790 795 800

His Lys Asp Asn Ile Gly Ser Gln Leu Leu Leu Asn Trp Cys Val Gln
805 810 815

Ile Ala Lys Gly Met Met Tyr Leu Glu Glu Arg Arg Leu Val His Arg
820 825 830

Asp Leu Ala Ala Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys
835 840 845

Ile Thr Asp Phe Gly Leu Ala Arg Leu Leu Glu Gly Asp Glu Lys Glu
850 855 860

Tyr Asn Ala Asp Gly Gly Lys Met Pro Ile Lys Trp Met Ala Leu Glu
865 870 875 880

Cys Ile His Tyr Arg Lys Phe Thr His Gln Ser Asp Val Trp Ser Tyr
885 890 895

Gly Val Thr Ile Trp Glu Leu Met Thr Phe Gly Gly Lys Pro Tyr Asp
900 905 910

Gly Ile Pro Thr Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg
915 920 925

Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Val Met Val
930 935 940

Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys Phe Lys Glu Leu
945 950 955 960

Ala Ala Glu Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Tyr Leu Val
965 970 975

Ile Gln Gly Asp Asp Arg Met Lys Leu Pro Ser Pro Asn Asp Ser Lys
980 985 990

Phe Phe Gln Asn Leu Leu Asp Glu Glu Asp Leu Glu Asp Met Met Asp
995 1000 1005

Ala Glu Glu Tyr Leu Val Pro Gln Ala Phe Asn Ile Pro Pro Pro
1010 1015 1020

Ile Tyr Thr Ser Arg Ala Arg Ile Asp Ser Asn Arg Ser Glu Ile
1025 1030 1035

Gly His Ser Pro Pro Pro Ala Tyr Thr Pro Met Ser Gly Asn Gln
1040 1045 1050

Phe Val Tyr Arg Asp Gly Gly Phe Ala Ala Glu Gln Gly Val Ser
1055 1060 1065

Val Pro Tyr Arg Ala Pro Thr Ser Thr Ile Pro Glu Ala Pro Val
1070 1075 1080

Ala Gln Gly Ala Thr Ala Glu Ile Phe Asp Asp Ser Cys Cys Asn
1085 1090 1095

Gly Thr Leu Arg Lys Pro Val Ala Pro His Val Gln Glu Asp Ser
1100 1105 1110

Ser Thr Gln Arg Tyr Ser Ala Asp Pro Thr Val Phe Ala Pro Glu
1115 1120 1125

Arg Ser Pro Arg Gly Glu Leu Asp Glu Glu Gly Tyr Met Thr Pro
1130 1135 1140

Met Arg Asp Lys Pro Lys Gln Glu Tyr Leu Asn Pro Val Glu Glu
1145 1150 1155

Asn Pro Phe Val Ser Arg Arg Lys Asn Gly Asp Leu Gln Ala Leu
1160 1165 1170

Asp Asn Pro Glu Tyr His Asn Ala Ser Asn Gly Pro Pro Lys Ala
1175 1180 1185

Glu Asp Glu Tyr Val Asn Glu Pro Leu Tyr Leu Asn Thr Phe Ala
1190 1195 1200

Asn Thr Leu Gly Lys Ala Glu Tyr Leu Lys Asn Asn Ile Leu Ser
1205 1210 1215

Met Pro Glu Lys Ala Lys Lys Ala Phe Asp Asn Pro Asp Tyr Trp
1220 1225 1230

Asn His Ser Leu Pro Pro Arg Ser Thr Leu Gln His Pro Asp Tyr
1235 1240 1245

Leu Gln Glu Tyr Ser Thr Lys Tyr Phe Tyr Lys Gln Asn Gly Arg
1250 1255 1260

Ile Arg Pro Ile Val Ala Glu Asn Pro Glu Tyr Leu Ser Glu Phe
1265 1270 1275

Ser Leu Lys Pro Gly Thr Val Leu Pro Pro Pro Pro Tyr Arg His
1280 1285 1290

Arg Asn Thr Val Val
1295

<210> 55

<211> 335

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 55

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
195 200 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
210 215 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225 230 235 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
245 250 255

His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
260 265 270

Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His
275 280 285

Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro
290 295 300

Thr Asn Gly Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala
305 310 315 320

Leu Leu Leu Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met
325 330 335

<210> 56
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 56
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60
acgaatatta aacacttcaa aaactgcacc tccatcagt gcatctcca catcctgccg 120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240
aggacggacc tccatgcctt tgagaacct a gaaatcatac gcggcaggac caagcaacat 300
ggtcagtttt ctcttgagc cgtcagcctg aacataacat ccttgggatt acgctccctc 360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttggt ctatgcaaat 420
acaataaact ggaaaaaact gtttgggacc tccggtcaga aaacaaaaat tataagcaac 480
agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttggt ccccccgag 540
ggctgctggg gcccgagacc cagggactgc gtctctggtg gcggtggctc gggcgggtggt 600
gggtcgggtg gcggcggatc tgggtggcggg ggctcggttt ggggtgctggt ggtggttggt 660
ggagtcctgg cttgctatag cttgctagta acagtggcct ttattatatt ctgggtgagg 720
agtaagagga gc 732

<210> 57
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 57
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile

20

25

30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
 35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
 50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
 65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
 85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
 115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
 130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
 145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
 165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
 180 185 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 195 200 205

Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
 210 215 220

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
 225 230 235 240

Ser Lys Arg Ser

<210> 58

<211> 771

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 58

cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct	60
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg	120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat	180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac	240
aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat	300
ggtcagtttt ctcttgagtg cgtcagcctg aacataacat ccttgggatt acgctccctc	360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttggt ctatgcaaat	420
acaataaaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaact tataagcaac	480
agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttggt ctcccccgag	540
ggctgctggg gcccgagacc cagggactgc gtctcttgcc ggaatgtcag ccgaggcagg	600
gaatgcgtgg acaagggtgg cgggtggctg ggcgggtggt ggtcgggtgg cggcggatct	660
ggtggcggtg gctcgttttg ggtgctggtg gtggttggtg gaggcttggtc ttgctatagc	720
ttgctagtaa cagtggcctt tattattttc tgggtgagga gtaagaggag c	771

<210> 59

<211> 257

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 59

Arg	Lys	Val	Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu
1				5				10					15		

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Gly Gly Gly
195 200 205

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
210 215 220

Ser	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser
225					230					235					240

Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg
				245					250					255	

Ser

<210> 60
 <211> 828
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 60	
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct	60
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg	120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat	180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac	240
aggacggacc tccatgcctt tgagaacctt gaaatcatac gcggcaggac caagcaacat	300
ggtcagtttt ctcttgagtg cgtcagcctg aacataacat ccttgggatt acgctccctc	360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaa	420
acaataaaact ggaaaaaact gtttgggacc tccggtcaga aaaccaa	480
agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctccccgag	540
ggctgctggg gcccgagacc cagggactgc gtctcttgcc ggaatgtcag ccgaggcagg	600
gaatgcgtgg acaagtgcaa ctttctggag ggtgagccaa gggagtttgt ggagaactct	660
gagtgcatag aggggtggcg tggctcgggc ggtggtgggt cgggtggcgg cggatctggt	720
ggcgggtggct cgttttgggt gctgggtggg gttggtggag tcctggcttg ctatagcttg	780
ctagtaacag tggcctttat tattttctgg gtgaggagta agaggagc	828

<210> 61
 <211> 276
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 61

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
195 200 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
210 215 220

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
225 230 235 240

Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
245 250 255

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
260 265 270

Ser Lys Arg Ser
275

<210> 62
<211> 885
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 62
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240
aggacggacc tccatgcctt tgagaacctt gaaatcatac gcggcaggac caagcaacat 300
ggtcagtttt ctcttgagtg cgtcagcctg aacataacat ccttgggatt acgctcctc 360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttggt ctatgcaaatt 420
acaataaact ggaaaaaact gtttgggacc tccggtcaga aaacaaaat tataagcaac 480
agaggtgaaa acagctgcaa ggccacaggc caggctctgcc atgccttggtg ctcccccgag 540
ggctgctggg gcccgagacc cagggactgc gtctcttgcc ggaatgtcag ccgaggcagg 600

gaatgcgtgg acaagtgcaa ccttctggag ggtgagccaa gggagtttgt ggagaactct	660
gagtgcatac agtgccaccc agagtgcctg cctcaggcca tgaacatcac ctgcacagga	720
cggggaccag acaactgtat ccagggcgga ggcggaagcg gaggcggagg ctccggcgga	780
ggcggaagct tttgggtgct ggtggtggtt ggtggagtcc tggcttgcta tagcttgcta	840
gtaacagtgg cctttattat tttctgggtg aggagtaaga ggagc	885

<210> 63

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 63

Arg	Lys	Val	Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu
1				5					10					15	

Ser	Ile	Asn	Ala	Thr	Asn	Ile	Lys	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile
		20					25						30		

Ser	Gly	Asp	Leu	His	Ile	Leu	Pro	Val	Ala	Phe	Arg	Gly	Asp	Ser	Phe
		35					40					45			

Thr	His	Thr	Pro	Pro	Leu	Asp	Pro	Gln	Glu	Leu	Asp	Ile	Leu	Lys	Thr
		50				55					60				

Val	Lys	Glu	Ile	Thr	Gly	Phe	Leu	Leu	Ile	Gln	Ala	Trp	Pro	Glu	Asn
65					70					75					80

Arg	Thr	Asp	Leu	His	Ala	Phe	Glu	Asn	Leu	Glu	Ile	Ile	Arg	Gly	Arg
			85						90					95	

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

Thr	Ser	Leu	Gly	Leu	Arg	Ser	Leu	Lys	Glu	Ile	Ser	Asp	Gly	Asp	Val
		115					120					125			

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
195 200 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
210 215 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225 230 235 240

Arg Gly Pro Asp Asn Cys Ile Gln Gly Gly Gly Gly Ser Gly Gly Gly
245 250 255

Gly Ser Gly Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly
260 265 270

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
275 280 285

Trp Val Arg Ser Lys Arg Ser
290 295

<210> 64

<211> 924

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 64

cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct	60
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg	120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat	180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac	240
aggacggacc tccatgcctt tgagaacctt gaaatcatac gcggcaggac caagcaacat	300
ggtcagtttt ctcttgagtg cgtcagcctg aacataacat ccttgggatt acgctccctc	360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttggt ctatgcaaat	420
acaataaaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaact tataagcaac	480
agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttggtg ctcccccgag	540
ggctgctggg gcccgaggcc cagggactgc gtctcttgcc ggaatgtcag ccgaggcagg	600
gaatgcgtgg acaagtgcaa ccttctggag ggtgagccaa gggagtttgt ggagaactct	660
gagtgcatat agtgccaccc agagtgcctg cctcaggcca tgaacatcac ctgcacagga	720
cggggaccag acaactgtat ccagtgtgcc cactacattg acggccccca ctgcgtcaag	780
accggcggag gcggaagcgg aggcggaggc tccggcggag gcggaagctt ttgggtgctg	840
gtggtggttg gtggagtcct ggcttgctat agcttgctag taacagtggc ctttattatt	900
ttctgggtga ggagtaagag gagc	924

<210> 65

<211> 308

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 65

Arg	Lys	Val	Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu
1				5					10					15	

Ser	Ile	Asn	Ala	Thr	Asn	Ile	Lys	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile
		20						25					30		

Ser	Gly	Asp	Leu	His	Ile	Leu	Pro	Val	Ala	Phe	Arg	Gly	Asp	Ser	Phe
		35					40					45			

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
195 200 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
210 215 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225 230 235 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
245 250 255

His Cys Val Lys Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

260

265

270

Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
 275 280 285

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
 290 295 300

Ser Lys Arg Ser
 305

<210> 66

<211> 984

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 66

cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct	60
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg	120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat	180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac	240
aggacggacc tccatgcctt tgagaacctt gaaatcatac gcggcaggac caagcaacat	300
ggtcagtttt ctcttgagtg cgtcagcctg aacataacat ccttgggatt acgctccctc	360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaa	420
acaataaact ggaaaaaact gtttgggacc tccggtcaga aaacaaaaat tataagcaac	480
agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctccccgag	540
ggctgctggg gcccggagcc cagggactgc gtctcttgcc ggaatgtcag ccgaggcagg	600
gaatgcgtgg acaagtgcaa ctttctggag ggtgagccaa gggagtttgt ggagaactct	660
gagtgcatat agtgccaccc agagtgcctg cctcaggcca tgaacatcac ctgcacagga	720
cggggaccag acaactgtat ccagtgtgcc cactacattg acggcccca ctgcgtcaag	780
acctgcccgg caggagtcac gggagaaaac aacaccctgg tctggaagta cgcagacgcc	840
ggccatgtgt gccacctggg cggaggcgga agcggaggcg gaggctcctt ttgggtgctg	900

gtggtggttg gtggagtcct ggcttgctat agcttgctag taacagtggc ctttattatt 960
 ttctgggtga ggagtaagag gagc 984

<210> 67
 <211> 328
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 67
 Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
 1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
 20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
 35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
 50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
 65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
 85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
 115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
 130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
 145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
195 200 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
210 215 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225 230 235 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
245 250 255

His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
260 265 270

Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Gly Gly
275 280 285

Gly Gly Ser Gly Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly
290 295 300

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

Phe Trp Val Arg Ser Lys Arg Ser
325

<210> 68

<211> 1032

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 68
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240
aggacggacc tccatgcctt tgagaacctt gaaatcatac gcggcaggac caagcaacat 300
ggtcagtttt ctcttgagtg cgtcagcctg aacataacat ccttgggatt acgctccctc 360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaatt 420
acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaatt tataagcaac 480
agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 540
ggctgctggg gcccgagacc cagggactgc gtctcttgcc ggaatgtcag ccgaggcagg 600
gaatgcgtgg acaagtgcaa ccttctggag ggtgagccaa gggagtttgt ggagaactct 660
gagtgcatac agtgccaccc agagtgcctg cctcaggcca tgaacatcac ctgcacagga 720
cggggaccag acaactgtat ccagtgtgcc cactacattg acggcccca ctgcgtcaag 780
acctgcccgg caggagtcatt gggagaaaac aacaccctgg tctggaagta cgcagacgcc 840
ggccatgtgt gccacctgtg ccatccaaac tgcacctacg gatgcactgg gccaggtctt 900
gaaggctgtc caggtggcgg tggcggcgga tctttttggg tgctggtggt ggttggtgga 960
gtcctggctt gctatagctt gctagtaaca gtggccttta ttattttctg ggtgaggagt 1020
aagaggagct aa 1032

<210> 69
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 69
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile

20

25

30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
 35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
 50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
 65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
 85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
 115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
 130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
 145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
 165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
 180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
 195 200 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
 210 215 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
 225 230 235 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
245 250 255

His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
260 265 270

Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His
275 280 285

Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro
290 295 300

Gly Gly Gly Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly
305 310 315 320

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
325 330 335

Trp Val Arg Ser Lys Arg Ser
340

<210> 70

<211> 786

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 70

atgaggctcc ctgctcagct cctggggctg ctaatgctct ggggtcccagg atccagtggg	60
cgcaaagtgt gtaacggaat aggtattggg gaatttaaag actcactctc cataaatgct	120
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg	180
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat	240
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac	300
aggacggacc tccatgcctt tgagaacctt gaaatcatat gcggcaggac caagcaacat	360
ggtcagtttt ctcttgagct cgtcagcctg aacataacat ccttgggatt acgctccctc	420
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat	480

acaataaaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaact tataagcaac	540
agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttggtg ctcccccgag	600
ggctgctggg gcccgagacc cagggactgc gtctctgggtg gcggtggctc gggcgggtgt	660
gggtcgggtg gcggcggatc tgggtggcggg ggctcggaga taacactcat tatttttggg	720
gtgatggctg gtgttattgg aacgatcctc ttaatttctt acggtattcg ccgaggaggt	780
ggaagc	786

<210> 71
 <211> 262
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 71
 Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro
 1 5 10 15

Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe
 20 25 30

Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn
 35 40 45

Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg
 50 55 60

Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp
 65 70 75 80

Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala
 85 90 95

Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile
 100 105 110

Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val
 115 120 125

Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser
130 135 140

Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn
145 150 155 160

Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys
165 170 175

Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val
180 185 190

Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg
195 200 205

Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Thr Leu Ile Ile Phe Gly
225 230 235 240

Val Met Ala Gly Val Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly Ile
245 250 255

Arg Arg Gly Gly Gly Ser
260

<210> 72
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 72
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac	240
aggacggacc tccatgcctt tgagaacctt gaaatcatac gcggcaggac caagcaacat	300
ggtcagtttt ctcttgagct cgtcagcctg aacataacat ccttgggatt acgctccctc	360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaa	420
acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaa	480
agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctccccgag	540
ggctgctggg gcccgagcc cagggactgc gtctctggtg gcggtggctc gggcggtggt	600
gggtcgggtg gcggcggatc tgggtggcgt ggctcggaga taacactcat tatttttggg	660
gtgatggctg gtgttattgg aacgatcctc ttaatttctt acggtattcg ccgaggaggt	720
ggaagc	726

<210> 73

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 73

Arg	Lys	Val	Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu
1				5					10					15	

Ser	Ile	Asn	Ala	Thr	Asn	Ile	Lys	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile
		20					25						30		

Ser	Gly	Asp	Leu	His	Ile	Leu	Pro	Val	Ala	Phe	Arg	Gly	Asp	Ser	Phe
	35						40					45			

Thr	His	Thr	Pro	Pro	Leu	Asp	Pro	Gln	Glu	Leu	Asp	Ile	Leu	Lys	Thr
	50					55					60				

Val	Lys	Glu	Ile	Thr	Gly	Phe	Leu	Leu	Ile	Gln	Ala	Trp	Pro	Glu	Asn
65					70					75					80

Arg	Thr	Asp	Leu	His	Ala	Phe	Glu	Asn	Leu	Glu	Ile	Ile	Arg	Gly	Arg
				85					90					95	

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
195 200 205

Gly Gly Gly Ser Glu Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly
210 215 220

Val Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly Ile Arg Arg Gly Gly
225 230 235 240

Gly Ser

<210> 74

<211> 777

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 74

atgaggctcc ctgctcagct cctggggctg ctaatgctct gggtcccagg atccagtggg 60

cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 120

acgaatatta aacacttcaa aaactgcacc tccatcagt gcatctcca catcctgccg 180
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 240
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 300
aggacggacc tccatgcctt tgagaacctt gaaatcatac gcggcaggac caagcaacat 360
ggtcagtttt ctcttgagc cgtcagcctg aacataacat ccttgggatt acgctccctc 420
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 480
acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaact tataagcaac 540
agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 600
ggctgctggg gcccgagacc cagggactgc gtctctgggt gcggtggctc gggcggtggt 660
gggtcgggtg gcggcggatc tgggtggcgt ggctcgataa cactcattat ttttggggtg 720
atggctggtg ttattggaac gacacctta atttcttacg gtattggagg tggaagc 777

<210> 75

<211> 259

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 75

Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro
1 5 10 15

Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe
20 25 30

Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn
35 40 45

Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg
50 55 60

Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp
65 70 75 80

Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala
85 90 95

Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile
100 105 110

Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val
115 120 125

Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser
130 135 140

Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn
145 150 155 160

Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys
165 170 175

Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val
180 185 190

Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg
195 200 205

Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val
225 230 235 240

Met Ala Gly Val Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly Ile Gly
245 250 255

Gly Gly Ser

<210> 76

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 76

cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct	60
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg	120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat	180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac	240
aggacggacc tccatgcctt tgagaaccta gaaatcatat gcggcaggac caagcaacat	300
ggtcagtttt ctcttgagtg cgtcagcctg aacataacat ccttgggatt acgctccctc	360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat	420
acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaact tataagcaac	480
agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttggtg ctcccccgag	540
ggctgctggg gcccggagcc cagggactgc gtctctggtg gcggtggctc gggcggtggt	600
gggtcgggtg gcggcggatc tgggtggcggg ggctcgataa cactcattat ttttgggggtg	660
atggctggtg ttattggaac gatcctctta atttcttacg gtattggagg tggaagc	717

<210> 77

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 77

Arg	Lys	Val	Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu
1				5					10					15	

Ser	Ile	Asn	Ala	Thr	Asn	Ile	Lys	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile
		20						25					30		

Ser	Gly	Asp	Leu	His	Ile	Leu	Pro	Val	Ala	Phe	Arg	Gly	Asp	Ser	Phe
		35					40					45			

Thr	His	Thr	Pro	Pro	Leu	Asp	Pro	Gln	Glu	Leu	Asp	Ile	Leu	Lys	Thr
	50					55					60				

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
195 200 205

Gly Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val
210 215 220

Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly Ile Gly Gly Gly Ser
225 230 235

<210> 78

<211> 777

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 78
atgaggctcc ctgctcagct cctggggctg ctaatgctct ggggtcccagg atccagtggg 60
cgcaaagtgt gtaacggaat aggtattggg gaatttaaag actcactctc cataaatgct 120
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 180
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 240
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 300
aggacggacc tccatgcctt tgagaacctg gaaatcatac gcggcaggac caagcaacat 360
ggtcagtttt ctcttgagtg cgtcagcctg aacataacat ccttgggatt acgctccctc 420
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaatt 480
acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaatt tataagcaac 540
agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttggtg ctcccccgag 600
ggctgctggg gcccgagacc cagggactgc gtctctgggtg gcggtggctc gggcggtggt 660
gggtcgggtg gcggcggatc tgggtggcggg ggctcgataa cactcattat ttttgggggtg 720
atggctggtg ttattggaac gacacctta gccctgctca tctggggagg tggaagc 777

<210> 79
<211> 259
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 79
Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro
1 5 10 15
Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe
20 25 30
Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn
35 40 45
Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg
50 55 60

Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp
65 70 75 80

Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala
85 90 95

Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile
100 105 110

Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val
115 120 125

Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser
130 135 140

Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn
145 150 155 160

Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys
165 170 175

Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val
180 185 190

Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg
195 200 205

Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val
225 230 235 240

Met Ala Gly Val Ile Gly Thr Ile Leu Leu Ala Leu Leu Ile Trp Gly
245 250 255

Gly Gly Ser

<210> 80
<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 80

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cgcaaagtgt gtaacggaat aggtattggg gaatttaaag actcactctc cataaatgct      60
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg      120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat      180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac      240
aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat      300
ggtcagtttt ctcttgagcgt cgtcagcctg aacataacat ccttgggatt acgctccctc      360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaatt      420
acaataaaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaatt tataagcaac      480
agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag      540
ggctgctggg gcccgagacc cagggactgc gtctctgggt gcggtggctc gggcggtggt      600
gggtcgggtg gcggcggatc tgggtggcgt ggctcgataa cactcattat ttttgggggtg      660
atggctgggtg ttattggaac gacacctta gccctgtca tctggggagg tggaagc      717
```

<210> 81

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 81

```
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1           5           10          15
```

```
Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
          20          25          30
```

```
Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
          35          40          45
```

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
195 200 205

Gly Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val
210 215 220

Ile Gly Thr Ile Leu Leu Ala Leu Leu Ile Trp Gly Gly Gly Ser
225 230 235

<210> 82

<211> 771

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 82

```
atgaggctcc ctgctcagct cctggggctg ctaatgctct ggggtcccagg atccagtggg      60
cgcaaagtgt gtaacggaat aggtattggg gaatttaaag actcactctc cataaatgct      120
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg      180
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat      240
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac      300
aggacggacc tccatgcctt tgagaacctt gaaatcatal gcggcaggac caagcaacat      360
ggtcagtttt ctcttgagc cgtcagcctg aacataacat ccttgggatt acgctccctc      420
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaatt      480
acaataaaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaatt tataagcaac      540
agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag      600
ggctgctggg gcccgagacc cagggactgc gtctctgggt gcggtggctc gggcggtggt      660
gggtcgggtg gcggcggatc tgggtggcgt ggctcgctct gctacctgct ggatggaatc      720
ctcttcatct atggtgtcat tctcactgcc ttgttcctgg gaggtggaag c              771
```

<210> 83

<211> 257

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 83

```
Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro
1           5           10          15
```

```
Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe
          20          25          30
```

```
Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn
          35          40          45
```

Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg
50 55 60

Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp
65 70 75 80

Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala
85 90 95

Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile
100 105 110

Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val
115 120 125

Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser
130 135 140

Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn
145 150 155 160

Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys
165 170 175

Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val
180 185 190

Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg
195 200 205

Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Leu Cys Tyr Leu Leu Asp Gly Ile
225 230 235 240

Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Gly Gly Gly
245 250 255

Ser

<210> 84
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 84
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240
aggacggacc tccatgcctt tgagaacctg gaaatcatac gcggcaggac caagcaacat 300
ggtcagtttt ctcttgagcgt cgtcagcctg aacataacat ccttgggatt acgctccctc 360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420
acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaact tataagcaac 480
agaggtgaaa acagctgcaa ggccacaggc caggctctgcc atgccttgtg ctcccccgag 540
ggctgctggg gcccggagcc cagggactgc gtctctgggtg gcggtggctc gggcgggtgt 600
gggtcgggtg gcggcggatc tgggtggcggg ggctcgtctt gctacctgct ggatggaatc 660
ctcttcatct atgggtgtcat tctcactgcc ttgttcctgg gaggtggaag c 711

<210> 85
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 85
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
195 200 205

Gly Gly Gly Ser Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr
210 215 220

Gly Val Ile Leu Thr Ala Leu Phe Leu Gly Gly Gly Ser
225 230 235

<211> 1077
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 86

atgcttctcc tggtgacaag ctttctgctc tgtgagttac cacaccagc attcctcctg	60
atccccacgca aagtgtgtaa cggaataggt attggtgaat ttaaagactc actctccata	120
aatgctacga atattaaaca cttcaaaaac tgcacctcca tcagtggcga tctccacatc	180
ctgccggtgg catttagggg tgactccttc acacatactc ctctcttgga tccacaggaa	240
ctggatattc tgaaaaccgt aaaggaaatc acagggtttt tgctgattca ggcttggcct	300
gaaaacagga cggacctcca tgcctttgag aacctagaaa tcatacgcgg caggaccaag	360
caacatggtc agttttctct tgcagtcgtc agcctgaaca taacatcctt gggattacgc	420
tccctcaagg agataagtga tggagatgtg ataatttcag gaaacaaaaa tttgtgctat	480
gcaaatacaa taaactggaa aaaactgttt gggacctccg gtcagaaaac caaaattata	540
agcaacagag gtgaaaacag ctgcaaggcc acaggccagg cctgccacca gctgtgcgcc	600
cgagggcact gctgggggtcc agggcccacc cagtgtgtca actgcagcca gttccttcgg	660
ggccaggagt gcgtggagga atgccgagta ctgcaggggc tcccagggga gtatgtgaat	720
gccaggcact gtttgccgtg ccaccctgag tgtcagcccc agaatggctc agtgacctgt	780
tttggaccgg aggctgacca gtgtgtggcc tgtgcccact ataaggacc tcccttctgc	840
gtggcccgct gccccagcgg tgtgaaacct gacctctctt acatgcccac ctggaagttt	900
ccagatgagg agggcgcatg ccagccttgc cccatcaact gcaccactc ctgtgtggac	960
ctggatgaca agggctgccc cgccgagcag agagccagcc ctctgacgtc catcatctct	1020
gcggtgggtg gcattctgct ggtcgtggtc ttgggggtgg tctttgggat cctcatc	1077

<210> 87
<211> 359
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 87

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
20 25 30

Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
35 40 45

Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
50 55 60

Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
65 70 75 80

Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
85 90 95

Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
100 105 110

Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala
115 120 125

Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
130 135 140

Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
145 150 155 160

Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys
165 170 175

Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
180 185 190

Gln Ala Cys His Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly
195 200 205

Pro Thr Gln Cys Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys
210 215 220

Val Glu Glu Cys Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn
225 230 235 240

Ala Arg His Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly
245 250 255

Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala
260 265 270

His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val
275 280 285

Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu
290 295 300

Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp
305 310 315 320

Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr
325 330 335

Ser Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly
340 345 350

Val Val Phe Gly Ile Leu Ile
355

<210> 88

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 88

cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

```

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat      180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac      240
aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat      300
ggtcagtttt ctcttgagct cgtcagcctg aacataacat ccttgggatt acgctccctc      360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaatt      420
acaataaaact ggaaaaaact gtttgggacc tccggtcaga aaacaaaaat tataagcaac      480
agaggtgaaa acagctgcaa ggccacaggc caggcctgcc accagctgtg cgcccagggg      540
cactgctggg gtccagggcc caccagtggt gtcaactgca gccagttcct tcggggccag      600
gagtgcgtgg aggaatgccg agtactgcag gggctcccca gggagtatgt gaatgccagg      660
cactgtttgc cgtgccaccc tgagtgtcag cccagaatg gctcagtga cgtttttgga      720
ccggaggctg accagtgtgt ggcctgtgcc cactataagg accctccctt ctgcgtggcc      780
cgctgccccca gcggtgtgaa acctgacctc tcctacatgc ccatctggaa gtttccagat      840
gaggagggcg catgccagcc ttgccccatc aactgcaccc actcctgtgt ggacctggat      900
gacaagggct gccccgccga gcagagagcc agccctctga cgtccatcat ctctgcggtg      960
gttggcattc tgctggctgt ggtcttgggg gtggtctttg ggatcctcat c              1011

```

<210> 89

<211> 337

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 89

```

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1           5           10          15

```

```

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
          20          25          30

```

```

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
          35          40          45

```

```

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr

```

50

55

60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Ala Cys His Gln Leu
165 170 175

Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys Val Asn
180 185 190

Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys Arg Val
195 200 205

Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys Leu Pro
210 215 220

Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys Phe Gly
225 230 235 240

Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp Pro Pro
245 250 255

Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr
260 265 270

Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys
275 280 285

Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly Cys
290 295 300

Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser Ala Val
305 310 315 320

Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly Ile Leu
325 330 335

Ile

<210> 90

<211> 1029

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 90

atgcttctcc tggtgacaag ctttctgctc tgtgagttac cacaccagc attcctcctg	60
atcccacgca aagtgtgtaa cggaataggt attggtgaat ttaaagactc actctccata	120
aatgctacga atattaaaca cttcaaaaac tgcacctcca tcagtggcga tctccacatc	180
ctgccggtgg catttagggg tgactccttc acacatactc ctctcttgga tccacaggaa	240
ctggatattc tgaaaaccgt aaaggaaatc acagggtttt tgctgattca ggcttggcct	300
gaaaacagga cggacctcca tgcctttgag aacctagaaa tcatacgcgg caggaccaag	360
caacatggtc agttttctct tgcagtcgtc agcctgaaca taacatcctt gggattacgc	420
tccctcaagg agataagtga tggagatgtg ataatttcag gaaacaaaaa tttgtgctat	480
gcaaatacaa taaactggaa aaaactgttt gggacctccg gtcagaaaac caaaattata	540
agcaacagag gtgaaaacag ctgcaaggcc acaggccagg cctgccacca gctgtgcgcc	600
cgagggcact gctggggtcc agggcccacc cagtgtgtca actgcagcca gttccttcgg	660
ggccaggagt gcgtggagga atgccgagta ctgcaggggc tccccaggga gtatgtgaat	720

gccaggcact gtttgccgtg ccaccctgag tgtcagcccc agaatggctc agtgacctgt	780
tttggaccgg aggctgacca gtgtgtggcc tgtgcccact ataaggaccc tcccttctgc	840
gtggcccgct gccccagcgg tgtgaaacct gacctctcct acatgcccac ctggaagttt	900
ccagatgagg agggcgcatg ccagccttgc cccatcaact gcaccactc ccctctgacg	960
tccatcatct ctgcggtggt tggcattctg ctggctgtgg tcttgggggt ggtctttggg	1020
atcctcatc	1029

<210> 91

<211> 343

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 91

Met	Leu	Leu	Leu	Val	Thr	Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro
1				5					10					15	

Ala	Phe	Leu	Leu	Ile	Pro	Arg	Lys	Val	Cys	Asn	Gly	Ile	Gly	Ile	Gly
		20						25					30		

Glu	Phe	Lys	Asp	Ser	Leu	Ser	Ile	Asn	Ala	Thr	Asn	Ile	Lys	His	Phe
		35					40					45			

Lys	Asn	Cys	Thr	Ser	Ile	Ser	Gly	Asp	Leu	His	Ile	Leu	Pro	Val	Ala
	50					55					60				

Phe	Arg	Gly	Asp	Ser	Phe	Thr	His	Thr	Pro	Pro	Leu	Asp	Pro	Gln	Glu
65					70					75					80

Leu	Asp	Ile	Leu	Lys	Thr	Val	Lys	Glu	Ile	Thr	Gly	Phe	Leu	Leu	Ile
			85						90					95	

Gln	Ala	Trp	Pro	Glu	Asn	Arg	Thr	Asp	Leu	His	Ala	Phe	Glu	Asn	Leu
			100					105					110		

Glu	Ile	Ile	Arg	Gly	Arg	Thr	Lys	Gln	His	Gly	Gln	Phe	Ser	Leu	Ala
		115					120					125			

Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
130 135 140

Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
145 150 155 160

Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys
165 170 175

Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
180 185 190

Gln Ala Cys His Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly
195 200 205

Pro Thr Gln Cys Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys
210 215 220

Val Glu Glu Cys Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn
225 230 235 240

Ala Arg His Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly
245 250 255

Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala
260 265 270

His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val
275 280 285

Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu
290 295 300

Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr His Ser Pro Leu Thr
305 310 315 320

Ser Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly
325 330 335

Val Val Phe Gly Ile Leu Ile
340

<210> 92
<211> 963
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 92
cgcaaagtgt gtaacggaat aggtattggg gaatttaaag actcactctc cataaatgct 60
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240
aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300
ggtcagtttt ctcttgagtg cgtcagcctg aacataacat ccttgggatt acgctccctc 360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaatt 420
acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaatt tataagcaac 480
agaggtgaaa acagctgcaa ggccacaggc caggcctgcc accagctgtg cgcccagggg 540
cactgctggg gtccagggcc caccagtggt gtcaactgca gccagttcct tcggggccag 600
gagtgcgtgg aggaatgccg agtactgcag gggctccca gggagtatgt gaatgccagg 660
cactgtttgc cgtgccacc tgagtgtcag cccagaatg gctcagtgac ctgttttgga 720
ccggaggctg accagtgtgt ggcctgtgcc cactataagg accctccctt ctgcgtggcc 780
cgctgccccca gcggtgtgaa acctgacctc tcctacatgc ccatctggaa gtttccagat 840
gaggagggcg catgccagcc ttgccccatc aactgcaccc actcccctct gacgtccatc 900
atctctgcgg tggttggcat tctgctggtc gtggtccttg gggtggtctt tgggatcctc 960
atc 963

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

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 93

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Ala Cys His Gln Leu
165 170 175

Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys Val Asn
180 185 190

Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys Arg Val

195

200

205

Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys Leu Pro
 210 215 220

Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys Phe Gly
 225 230 235 240

Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp Pro Pro
 245 250 255

Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr
 260 265 270

Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys
 275 280 285

Pro Ile Asn Cys Thr His Ser Pro Leu Thr Ser Ile Ile Ser Ala Val
 290 295 300

Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly Ile Leu
 305 310 315 320

Ile

<210> 94

<211> 1080

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 94

atgcttctcc tggtagacaag ctttctgctc tgtgagttac cacaccagc attcctcctg 60

atcccacgca aagtgtgtaa cggaataggt attggtgaat ttaaagactc actctccata 120

aatgctacga atattaaaca cttcaaaaac tgcacctcca tcagtggcga tctccacatc 180

ctgccggtgg catttagggg tgactccttc acacatactc ctcctctgga tccacaggaa 240

ctggatattc tgaaaaccgt aaaggaaatc acagggtttt tgctgattca ggcttggcct 300

gaaaacagga cggacctcca tgcctttgag aacctagaaa tcatacgcgg caggaccaag	360
caacatgggtc agttttctct tgcagtcgtc agcctgaaca taacatcctt gggattacgc	420
tccctcaagg agataagtga tggagatgtg ataatttcag gaaacaaaaa tttgtgctat	480
gcaaatacaa taaactggaa aaaactgttt gggacctccg gtcagaaaac caaaattata	540
agcaacagag gtgaaaacag ctgcaaggcc acaggccagg tgtgtgaccc actgtgctcc	600
tctgggggat gctggggccc aggccctggt cagtgcctgt cctgtcgaaa ttatagccga	660
ggaggtgtct gtgtgaccca ctgcaacttt ctgaatgggg agcctcgaga atttgcccat	720
gaggccgaat gcttctcctg ccacccggaa tgccaacca tggagggcac tgccacatgc	780
aatggctcgg gctctgatac ttgtgctcaa tgtgcccatt ttcgagatgg gccccactgt	840
gtgagcagct gccccatgg agtcctaggt gccaaaggcc caatctacaa gtaccagat	900
gttcagaatg aatgtcggcc ctgccatgag aactgcaccc aggggtgtaa aggaccagag	960
cttcaagact gtttaggaca aacactggtg ctgatcggca aaacccatct gacaatggct	1020
ttgacagtga tagcaggatt ggtagtgatt ttcatgatgc tgggcggcac ttttctctac	1080

<210> 95

<211> 360

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 95

Met	Leu	Leu	Leu	Val	Thr	Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro
1				5					10				15		

Ala	Phe	Leu	Leu	Ile	Pro	Arg	Lys	Val	Cys	Asn	Gly	Ile	Gly	Ile	Gly
		20						25					30		

Glu	Phe	Lys	Asp	Ser	Leu	Ser	Ile	Asn	Ala	Thr	Asn	Ile	Lys	His	Phe
		35					40				45				

Lys	Asn	Cys	Thr	Ser	Ile	Ser	Gly	Asp	Leu	His	Ile	Leu	Pro	Val	Ala
	50					55					60				

Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
65 70 75 80

Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
85 90 95

Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
100 105 110

Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala
115 120 125

Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
130 135 140

Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
145 150 155 160

Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys
165 170 175

Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
180 185 190

Gln Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro Gly
195 200 205

Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val Cys
210 215 220

Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala His
225 230 235 240

Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu Gly
245 250 255

Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys Ala
260 265 270

His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly Val
275 280 285

Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn Glu
 290 295 300

Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro Glu
 305 310 315 320

Leu Gln Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr His
 325 330 335

Leu Thr Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe Met
 340 345 350

Met Leu Gly Gly Thr Phe Leu Tyr
 355 360

<210> 96

<211> 1014

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 96

cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct	60
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg	120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat	180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac	240
aggacggacc tccatgcctt tgagaacctt gaaatcatat gcggcaggac caagcaacat	300
ggtcagtttt ctcttgagtg cgtcagcctg aacataacat ccttgggatt acgctccctc	360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaa	420
acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaa	480
agaggtgaaa acagctgcaa ggccacaggc caggtgtgtg acccactgtg ctcctctggg	540
ggatgctggg gccaggccc tggtcagtg ttgtcctgtc gaaattatag ccgaggaggt	600
gtctgtgtga cccactgcaa ctttctgaat ggggagcctc gagaatttgc ccatgaggcc	660

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gaatgcttct cctgccaccc ggaatgccaa cccatggagg gcactgccac atgcaatggc      720
tcgggctctg atacttgtgc tcaatgtgcc cattttcgag atgggccccca ctgtgtgagc      780
agctgcccc atggagtcct aggtgccaa ggcccaatct acaagtaccc agatgttcag      840
aatgaatgtc ggccctgcc tgagaactgc acccaggggt gtaaaggacc agagcttcaa      900
gactgtttag gacaaacact ggtgctgac ggcaaaaccc atctgacaat ggctttgaca      960
gtgatagcag gattggtagt gattttcatg atgctgggcg gcacttttct ctac      1014

```

<210> 97

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 97

```

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1           5           10          15

```

```

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
          20          25          30

```

```

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
          35          40          45

```

```

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
          50          55          60

```

```

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65          70          75          80

```

```

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
          85          90          95

```

```

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

```

```

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
          115         120         125

```

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys Asp Pro Leu
165 170 175

Cys Ser Ser Gly Gly Cys Trp Gly Pro Gly Pro Gly Gln Cys Leu Ser
180 185 190

Cys Arg Asn Tyr Ser Arg Gly Gly Val Cys Val Thr His Cys Asn Phe
195 200 205

Leu Asn Gly Glu Pro Arg Glu Phe Ala His Glu Ala Glu Cys Phe Ser
210 215 220

Cys His Pro Glu Cys Gln Pro Met Glu Gly Thr Ala Thr Cys Asn Gly
225 230 235 240

Ser Gly Ser Asp Thr Cys Ala Gln Cys Ala His Phe Arg Asp Gly Pro
245 250 255

His Cys Val Ser Ser Cys Pro His Gly Val Leu Gly Ala Lys Gly Pro
260 265 270

Ile Tyr Lys Tyr Pro Asp Val Gln Asn Glu Cys Arg Pro Cys His Glu
275 280 285

Asn Cys Thr Gln Gly Cys Lys Gly Pro Glu Leu Gln Asp Cys Leu Gly
290 295 300

Gln Thr Leu Val Leu Ile Gly Lys Thr His Leu Thr Met Ala Leu Thr
305 310 315 320

Val Ile Ala Gly Leu Val Val Ile Phe Met Met Leu Gly Gly Thr Phe
325 330 335

Leu Tyr

<210> 98
<211> 1101
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 98
atgcttctcc tggtgacaag ctttctgctc tgtgagttac cacaccagc attcctcctg 60
atcccacgca aagtgtgtaa cggaataggt attggtgaat ttaaagactc actctccata 120
aatgctacga atattaaaca cttcaaaaac tgcacctcca tcagtggcga tctccacatc 180
ctgccggtgg catttagggg tgactccttc acacatactc ctctcttgga tccacaggaa 240
ctggatattc tgaaaaccgt aaaggaaatc acagggtttt tgctgattca ggcttggcct 300
gaaaacagga cggacctcca tgcctttgag aacctagaaa tcatacgcgg caggaccaag 360
caacatggtc agttttctct tgcagtcgtc agcctgaaca taacatcctt gggattacgc 420
tccctcaagg agataagtga tggagatgtg ataatttcag gaaacaaaaa tttgtgctat 480
gcaaatacaa taaactggaa aaaactgttt gggacctccg gtcagaaaac caaaattata 540
agcaacagag gtgaaaacag ctgcaaggcc acaggccagg tgtgcaacca tctgtgttcc 600
agtgatggct gttggggacc tgggccagac caatgtctgt cgtgtcgccg cttcagtaga 660
ggaaggatct gcatagagtc ttgtaacctc tatgatgggtg aatttcggga gtttgagaat 720
ggctccatct gtgtggagtg tgacccccag tgtgagaaga tggaagatgg cctcctcaca 780
tgccatggac cgggtcctga caactgtaca aagtgtcttc attttaaaga tggcccaaac 840
tgtgtggaaa aatgtccaga tggcttacag ggggcaaaca gtttcatttt caagtatgct 900
gatccagatc gggagtgcc aacatgccat ccaaactgca cccaagggtg taacgggtccc 960
actagtcatg actgcattta ctacccatgg acgggccatt ccactttacc acaacatgct 1020
agaactcccc tgattgcagc tggagtaatt ggtgggctct tcattctggt cattgtgggt 1080
ctgacatttg ctgtttatgt t 1101

<210> 99
<211> 367

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 99

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
20 25 30

Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
35 40 45

Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
50 55 60

Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
65 70 75 80

Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
85 90 95

Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
100 105 110

Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala
115 120 125

Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
130 135 140

Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
145 150 155 160

Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys
165 170 175

Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
180 185 190

Gln Val Cys Asn His Leu Cys Ser Ser Asp Gly Cys Trp Gly Pro Gly
195 200 205

Pro Asp Gln Cys Leu Ser Cys Arg Arg Phe Ser Arg Gly Arg Ile Cys
210 215 220

Ile Glu Ser Cys Asn Leu Tyr Asp Gly Glu Phe Arg Glu Phe Glu Asn
225 230 235 240

Gly Ser Ile Cys Val Glu Cys Asp Pro Gln Cys Glu Lys Met Glu Asp
245 250 255

Gly Leu Leu Thr Cys His Gly Pro Gly Pro Asp Asn Cys Thr Lys Cys
260 265 270

Ser His Phe Lys Asp Gly Pro Asn Cys Val Glu Lys Cys Pro Asp Gly
275 280 285

Leu Gln Gly Ala Asn Ser Phe Ile Phe Lys Tyr Ala Asp Pro Asp Arg
290 295 300

Glu Cys His Pro Cys His Pro Asn Cys Thr Gln Gly Cys Asn Gly Pro
305 310 315 320

Thr Ser His Asp Cys Ile Tyr Tyr Pro Trp Thr Gly His Ser Thr Leu
325 330 335

Pro Gln His Ala Arg Thr Pro Leu Ile Ala Ala Gly Val Ile Gly Gly
340 345 350

Leu Phe Ile Leu Val Ile Val Gly Leu Thr Phe Ala Val Tyr Val
355 360 365

<210> 100

<211> 1035

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 100

cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct	60
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg	120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat	180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac	240
aggacggacc tccatgcctt tgagaaccta gaaatcatat gcggcaggac caagcaacat	300
ggtcagtttt ctcttgagct cgtcagcctg aacataacat ccttgggatt acgctccctc	360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat	420
acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaact tataagcaac	480
agaggtgaaa acagctgcaa ggccacaggc caggtgtgca accatctgtg ttccagtgat	540
ggctgttggg gacctgggcc agaccaatgt ctgtcgtgtc gccgcttcag tagaggaagg	600
atctgcatag agtcttgtaa cctctatgat ggtgaatttc gggagtttga gaatggctcc	660
atctgtgtgg agtgtgaccc ccagtgtgag aagatggaag atggcctcct cacatgccat	720
ggaccgggtc ctgacaactg tacaaagtgc tctcatttta aagatggccc aaactgtgtg	780
gaaaaatgtc cagatggctt acagggggca aacagtttca ttttcaagta tgctgatcca	840
gatcgggagt gccacccatg ccatccaaac tgcacccaag ggtgtaacgg tcccactagt	900
catgactgca tttactaccc atggacgggc cattccactt taccacaaca tgctagaact	960
cccctgattg cagctggagt aattgggtggg ctcttcattc tggtcattgt gggctctgaca	1020
tttgctgttt atgtt	1035

<210> 101

<211> 345

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 101

Arg	Lys	Val	Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu
1				5			10					15			

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile

20

25

30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
 35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
 50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
 65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
 85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
 115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
 130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
 145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys Asn His Leu
 165 170 175

Cys Ser Ser Asp Gly Cys Trp Gly Pro Gly Pro Asp Gln Cys Leu Ser
 180 185 190

Cys Arg Arg Phe Ser Arg Gly Arg Ile Cys Ile Glu Ser Cys Asn Leu
 195 200 205

Tyr Asp Gly Glu Phe Arg Glu Phe Glu Asn Gly Ser Ile Cys Val Glu
 210 215 220

Cys Asp Pro Gln Cys Glu Lys Met Glu Asp Gly Leu Leu Thr Cys His
 225 230 235 240

Gly Pro Gly Pro Asp Asn Cys Thr Lys Cys Ser His Phe Lys Asp Gly
245 250 255

Pro Asn Cys Val Glu Lys Cys Pro Asp Gly Leu Gln Gly Ala Asn Ser
260 265 270

Phe Ile Phe Lys Tyr Ala Asp Pro Asp Arg Glu Cys His Pro Cys His
275 280 285

Pro Asn Cys Thr Gln Gly Cys Asn Gly Pro Thr Ser His Asp Cys Ile
290 295 300

Tyr Tyr Pro Trp Thr Gly His Ser Thr Leu Pro Gln His Ala Arg Thr
305 310 315 320

Pro Leu Ile Ala Ala Gly Val Ile Gly Gly Leu Phe Ile Leu Val Ile
325 330 335

Val Gly Leu Thr Phe Ala Val Tyr Val
340 345

<210> 102

<211> 1071

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 102

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atcccacgca aagtgtgtaa cggaataggt attggtgaat ttaaagactc actctccata	120
aatgctacga atattaaaca cttcaaaaac tgcacctcca tcagtggcga tctccacatc	180
ctgccggtgg catttagggg tgactccttc acacatactc ctctcttgga tccacaggaa	240
ctggatattc tgaaaaccgt aaaggaaatc acagggtttt tgctgattca ggcttggcct	300
gaaaacagga cggacctcca tgcctttgag aacctagaaa tcatacgcgg caggaccaag	360
caacatggtc agttttctct tgcagtcgtc agcctgaaca taacatcctt gggattacgc	420
tccctcaagg agataagtga tggagatgtg ataatttcag gaaacaaaaa tttgtgctat	480

gcaaatacaa taaactggaa aaaactgttt gggacctccg gtcagaaaac caaaattata	540
agcaacagag gtgaaaacag ctgcaaggcc acaggccagg tgtgcaacca tctgtgttcc	600
agtgatggct gttggggacc tgggccagac caatgtctgt cgtgtcgccg cttcagtaga	660
ggaaggatct gcatagagtc ttgtaacctc tatgatggtg aatttcggga gtttgagaat	720
ggctccatct gtgtggagtg tgacccccag tgtgagaaga tggaagatgg cctcctcaca	780
tgccatggac cgggtcctga caactgtaca aagtgtcttc attttaaaga tggcccaaac	840
tgtgtggaaa aatgtccaga tggcttacag ggggcaaaca gtttcatttt caagtatgct	900
gatccagatc gggagtgcc cccatgccat ccaaactgca cccaagggtg cataggctca	960
agtattgaag actgcatcgg cctgatggat agaactcccc tgattgcagc tggagtaatt	1020
ggtgggctct tcattctggt cattgtgggt ctgacatttg ctgtttatgt t	1071

<210> 103

<211> 357

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 103

Met	Leu	Leu	Leu	Val	Thr	Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro
1				5					10					15	

Ala	Phe	Leu	Leu	Ile	Pro	Arg	Lys	Val	Cys	Asn	Gly	Ile	Gly	Ile	Gly
			20					25					30		

Glu	Phe	Lys	Asp	Ser	Leu	Ser	Ile	Asn	Ala	Thr	Asn	Ile	Lys	His	Phe
		35					40					45			

Lys	Asn	Cys	Thr	Ser	Ile	Ser	Gly	Asp	Leu	His	Ile	Leu	Pro	Val	Ala
	50					55					60				

Phe	Arg	Gly	Asp	Ser	Phe	Thr	His	Thr	Pro	Pro	Leu	Asp	Pro	Gln	Glu
65					70					75					80

Leu	Asp	Ile	Leu	Lys	Thr	Val	Lys	Glu	Ile	Thr	Gly	Phe	Leu	Leu	Ile
			85						90					95	

Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
100 105 110

Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala
115 120 125

Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
130 135 140

Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
145 150 155 160

Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys
165 170 175

Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
180 185 190

Gln Val Cys Asn His Leu Cys Ser Ser Asp Gly Cys Trp Gly Pro Gly
195 200 205

Pro Asp Gln Cys Leu Ser Cys Arg Arg Phe Ser Arg Gly Arg Ile Cys
210 215 220

Ile Glu Ser Cys Asn Leu Tyr Asp Gly Glu Phe Arg Glu Phe Glu Asn
225 230 235 240

Gly Ser Ile Cys Val Glu Cys Asp Pro Gln Cys Glu Lys Met Glu Asp
245 250 255

Gly Leu Leu Thr Cys His Gly Pro Gly Pro Asp Asn Cys Thr Lys Cys
260 265 270

Ser His Phe Lys Asp Gly Pro Asn Cys Val Glu Lys Cys Pro Asp Gly
275 280 285

Leu Gln Gly Ala Asn Ser Phe Ile Phe Lys Tyr Ala Asp Pro Asp Arg
290 295 300

Glu Cys His Pro Cys His Pro Asn Cys Thr Gln Gly Cys Ile Gly Ser
 305 310 315 320

Ser Ile Glu Asp Cys Ile Gly Leu Met Asp Arg Thr Pro Leu Ile Ala
 325 330 335

Ala Gly Val Ile Gly Gly Leu Phe Ile Leu Val Ile Val Gly Leu Thr
 340 345 350

Phe Ala Val Tyr Val
 355

<210> 104

<211> 1005

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 104

cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct	60
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg	120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat	180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac	240
aggacggacc tccatgcctt tgagaacctg gaaatcatac gcggcaggac caagcaacat	300
ggtcagtttt ctcttgagtg cgtcagcctg aacataacat ccttgaggatt acgctccctc	360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat	420
acaataaaact ggaaaaaact gtttgggacc tccggtcaga aaacaaaaat tataagcaac	480
agaggtgaaa acagctgcaa ggccacaggc caggtgtgca accatctgtg ttccagtgat	540
ggctgttggg gacctgggcc agaccaatgt ctgtcgtgtc gccgcttcag tagaggaagg	600
atctgcatag agtcttgtaa cctctatgat ggtgaatttc gggagtttga gaatggctcc	660
atctgtgtgg agtgtgacct ccagtgtgag aagatggaag atggcctcct cacatgccat	720
ggaccgggtc ctgacaactg taaaagtgc tctcatttta aagatggccc aaactgtgtg	780
gaaaaatgtc cagatggctt acagggggca aacagtttca ttttcaagta tgctgatcca	840

gatcgggagt gccacccatg ccatccaaac tgcacccaag ggtgcatagg ctcaagtatt 900
gaagactgca tcggcctgat ggatagaact cccctgattg cagctggagt aattggtggg 960
ctcttcattc tggtcattgt gggctctgaca tttgctgttt atgtt 1005

<210> 105
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 105
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn

145		150		155		160
Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys Asn His Leu						
		165		170		175
Cys Ser Ser Asp Gly Cys Trp Gly Pro Gly Pro Asp Gln Cys Leu Ser						
		180		185		190
Cys Arg Arg Phe Ser Arg Gly Arg Ile Cys Ile Glu Ser Cys Asn Leu						
		195		200		205
Tyr Asp Gly Glu Phe Arg Glu Phe Glu Asn Gly Ser Ile Cys Val Glu						
		210		215		220
Cys Asp Pro Gln Cys Glu Lys Met Glu Asp Gly Leu Leu Thr Cys His						
		225		230		235
Gly Pro Gly Pro Asp Asn Cys Thr Lys Cys Ser His Phe Lys Asp Gly						
		245		250		255
Pro Asn Cys Val Glu Lys Cys Pro Asp Gly Leu Gln Gly Ala Asn Ser						
		260		265		270
Phe Ile Phe Lys Tyr Ala Asp Pro Asp Arg Glu Cys His Pro Cys His						
		275		280		285
Pro Asn Cys Thr Gln Gly Cys Ile Gly Ser Ser Ile Glu Asp Cys Ile						
		290		295		300
Gly Leu Met Asp Arg Thr Pro Leu Ile Ala Ala Gly Val Ile Gly Gly						
		305		310		315
Leu Phe Ile Leu Val Ile Val Gly Leu Thr Phe Ala Val Tyr Val						
		325		330		335

<210> 106

<211> 891

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown:

Full length CD20 sequence

<400> 106

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atgacaacac ccagaaattc agtaaattggg actttcccgg cagagccaat gaaaggccct      60
attgctatgc aatctggtcc aaaaccactc ttcaggagga tgtcttcact ggtgggcccc      120
acgcaaagct tcttcattgag ggaatctaag actttggggg ctgtccagat tatgaatggg      180
ctcttccaca ttgccctggg gggctcttctg atgatcccag cagggatcta tgcacccatc      240
tgtgtgactg tgtggtaccc tctctgggga ggcattatgt atattatttc cggatcactc      300
ctggcagcaa cggagaaaaa ctccaggaag tgtttggtca aaggaaaaat gataatgaat      360
tcattgagcc tctttgctgc catttctgga atgattcttt caatcatgga cataacttaat      420
attaaaattt cccatttttt aaaaatggag agtctgaatt ttattagagc tcacacacca      480
tatattaaca tatacaactg tgaaccagct aatccctctg agaaaaactc cccatctacc      540
caatactgtt acagcataca atctctgttc ttgggcattt tgtcagtgat gctgatcttt      600
gccttcttcc aggaacttgt aatagctggc atcgttgaga atgaatggaa aagaacgtgc      660
tccagacca aatctaacat agttctcctg tcagcagaag aaaaaaaga acagactatt      720
gaaataaaag aagaagtggg tgggctaact gaaacatctt cccaacaaa gaatgaagaa      780
gacattgaaa ttattccaat ccaagaagag gaagaagaag aaacagagac gaactttcca      840
gaacctcccc aagatcagga atcctcacca atagaaaatg acagctctcc t              891

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<210> 107

<211> 297

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

Full length CD20 sequence

<400> 107

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Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1           5           10          15

```

```

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
          20          25          30

```

```

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
          35          40          45

```

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
50 55 60

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
65 70 75 80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
85 90 95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
100 105 110

Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
115 120 125

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
130 135 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
145 150 155 160

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
165 170 175

Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
180 185 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
195 200 205

Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
210 215 220

Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
225 230 235 240

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
245 250 255

Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu
260 265 270

Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
275 280 285

Ser Pro Ile Glu Asn Asp Ser Ser Pro
290 295

<210> 108
<211> 789
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 108
atgaccacac cacggaactc tgtgaatggc accttcccag cagagccaat gaagggacca 60
atcgcaatgc agagcggacc caagcctctg tttcggagaa tgagctccct ggtgggcccc 120
acccagtcct tctttatgag agagtctaag aacttgggcg ccgtgcagat catgaacgga 180
ctgttccaca tcgccctggg aggactgctg atgatcccag ccggcatcta cgcccctatc 240
tgcgtgaccg tgtggtaccc tctgtggggc ggcatcatgt atatcatctc cggctctctg 300
ctggccgcca cagagaagaa cagcaggaag tgtctggtga agggcaagat gatcatgaat 360
agcctgtccc tgtttgccgc catctctggc atgatcctga gcatcatgga catcctgaac 420
atcaagatca gccacttcct gaagatggag agcctgaact tcatcagagc ccacaccct 480
tacatcaaca tctataattg cgagcctgcc aaccatccg agaagaattc tccaagcaca 540
cagtactgtt attccatcca gtctctgttc ctgggcatcc tgtctgtgat gctgatcttt 600
gccttctttc aggagctggt catcgccggc atcgtggaga acgagtggaa gaggacctgc 660
agccgcccc agtccaatat cgtgctgctg tccgccgagg agaagaagga gcagacaatc 720
gagatcaagg aggaggtggt gggcctgacc gagacatcta gccagcctaa gaatgaggag 780
gatatcgag 789

<210> 109
<211> 263
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 109

Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
35 40 45

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
50 55 60

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
65 70 75 80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
85 90 95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
100 105 110

Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
115 120 125

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
130 135 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
145 150 155 160

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
165 170 175

Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
180 185 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
195 200 205

Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
210 215 220

Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
225 230 235 240

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
245 250 255

Lys Asn Glu Glu Asp Ile Glu
260

<210> 110
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 110
atgataatga attcattgag cctctttgct gccatttctg gaatgattct ttcaatcatg 60
gacataactta atattaaaat ttcccatgtt ttaaaaatgg agagtctgaa ttttattaga 120
gctcacacac catatattaa catatacaac tgtgaaccag ctaatccctc tgagaaaaac 180
tccccatcta cccaatactg ttacagcata caatctctgt tcttgggcat tttgtcagtg 240
atgctgatct ttgccttctt ccaggaactt gtaatagctg gcatcgttga gaat 294

<210> 111
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 111
Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile
1 5 10 15

Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys
20 25 30

Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile
35 40 45

Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr
50 55 60

Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val
65 70 75 80

Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val
85 90 95

Glu Asn

<210> 112

<211> 267

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 112

atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgaaaattt cccatttttt aaaaatggag agtctgaatt ttattagagc tcacacacca 120

tatattaaca tatacaactg tgaaccagct aatccctctg agaaaaactc cccatctacc 180

caatactgtt acagcataca atctatctac atctgggcgc ccttggccgg gacttgtggg 240

gtccttctcc tgcactggt tacc 267

<210> 113

<211> 89

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 113

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu
35 40 45

Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr
50 55 60

Ser Ile Gln Ser Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
65 70 75 80

Val Leu Leu Leu Ser Leu Val Ile Thr
85

<210> 114

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 114

atgacaacac ccagaaattc agtaaatggg actttcccgg cagagccaat gaaaggccct	60
attgctatgc aatctggtcc aaaaccactc ttcaggagga tgtcttcact ggtgggcccc	120
acgcaaagct tcttcatgag ggaatctaag actttggggg ctgtccagat tatgaatggg	180
ctcttcacac ttgccctggg gggtcttctg atgatcccag cagggatcta tgcacccatc	240
tgtgtgactg tgtggtaccc tctctgggga ggcattatgt atattatttc cggatcactc	300
ctggcagcaa cggagaaaaa ctccaggaag tgtttggtca aaggaaaaat gataatgaat	360
tcattgagcc tctttgctgc catttctgga atgattcttt caatcatgga catacttaat	420
attaaaattt cccatttttt aaaaatggag agtctgaatt ttattagagc tcacacacca	480
tatattaaca tatacaactg tgaaccagct aatccctctg agaaaaactc cccatctacc	540

caatactgtt acagcataca atctctgttc ttgggcattt tgtcagtgat gctgatcttt 600

gccttcttcc aggaacttgt aatagctggc atcgttgaga at 642

<210> 115

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 115

Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
35 40 45

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
50 55 60

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
65 70 75 80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
85 90 95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
100 105 110

Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
115 120 125

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
130 135 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
145 150 155 160

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
165 170 175

Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
180 185 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
195 200 205

Ala Gly Ile Val Glu Asn
210

<210> 116
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 116
gtgactgtgt ggtaccctct ctggggaggc attatgtata ttatttcgg atcactcctg 60
gcagcaacgg agaaaaactc caggaagtgt ttggtcaaag gaaaaatgat aatgaattca 120
ttgagcctct ttgctgcat ttctggaatg attctttcaa tcatggacat acttaatat 180
aaaatttccc attttttaaa aatggagagt ctgaatttta ttagagctca cacaccatat 240
attaacatat acaactgtga accagctaat ccctctgaga aaaactcccc atctacccaa 300
tactgttaca gcatacaatc tctgttcttg ggcattttgt cagtgatgct gatctttgcc 360
ttcttccagg aacttgtaat agctggcatc gttgagaat 399

<210> 117
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 117
Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile Ser

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

<210> 118
 <211> 315
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 118	
gtgactgtgt ggtaccctct ctggggaggc attatgtata ttatttccgg atcactcctg	60
gcagcaacgg agaaaaactc caggaagtgt ttggtcaaag gaaaaatgat aatgaattca	120
ttgagcctct ttgctgcat ttctggaatg attctttcaa tcatggacat acttaatatt	180
aaaatttccc attttttaaa aatggagagt ctgaatttta ttagagctca cacaccatat	240
attaacatat acaactgtga accagctaat ccctctgaga aaaactcccc atctacccaa	300

tactgttaca gcata

315

<210> 119

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 119

Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile Ser
1 5 10 15

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

Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile Ser
35 40 45

Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser His
50 55 60

Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr
65 70 75 80

Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser
85 90 95

Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile
100 105 110

Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala
115 120 125

Gly Ile Val Glu Asn
130

<210> 120

<211> 333

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 120

```
ccatatatta acatatacaa ctgtgaacca gctaatccct ctgagaaaaa ctccccatct      60
acccaatact gttacagcat acaatcgggt ggcggcggat ctattgaagt tatgtatcct      120
cctccttacc tagacaatga gaagagcaat ggaaccatta tccatgtgaa agggaaacac      180
ctttgtccaa gtcccctatt tcccggacct tctaagccct tttgggtgct ggtggtggtt      240
ggtggagtcc tggcttgcta tagcttgcta gtaacagtgg cctttattat tttctgggtg      300
aggagtaaga ggagcaggct cctgcacagt gac                                     333
```

<210> 121

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 121

```
Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys
1           5           10          15
```

```
Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Gly Gly Gly
          20          25          30
```

```
Gly Ser Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys
          35          40          45
```

```
Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser
          50          55          60
```

```
Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val
          65          70          75          80
```

```
Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
          85          90          95
```

```
Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
```

100

105

110

<210> 122

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 122

```

ccatatatta acatatacaa ctgtgaacca gctaatccct ctgagaaaaa ctcccatctt      60
acccaatact gttacagcat acaatcgggt ggcggcggat ctccatatat taacatatatac    120
aactgtgaac cagctaatcc ctctgagaaa aactcccat ctaccaata ctgttacagc      180
atacaatcgg gtggcggcgg atctattgaa gttatgtatc ctctcctta cctagacaat      240
gagaagagca atggaacat tatccatgtg aaagggaac acctttgtcc aagtccccta      300
tttcccgac cttctaagcc cttttgggtg ctggtggtgg ttggtggagt cctggcttgc      360
tatagcttgc tagtaacagt ggcctttatt attttctggg tgaggagtaa gaggagcagg      420
ctcctgcaca gtgac                                     435

```

<210> 123

<211> 145

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 123

```

Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys
1           5           10           15

Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Gly Gly Gly
          20           25           30

Gly Ser Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser
          35           40           45

Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Gly
50           55           60

```

Gly Gly Gly Ser Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn
65 70 75 80

Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys
85 90 95

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

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
115 120 125

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
130 135 140

Asp
145

<210> 124
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 124
ccatatatta acatatacaa ctgtgaacca gctaatccct ctgagaaaaa ctcccatct 60
acccaatact gttacagcat acaatcgggt ggcggcggat ctccagcgcc gcgaccacca 120
acaccggcgc ccaccatcgc gtcgcagccc ctgtccctgc gcccagaggc gtgccggcca 180
gcggcggggg gcgcagtgca cacgaggggg ctggacttcg cctgtgatat ctacatctgg 240
gcgcccttgg ccgggacttg tggggtcctt ctcctgtcac tggttatcac cttttactgc 300
aaccacagga accgaagacg tgtttgcaaa tgtccccggc ctgtggtc 348

<210> 125
<211> 116
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 125

Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys
1 5 10 15

Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Gly Gly Gly
20 25 30

Gly Ser Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
35 40 45

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
50 55 60

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
65 70 75 80

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
85 90 95

Thr Leu Tyr Cys Asn His Arg Asn Arg Arg Arg Val Cys Lys Cys Pro
100 105 110

Arg Pro Val Val
115

<210> 126

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 126

tgtgaaccag ctaatccctc tgagaaaaac tccccatcta cccaatactg ttcgggtggc 60

ggcggatcta ttgaagttat gtatcctcct cttacctag acaatgagaa gagcaatgga 120

accattatcc atgtgaaagg gaaacacctt tgtccaagtc ccctatttcc cggaccttct 180

aagccctttt ggggtgctggg ggtgggttggg ggagtcctgg cttgctatag cttgctagta 240

acagtggcct ttattatattt ctgggtgagg agtaagagga gcaggctcct gcacagtgac 300

<210> 127
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 127
Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr
1 5 10 15

Cys Ser Gly Gly Gly Gly Ser Ile Glu Val Met Tyr Pro Pro Pro Tyr
20 25 30

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

His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp
50 55 60

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
65 70 75 80

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
85 90 95

Leu His Ser Asp
100

<210> 128
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 128
tgtgaaccag ctaatccctc tgagaaaaac tccccatcta cccaatactg ttcgggtggc 60

```

ggcggatctt gtgaaccagc taatccctct gagaaaaact ccccatctac ccaatactgt      120
tcgggtggcg gcggatctat tgaagttatg tatcctcctc cttacctaga caatgagaag      180
agcaatggaa ccattatcca tgtgaaaggg aaacaccttt gtccaagtcc cctatttccc      240
ggaccttcta agcccttttg ggtgctggtg gtggttggtg gagtcctggc ttgctatagc      300
ttgctagtaa cagtggcctt tattattttc tgggtgagga gtaagaggag caggctcctg      360
cacagtgac                                                                    369

```

<210> 129

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 129

```

Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr
1           5           10           15

```

```

Cys Ser Gly Gly Gly Gly Ser Cys Glu Pro Ala Asn Pro Ser Glu Lys
          20           25           30

```

```

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

```

```

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

```

```

Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro
65           70           75           80

```

```

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

```

```

Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
          100          105          110

```

```

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
          115          120

```

<210> 130
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 130
tgtgaaccag ctaatccctc tgagaaaaac tccccatcta cccaatactg ttcgggtggc 60
ggcggatctc cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg 120
tccctgcgcc cagaggcgtg ccggccagcg gcggggggcg cagtgcacac gagggggctg 180
gacttcgcct gtgatatcta catctgggcg cccttggccg ggacttgtgg ggtccttctc 240
ctgtcactgg ttatcacctt ttactgcaac cacaggaacc gaagacgtgt ttgcaaattg 300
ccccggcctg tggtc 315

<210> 131
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 131
Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr
1 5 10 15

Cys Ser Gly Gly Gly Gly Ser Pro Ala Pro Arg Pro Pro Thr Pro Ala
20 25 30

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
35 40 45

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
50 55 60

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
65 70 75 80

Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Arg Arg
85 90 95

Val Cys Lys Cys Pro Arg Pro Val Val
100 105

<210> 132
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 132
atgaccacac cccggaactc cgtgaatggc accttcctg ccgagccaat gaagggccct 60
atgccatgc agtctggccc aaagcccctg tttcggagaa tgagctcct ggtgggcccc 120
accagagct tctttatgag ggagtccaag acactgggcg cctgcctggt gaagggcaag 180
atgatcatga actctctgag cctgttcgcc gccatctccg gcatgacct gtctatcatg 240
gacatcctga acatcaagat ctctcacttc ctgaagatgg agagcctgaa cttcatccgg 300
gccacaccc catacatcaa catctataat tgcgagcccg ccaaccctag cgagaagaat 360
tccccctcta cacagtactg ttatagcatc cagtccctgt tcctgggcat cctgtccgtg 420
atgctgatct ttgccttctt tcaggagctg gtcatcgccg gcatcgtgga gaacgagtgg 480
aagaggacct gttctcgccc taagagcaat atcgtgctgc tgagcgccga ggagaagaag 540
gagcagacaa tcgagatcaa ggaggaggtg gtgggcctga ccgagacatc tagccagcct 600
aagaatgagg aggatatcga gatcatccca atccaggagg aggaggagga ggagaccgag 660
acaaactttc cagagccccc tcaggaccag gagtcctctc caatcgagaa tgatagctcc 720
ccctgataa 729

<210> 133
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 133

Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
35 40 45

Ser Lys Thr Leu Gly Ala Cys Leu Val Lys Gly Lys Met Ile Met Asn
50 55 60

Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser Ile Met
65 70 75 80

Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met Glu Ser Leu
85 90 95

Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu
100 105 110

Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr
115 120 125

Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile Phe
130 135 140

Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn Glu Trp
145 150 155 160

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

Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val Val Gly
180 185 190

Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile Glu Ile
195 200 205

Ile Pro Ile Gln Glu Glu Glu Glu Glu Thr Glu Thr Asn Phe Pro

210

215

220

Glu Pro Pro Gln Asp Gln Glu Ser Ser Pro Ile Glu Asn Asp Ser Ser
 225 230 235 240

<210> 134

<211> 681

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 134

atgaccacac cacggaacag cgtgaatggc accttcccag cagagccaat gaagggacca 60
 atcgcaatgc agtccggacc caagcctctg tttcggagaa tgagctccct ggtgggcccc 120
 acccagtctt tctttatgag ggagagcaag aacttgggag cctgcctggt gaagggcaag 180
 atgatcatga actccctgtc tctgttcgcc gccatcagcg gcatgacatc gtccatcatg 240
 gacatcctga acatcaagat ctcccacttc ctgaagatgg agagcctgaa cttcatccgg 300
 gccacacccc cttacatcaa catctataat tgcgagcctg ccaacccatc tgagaagaat 360
 agcccatcca cacagtactg ttattctatc cagagcctgt tcctgggcat cctgtccgtg 420
 atgctgatct ttgccttctt tcaggagctg gtcacgccc gcatcgtgga gaacgagtgg 480
 aagaggacct gttcccgccc caagtctaata atcgtgctgc tgagcgccga ggagaagaag 540
 gagcagacaa tcgagatcaa ggaggaggtg gtgggcctga ccgagacatc tagccagccc 600
 aagaacgagg aggatatcga gatcatccct atccaggagg aggaggagga ggagaccgag 660
 acaaattttc ctgagtata a 681

<210> 135

<211> 225

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 135

Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
 1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
35 40 45

Ser Lys Thr Leu Gly Ala Cys Leu Val Lys Gly Lys Met Ile Met Asn
50 55 60

Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser Ile Met
65 70 75 80

Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met Glu Ser Leu
85 90 95

Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu
100 105 110

Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr
115 120 125

Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile Phe
130 135 140

Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn Glu Trp
145 150 155 160

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

Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val Val Gly
180 185 190

Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile Glu Ile
195 200 205

Ile Pro Ile Gln Glu Glu Glu Glu Glu Thr Glu Thr Asn Phe Pro
210 215 220

Glu
225

<210> 136
<211> 627
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 136
atgaccacac cccggaacag cgtgaatggc accttcccag ccgagcccat gaagggccct 60
atcgccatgc agtccggccc caagcctctg tttcggagaa tgagctccct ggtgggcccc 120
accagtcctt tctttatgag ggagagcaag acactgggcg cctgcctggt gaagggcaag 180
atgatcatga actccctgtc tctgttcgcc gccatcagcg gcatgatcct gtccatcatg 240
gacatcctga acatcaagat ctcccacttc ctgaagatgg agagcctgaa cttcatccgg 300
gcccacaccc catacatcaa catctataat tgcgagcctg ccaacccatc tgagaagaat 360
agcccctcca cacagtactg ttattctatc cagagcctgt tcctgggcat cctgtccgtg 420
atgctgatct ttgccttctt tcaggagctg gtcacgccc gcatcgtgga gaacgagtgg 480
aagaggacct gttcccgccc taagtcta atcgtgctgc tgagcgccga ggagaagaag 540
gagcagacaa tcgagatcaa ggaggaggtg gtgggcctga ccgagacatc tagccagcca 600
aagaatgagg aggatatcga gtgataa 627

<210> 137
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 137
Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
35 40 45

Ser Lys Thr Leu Gly Ala Cys Leu Val Lys Gly Lys Met Ile Met Asn
50 55 60

Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser Ile Met
65 70 75 80

Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met Glu Ser Leu
85 90 95

Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu
100 105 110

Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr
115 120 125

Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile Phe
130 135 140

Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn Glu Trp
145 150 155 160

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

Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val Val Gly
180 185 190

Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile Glu
195 200 205

<210> 138

<211> 522

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 138
atgaccacac cccggaactc cgtgaatggc accttcccag ccgagcccat gaagggccct 60
atcgccatgc agtctggccc caagcctctg tttcggagaa tgagctcct ggtgggcccct 120
accagagct tctttatgag ggagtccaag acactgggcg cctgcctggt gaagggcaag 180
atgatcatga actctctgag cctgttcgcc gccatctccg gcatgacct gtctatcatg 240
gacatcctga acatcaagat ctctcacttc ctgaagatgg agagcctgaa cttcatccgg 300
gccacacccc catacatcaa catctataat tgcgagcctg ccaaccaag cgagaagaat 360
tccccctcta cacagtactg ttatagcatc cagtccctgt tcctgggcat cctgtccgtg 420
atgctgatct ttgccttctt tcaggagctg gtcacgccg gcatcgtgga gaacgagtgg 480
aagaggacat gttctcgccc caagagcaat atcgtgtgat aa 522

<210> 139
<211> 172
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 139
Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
35 40 45

Ser Lys Thr Leu Gly Ala Cys Leu Val Lys Gly Lys Met Ile Met Asn
50 55 60

Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser Ile Met
65 70 75 80

Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met Glu Ser Leu
85 90 95

Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu
100 105 110

Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr
115 120 125

Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile Phe
130 135 140

Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn Glu Trp
145 150 155 160

Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile Val
165 170

<210> 140
<211> 591
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 140
atgaccacac ccaggaacag cgtgtgcctg gtgaaggcca agatgatcat gaatagcctg 60
tccctgttcg ccgccatctc tggcatgatc ctgagcatca tggacatcct gaacatcaag 120
atctcccact tcctgaagat ggagagcctg aacttcatcc gggcccacac cccatacatc 180
aacatctata attgcgagcc agccaacccc agcgagaaga attctcccag cacacagtac 240
tgttattcca tccagtctct gttcctgggc atcctgtccg tgatgctgat ctttgccttc 300
tttcaggagc tggatcatcg cggcatcgtg gagaacgagt ggaagcggac ctgtagcaga 360
cctaagtcca atatcgtgct gctgtccgcc gaggagaaga aggagcagac aatcgagatc 420
aaggaggagg tgggtgggcct gaccgagaca agctcccagc ccaagaacga ggaggatatc 480
gagatcatcc ctatccagga ggaggaggag gaggagaccg agacaaactt tccagagccc 540
cctcaggacc aggagtctag ccctatcgag aatgattcct ctccatgata a 591

<210> 141
<211> 195
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 141

Met Thr Thr Pro Arg Asn Ser Val Cys Leu Val Lys Gly Lys Met Ile
1 5 10 15

Met Asn Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser
20 25 30

Ile Met Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met Glu
35 40 45

Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn
50 55 60

Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr
65 70 75 80

Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu
85 90 95

Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn
100 105 110

Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile Val Leu Leu
115 120 125

Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val
130 135 140

Val Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile
145 150 155 160

Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu Glu Thr Glu Thr Asn
165 170 175

Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser Ser Pro Ile Glu Asn Asp
180 185 190

Ser Ser Pro
195

<210> 142
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 142
ggacaaaacg acaccagcca aaccagcagc ccctca 36

<210> 143
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 143
Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser
1 5 10

<210> 144
<211> 279
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 144
atgaagcgct tcctcttcct cctactcacc atcagcctcc tggttatggt acagatacaa 60
actggactct caggacaaaa cgacaccagc caaaccagca gccctcagg cagcacctcc 120
ggcagcggca agcctggcag cggcgagggc agcaccaagg gcggcggagg cggaagcgga 180
ggcggagggt ccaagccctt ctgggtgctg gtcgtggtcg gcggagtgtt ggcctgttac 240
agcctgtgtg tcaccgtggc cttcatcatc ttttgggtc 279

<210> 145

<211> 93
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 145

Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
20 25 30

Ser Ser Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly
35 40 45

Glu Gly Ser Thr Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
50 55 60

Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
65 70 75 80

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
85 90

<210> 146
<211> 369
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 146

atgaagcgct tcctcttcct cctactcacc atcagcctcc tggttatggt acagatacaa	60
actggactct caggacaaaa cgacaccagc caaaccagca gccctcagg cagcacctcc	120
ggcagcggca agcctggcag cggcgagggc agcaccaagg gcggccagaa tgatacatct	180
cagacttcat ctctagcgg atccacttct ggttcggta aaccaggttc tggggaaggt	240
agtacaaaag gaggcggagg cggaagcgga ggcggaggct ccaagccctt ctgggtgctg	300
gtcgtggtcg gcggagtgtt ggcctgttac agcctgtctg tcaccgtggc cttcatcatc	360

ttttgggtc

369

<210> 147

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 147

Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
20 25 30

Ser Ser Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly
35 40 45

Glu Gly Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser
50 55 60

Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
65 70 75 80

Ser Thr Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Pro
85 90 95

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
100 105 110

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
115 120

<210> 148

<211> 459

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 148
atgaagcgct tcctcttcct cctactcacc atcagcctcc tggttatggt acagatacaa 60
actggactct caggacaaaa cgacaccagc caaaccagca gcccctcagg cagcacctcc 120
ggcagcggca agcctggcag cggcgagggc agcaccaagg gcggccagaa tgatacatct 180
cagacttcat ctctagcgg atccacttct ggttccggta aaccaggttc tggggaaggt 240
agtacaaaag gaggtcagaa cgacacttca cagacatcta gtccatccgg cagtacaagc 300
ggaagtggaa agcccggaag tggtgagggg tcaactaagg gtggcggagg cggaagcgga 360
ggcggaggct ccaagccctt ctgggtgctg gtcgtggtcg gcggagtgct ggcctgttac 420
agcctgctgg tcaccgtggc cttcatcatc ttttgggtc 459

<210> 149
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 149
Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
20 25 30

Ser Ser Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly
35 40 45

Glu Gly Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser
50 55 60

Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
65 70 75 80

Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser
85 90 95

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr

100

105

110

Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Pro Phe Trp
 115 120 125

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
 130 135 140

Thr Val Ala Phe Ile Ile Phe Trp Val
 145 150

<210> 150

<211> 163

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 150

Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
 1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
 20 25 30

Ser Ser Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly
 35 40 45

Glu Gly Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser
 50 55 60

Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
 65 70 75 80

Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser
 85 90 95

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
 100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115

120

125

Gly Gly Gly Gly Ser Glu Ile Thr Leu Ile Ile Phe Gly Val Met Ala
 130 135 140

Gly Val Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly Ile Arg Arg Gly
 145 150 155 160

Gly Gly Ser

<210> 151

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 151

Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
 1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
 20 25 30

Ser Ser Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly
 35 40 45

Glu Gly Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser
 50 55 60

Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
 65 70 75 80

Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser
 85 90 95

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
 100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115

120

125

Gly Gly Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly
 130 135 140

Val Ile Gly Thr Ile Leu Leu Ala Leu Leu Ile Trp Gly Gly Gly Ser
 145 150 155 160

<210> 152

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 152

Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
 1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
 20 25 30

Ser Ser Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly
 35 40 45

Glu Gly Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser
 50 55 60

Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
 65 70 75 80

Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser
 85 90 95

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
 100 105 110

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

Gly Gly Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly

130

135

140

Val Ile Gly Thr Ile Leu Leu Ala Leu Leu Ile Trp Gly Gly Gly Ser
 145 150 155 160

<210> 153

<211> 1284

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown:

Low-affinity nerve growth factor receptor (LNGFR, TNFRSF16)
 sequence

<400> 153

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atgggggcag gtgccaccgg ccgcgccatg gacgggccgc gcctgctgct gttgctgctt      60
ctgggggtgt cccttgaggg tgccaaggag gcatgcccc aaggcctgta cacacacagc      120
ggtgagtgtg gcaaagcctg caacctgggc gaggggtgtgg cccagccttg tggagccaac      180
cagaccgtgt gtgagccctg cctggacagc gtgacgttct ccgacgtggt gagcgcgacc      240
gagccgtgca agccgtgcac cgagtgcgtg gggctccaga gcatgtcggc gccgtgcgtg      300
gaggccgacg acgccgtgtg ccgctgcgcc tacggctact accaggatga gacgactggg      360
cgctgcgagg cgtgccgcgt gtgcgaggcg ggctcggggc tcgtgtttctc ctgccaggac      420
aagcagaaca ccgtgtgcga ggagtgtccc gacggcacgt attccgacga ggccaaccac      480
gtggacccgt gcctgccctg caccgtgtgc gaggacaccg agcgccagct ccgcgagtgc      540
acacgctggg ccgacgccga gtgcgaggag atccctggcc gttggattac acggtccaca      600
ccccagagg gctcggacag cacagcccc agcaccaggg agcctgaggc acctccagaa      660
caagacctca tagccagcac ggtggcaggt gtggtgacca cagtgatggg cagctcccag      720
cccgtgggtg cccgaggcac caccgacaac ctcatccctg tctattgctc catcctggct      780
gctgtggttg tgggccttgt ggcctacata gccttcaaga ggtggaacag ctgcaagcag      840
aacaagcaag gagccaacag ccggccagtg aaccagacgc ccccaccaga gggagaaaaa      900
ctccacagcg acagtggcat ctccgtggac agccagagcc tgcattgacca gcagccccac      960
acgcagacag cctcggggca ggccctcaag ggtgacggag gcctctacag cagcctgccc     1020
ccagccaagc gggaggaggt ggagaagctt ctcaacggct ctgcggggga cacctggcgg     1080

```

cacctggcgg gcgagctggg ctaccagccc gagcacatag actcctttac ccatgaggcc	1140
tgccccgttc gcgccctgct tgcaagctgg gccacccagg acagcgccac actggacgcc	1200
ctcctggccg ccctgcgccg catccagcga gccgacctcg tggagagtct gtgcagtgag	1260
tccactgcca catccccggt gtga	1284

<210> 154
 <211> 427
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Low-affinity nerve growth factor receptor (LNGFR, TNFRSF16)
 sequence

<400> 154
 Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu
 1 5 10 15

Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys
 20 25 30

Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn
 35 40 45

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

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

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
 85 90 95

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
 100 105 110

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

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
 130 135 140

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
145 150 155 160

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
165 170 175

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
180 185 190

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
195 200 205

Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile
210 215 220

Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln
225 230 235 240

Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys
245 250 255

Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe
260 265 270

Lys Arg Trp Asn Ser Cys Lys Gln Asn Lys Gln Gly Ala Asn Ser Arg
275 280 285

Pro Val Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu His Ser Asp
290 295 300

Ser Gly Ile Ser Val Asp Ser Gln Ser Leu His Asp Gln Gln Pro His
305 310 315 320

Thr Gln Thr Ala Ser Gly Gln Ala Leu Lys Gly Asp Gly Gly Leu Tyr
325 330 335

Ser Ser Leu Pro Pro Ala Lys Arg Glu Glu Val Glu Lys Leu Leu Asn
340 345 350

Gly Ser Ala Gly Asp Thr Trp Arg His Leu Ala Gly Glu Leu Gly Tyr
 355 360 365

Gln Pro Glu His Ile Asp Ser Phe Thr His Glu Ala Cys Pro Val Arg
 370 375 380

Ala Leu Leu Ala Ser Trp Ala Thr Gln Asp Ser Ala Thr Leu Asp Ala
 385 390 395 400

Leu Leu Ala Ala Leu Arg Arg Ile Gln Arg Ala Asp Leu Val Glu Ser
 405 410 415

Leu Cys Ser Glu Ser Thr Ala Thr Ser Pro Val
 420 425

<210> 155
 <211> 666
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown:
 LNGFR Extracellular Domain (K29-N250) sequence

<400> 155
 aaggaggcat gccccacagg cctgtacaca cacagcgggtg agtgctgcaa agcctgcaac 60
 ctgggcgagg gtgtggccca gccttgtgga gccaaccaga ccgtgtgtga gccctgcctg 120
 gacagcgtga cgttctccga cgtgggtgagc gcgaccgagc cgtgcaagcc gtgcaccgag 180
 tgcgtggggc tccagagcat gtcggcgccg tgcgtggagg ccgacgacgc cgtgtgccgc 240
 tgcgcctacg gctactacca ggatgagacg actgggcgct gcgaggcgtg ccgcgtgtgc 300
 gaggcgggct cgggcctcgt gttctcctgc caggacaagc agaacaccgt gtgcgaggag 360
 tgccccgacg gcacgtattc cgacgaggcc aaccacgtgg acccgtgcct gccctgcacc 420
 gtgtgcgagg acaccgagcg ccagctccgc gagtgcacac gctgggcca cgccgagtgc 480
 gaggagatcc ctggccgttg gattacacgg tccacacccc cagagggctc ggacagcaca 540
 gccccagca cccaggagcc tgaggcacct ccagaacaag acctcatagc cagcacgggtg 600
 gcaggtgtgg tgaccacagt gatgggcagc tcccagcccc tggtgacctg aggcaccacc 660
 gacaac 666

<210> 156
<211> 222
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
LNGFR Extracellular Domain (K29-N250) sequence

<400> 156

Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys
1 5 10 15

Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn
20 25 30

Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val
35 40 45

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

Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg
65 70 75 80

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

Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp
100 105 110

Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp
115 120 125

Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp
130 135 140

Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys
145 150 155 160

Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly
165 170 175

Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu
180 185 190

Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met
195 200 205

Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn
210 215 220

<210> 157
<211> 558
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 157
gagccctgcc tggacagcgt gacgttctcc gacgtggtga gcgcgaccga gccgtgcaag 60
ccgtgcaccg agtgcgtggg gctccagagc atgtcggcgc cgtgcgtgga ggccgacgac 120
gccgtgtgcc gctgcgccta cggctactac caggatgaga cgactgggcg ctgcgaggcg 180
tgccgcgtgt gcgaggcggg ctcgggcctc gtgttctcct gccaggacaa gcagaacacc 240
gtgtgcgagg agtgccccga cggcacgtat tccgacgagg ccaaccacgt ggacccgtgc 300
ctgccctgca ccgtgtgcga ggacaccgag cgccagctcc gcgagtgcac acgctgggcc 360
gacgccgagt gcgaggagat ccctggccgt tggattacac ggtccacacc cccagagggc 420
tcggacagca cagccccag caccagagg cctgaggcac ctccagaaca agacctcata 480
gccagcacgg tggcaggtgt ggtgaccaca gtgatgggca gctcccagcc cgtggtgacc 540
cgaggcacca ccgacaac 558

<210> 158
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 158

Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
1 5 10 15

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
20 25 30

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
35 40 45

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
50 55 60

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
65 70 75 80

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
85 90 95

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
100 105 110

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
115 120 125

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
130 135 140

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

Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln
165 170 175

Pro Val Val Thr Arg Gly Thr Thr Asp Asn
180 185

<210> 159

<211> 429

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 159

```
cgctgcgctt acggctacta ccaggatgag acgactgggc gctgcgaggc gtgccgcgtg      60
tgcgaggcgg gctcgggcct cgtgttctcc tgccaggaca agcagaacac cgtgtgctgag      120
gagtgcctcg acggcacgta ttccgacgag gcccaaccacg tggacccgtg cctgccctgc      180
accgtgtgctg aggacaccga gcgccagctc cgcgagtgcg cacgctgggc cgacgccgag      240
tgcgaggaga tccctggccg ttggattaca cggtccacac cccagagagg ctcggacagc      300
acagccccca gcaccagga gcctgaggca cctccagaac aagacctcat agccagcacg      360
gtggcaggtg tggtgaccac agtgatgggc agctcccagc ccgtggtgac ccgaggcacc      420
accgacaac                                     429
```

<210> 160

<211> 143

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 160

```
Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
1           5           10          15
```

```
Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
          20          25          30
```

```
Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser
          35          40          45
```

```
Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
          50          55          60
```

```
Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
          65          70          75          80
```

```
Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
          85          90          95
```

Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro
100 105 110

Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val
115 120 125

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn
130 135 140

<210> 161
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 161
aaggaggcat gccccacagg cctgtacaca cacagcgggtg agtgctgcaa agcctgcaac 60
ctgggcgagg gtgtggccca gccttgtgga gccaaccaga ccgtgtgtga gccctgcctg 120
gacagcgtga cgttctccga cgtgggtgagc gcgaccgagc cgtgcaagcc gtgcaccgag 180
tgcgtggggc tccagagcat gtcggcgccg tgcgtggagg ccgacgacgc cgtgtgccgc 240
tgcgcctacg gctactacca ggatgagacg actgggcgct gcgaggcgtg ccgctgtgtc 300
gaggcgggct cgggcctcgt gttctcctgc caggacaagc agaacaccgt gtgagaggag 360
tgccccgacg gcacgtattc cgacagggcc aaccacgtgg acccgtgcct gccctgcacc 420
gtgtgagagg acaccgagcg ccagctccgc gagtgcacac gctgggccga cgccgagtgc 480
gaggagatcc ctggccgttg gattacacgg tccacacccc cagagggtc ggacagcaca 540
gccccagca cccaggagcc tgaggcacct ccagaacaag acctcatagc cagcacgggtg 600
gcaggtgtgg tgaccacagt gatgggcagc tcccagcccg tggtgacctg aggcaccacc 660
gacaacctca tccctgtcta ttgctccatc ctggctgctg tggttgtggg ccttgtggcc 720
tacatagcct tc 732

<210> 162
<211> 244
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 162

Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys
1 5 10 15

Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn
20 25 30

Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val
35 40 45

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

Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg
65 70 75 80

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

Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp
100 105 110

Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp
115 120 125

Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp
130 135 140

Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys
145 150 155 160

Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly
165 170 175

Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu
180 185 190

Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met
195 200 205

Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile
210 215 220

Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala
225 230 235 240

Tyr Ile Ala Phe

<210> 163

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 163

Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys
1 5 10 15

Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn
20 25 30

Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val
35 40 45

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

Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg
65 70 75 80

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

Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp
100 105 110

Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp
115 120 125

Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp
130 135 140

Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys
145 150 155 160

Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly
165 170 175

Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu
180 185 190

Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met
195 200 205

Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
225 230 235 240

Gly Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
245 250 255

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
260 265 270

Arg Ser

<210> 164

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 164

Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
1 5 10 15

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
20 25 30

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
35 40 45

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
50 55 60

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
65 70 75 80

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
85 90 95

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
100 105 110

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
115 120 125

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
130 135 140

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

Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln
165 170 175

Pro Val Val Thr Arg Gly Thr Thr Asp Asn Gly Gly Gly Gly Ser Gly
180 185 190

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe Trp
195 200 205

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
210 215 220

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
225 230 235

<210> 165

<211> 195

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 165

Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
1 5 10 15

Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
20 25 30

Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser
35 40 45

Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
50 55 60

Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
65 70 75 80

Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
85 90 95

Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro
100 105 110

Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val
115 120 125

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
165 170 175

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
180 185 190

Lys Arg Ser
195

<210> 166

<211> 193

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 166

Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
1 5 10 15

Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
20 25 30

Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser
35 40 45

Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
50 55 60

Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
65 70 75 80

Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
85 90 95

Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro
100 105 110

Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val
115 120 125

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Glu Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val
165 170 175

Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly Ile Arg Arg Gly Gly Gly
180 185 190

Ser

<210> 167

<211> 190

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 167

Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
1 5 10 15

Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
20 25 30

Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser
35 40 45

Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
50 55 60

Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
65 70 75 80

Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
85 90 95

Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro
100 105 110

Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val
115 120 125

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile
165 170 175

Gly Thr Ile Leu Leu Ala Leu Leu Ile Trp Gly Gly Gly Ser
180 185 190

<210> 168

<211> 190

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 168

Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
1 5 10 15

Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
20 25 30

Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser
35 40 45

Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
50 55 60

Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
65 70 75 80

Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
85 90 95

Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro
100 105 110

Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val
115 120 125

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile
165 170 175

Gly Thr Ile Leu Leu Ala Leu Leu Ile Trp Gly Gly Gly Ser
180 185 190

<210> 169
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 169
atggcgctgc ccgtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
ccggacatcc agatgacaca gactacatcc tccctgtctg cctctctggg agacagagtc 120
accatcagtt gcagggcaag tcaggacatt agtaaattatt taaattggta tcagcagaaa 180
ccagatggaa ctgttaaact cctgatctac catacatcaa gattacactc aggagtccca 240
tcaaggttca gtggcagtgg gtctggaaca gattattctc tcaccattag caatttggag 300
caggaagata ttgccactta cttttgccaa cagggttaata cgcttccgta cacgttcgga 360
ggggggacca agctggagat cacaggtggc ggtggctcgg gcggtggtgg gtcgggtggc 420

ggcggatctg aggtgaaact gcaggagtca ggacctggcc tgggtggcgcc ctcacagagc	480
ctgtccgtca catgcactgt ctcaggggtc tcattaccgc actatggtgt aagctggatt	540
cgccagcctc cacgaaaggg tctggagtgg ctgggagtaa tatggggtag tgaaaccaca	600
tactataatt cagctctcaa atccagactg accatcatca aggacaactc caagagccaa	660
gttttcttaa aaatgaacag tctgcaaact gatgacacag ccatttacta ctgtgccaaa	720
cattattact acggtggtag ctatgctatg gactactggg gccaaaggaac ctcagtcacc	780
gtctcctcaa ccacgacgcc agcgccgcga ccaccaacac cggcgccac catcgcgctc	840
cagcccctgt ccctgcgccc agaggcgtgt agaccggctg caggtggagc agtgcacacg	900
agggggctgg acttcgcctg tgatatctac atctgggcgc ccttggccgg gacttgtggg	960
gtccttctcc tgtcactggt tatcacctt tactgccgcg tcaagttcag caggagcgca	1020
gacgccccg cgtacaagca gggccagaac cagctctata acgagctcaa tctaggacga	1080
agagaggagt acgatgtttt ggacaagaga cgtggccggg accctgagat ggggggaaag	1140
ccgagaagga agaaccctca ggaaggcctg tacaatgaac tgcagaaaga taagatggcg	1200
gaggcctaca gtgagattgg gatgaaaggc gagcgccgga ggggcaaggg gcacgatggc	1260
ctttaccagg gtctcagtac agccaccaag gacacctacg acgcccttca catgcaggcc	1320
ctgccccctc gc	1332

<210> 170

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 170

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	

His	Ala	Ala	Arg	Pro	Asp	Ile	Gln	Met	Thr	Gln	Thr	Thr	Ser	Ser	Leu
			20					25					30		

Ser	Ala	Ser	Leu	Gly	Asp	Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Gln
			35				40					45			

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

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

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

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

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
165 170 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly
180 185 190

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
195 200 205

Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
210 215 220

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
225 230 235 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
245 250 255

Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro

260

265

270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
 275 280 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
 290 295 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
 305 310 315 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Val Lys Phe
 325 330 335

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu
 340 345 350

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
 355 360 365

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
 370 375 380

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
 385 390 395 400

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
 405 410 415

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
 420 425 430

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 435 440

<210> 171

<211> 1467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polynucleotide

<400> 171

atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg	60
ccggacatcc agatgacaca gactacatcc tccctgtctg cctctctggg agacagagtc	120
accatcagtt gcagggcaag tcaggacatt agtaaattatt taaattggta tcagcagaaa	180
ccagatggaa ctgttaaact cctgatctac catacatcaa gattacactc aggagtccca	240
tcaaggttca gtggcagtgg gtctggaaca gattattctc tcaccattag caacctggag	300
caagaagata ttgccactta cttttgccaa cagggttaata cgcttccgta cacgttcgga	360
ggggggacca agctggagat cacaggcagc acctccggca gcggcaagcc tggcagcggc	420
gagggcagca ccaagggcga ggtgaaactg caggagtcag gacctggcct ggtggcgccc	480
tcacagagcc tgtccgtcac atgcactgtc tcaggggtct cattaccga ctatggtgta	540
agctggattc gccagcctcc acgaaagggt ctggagtggc tgggagtaat atggggtagt	600
gaaaccacat actataattc agctctcaaa tccagactga ccatcatcaa ggacaactcc	660
aagagccaag ttttcttaaa aatgaacagt ctgcaaactg atgacacagc cattttactac	720
tgtgccaaac attattacta cggtggtagc tatgctatgg actactgggg ccaaggaacc	780
tcagtcaccg tctcctcaac cacgacgcca gcgccgcgac caccaacacc ggcgcccacc	840
atcgctcgc agcccctgtc cctgcgcca gaggcgtgcc ggccagcggc ggggggcgca	900
gtgcacacga gggggctgga cttcgcctgt gatattctaca tctgggcgcc cttggccggg	960
acttgtgggg tccttctcct gtcactggtt atcacccttt actgcaaacg gggcagaaag	1020
aaactcctgt atatattcaa acaaccattt atgagaccag taaaactac tcaagaggaa	1080
gatggctgta gctgccgatt tccagaagaa gaagaaggag gatgtgaact gagagtgaag	1140
ttcagcagga gcgcagacgc ccccgcttac aagcagggcc agaaccagct ctataacgag	1200
ctcaatctag gacgaagaga ggagtacgat gttttggaca agagacgtgg ccgggaccct	1260
gagatggggg gaaagccgag aaggaagaac cctcaggaag gcctgtacaa tgaactgcag	1320
aaagataaga tggcggaggc ctacagtgag attgggatga aaggcgagcg ccggaggggc	1380
aaggggcacg atggccttta ccagggtctc agtacagcca ccaaggacac ctacgacgcc	1440
cttcacatgc aggccctgcc ccctcgc	1467

<210> 172
<211> 489
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 172

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
20 25 30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

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

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
130 135 140

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

Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro
165 170 175

Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu
180 185 190

Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala
195 200 205

Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val
210 215 220

Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr
225 230 235 240

Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp
245 250 255

Gly Gln Gly Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro
260 265 270

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
275 280 285

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
290 295 300

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
305 310 315 320

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys
325 330 335

Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg
340 345 350

Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro
355 360 365

Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser
370 375 380

Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu
385 390 395 400

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
405 410 415

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
420 425 430

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
435 440 445

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
450 455 460

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
465 470 475 480

Leu His Met Gln Ala Leu Pro Pro Arg
485

<210> 173

<211> 1455

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 173

atggcgctgc ccgtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg	60
ccggacatcc agatgacaca gactacatcc tccctgtctg cctctctggg agacagagtc	120
accatcagtt gcagggcaag tcaggacatt agtaaattatt taaattggta tcagcagaaa	180
ccagatggaa ctgttaaact cctgatctac catacatcaa gattacactc aggagtccca	240
tcaaggttca gtggcagtgg gtctggaaca gattattctc tcaccattag caatttggag	300
caggaagata ttgccactta cttttgccaa cagggttaata cgcttccgta cacgttcgga	360
ggggggacca agctggagat cacaggtggc ggtggctcgg gcggtggtgg gtcgggtggc	420
ggcggatctg aggtgaaact gcaggagtca ggacctggcc tggtggcgcc ctcacagagc	480
ctgtccgtca catgcactgt ctcaggggtc tcattaccgc actatggtgt aagctggatt	540

cgccagcctc cacgaaaggg tctggagtgg ctgggagtaa tatggggtag tgaaaccaca	600
tactataatt cagctctcaa atccagactg accatcatca aggacaactc caagagccaa	660
gttttcttaa aaatgaacag tctgcaaact gatgacacag ccatttacta ctgtgccaaa	720
cattattact acggtggttag ctatgctatg gactactggg gccaaaggaac ctcagtcacc	780
gtctcctcaa ccacgacgcc agcgccgcga ccaccaacac cggcgcccac catcgcgtcg	840
cagccccctgt ccctgcgccc agaggcgtgt agaccggctg caggtggagc agtgcacacg	900
agggggctgg acttcgcctg tgatatctac atctgggcgc ccttggccgg gacttgtggg	960
gtccttctcc tgtcactggt tatcaccctt tactgcagga gtaagaggag caggctcctg	1020
cacagtgact acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag	1080
ccctatgccc caccacgcga cttcgagcc tatcgctccc gcgtcaagtt cagcaggagc	1140
gcagacgccc ccgcgtacaa gcagggccag aaccagctct ataacgagct caatctagga	1200
cgaagagagg agtacgatgt tttggacaag agacgtggcc gggaccctga gatgggggga	1260
aagccgagaa ggaagaacct tcaggaaggc ctgtacaatg aactgcagaa agataagatg	1320
gcggaggcct acagtgagat tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat	1380
ggcctttacc aggttctcag tacagccacc aaggacacct acgacgccct tcacatgcag	1440
gccctgcccc ctgc	1455

<210> 174

<211> 485

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 174

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5					10					15	

His	Ala	Ala	Arg	Pro	Asp	Ile	Gln	Met	Thr	Gln	Thr	Thr	Ser	Ser	Leu
			20					25					30		

Ser	Ala	Ser	Leu	Gly	Asp	Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Gln
			35				40					45			

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

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

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

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

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
165 170 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly
180 185 190

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
195 200 205

Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
210 215 220

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
225 230 235 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
245 250 255

Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro

260

265

270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
 275 280 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
 290 295 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
 305 310 315 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg
 325 330 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
 340 345 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
 355 360 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
 370 375 380

Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
 385 390 395 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
 405 410 415

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
 420 425 430

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
 435 440 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
 450 455 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
 465 470 475 480

Ala Leu Pro Pro Arg
485

<210> 175
<211> 2031
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 175
atgctgctgc tggtagaccag cctgctgctg tgtgagctgc cccaccccgc ctttctgctg 60
atccccgaca tccagatgac ccagaccacc tccagcctga gcgccagcct gggcgaccgg 120
gtgaccatca gctgccgggc cagccaggac atcagcaagt acctgaactg gtatcagcag 180
aagcccgcgc gcaccgtcaa gctgctgata taccacacca gccggctgca cagcggcgtg 240
cccagccggc ttagcggcag cggctccggc accgactaca gcctgaccat ctccaacctg 300
gagcaggagg acatcgccac ctacttttgc cagcagggca acacactgcc ctacaccttt 360
ggcggcgaggaa caaagctgga gatcaccggc agcacctccg gcagcggcaa gcctggcagc 420
ggcgagggca gcaccaaggc cgaggtgaag ctgcaggaga gcggccctgg cctggtggcc 480
cccagccaga gcctgagcgt gacctgtacc gtgtccggcg tgtccctgcc cgactacggc 540
gtgtcctgga tccggcagcc ccctaggaag ggcctggagt ggctgggcgt gatctggggc 600
agcgagacca cctactacaa cagcgccctg aagagccggc tgaccatcat caaggacaac 660
agcaagagcc aggtgttcct gaagatgaac agcctgcaga ccgacgacac cgccatctac 720
tactgtgcca agcactacta ctacggcggc agctacgcca tggactactg gggccagggc 780
accagcgtga ccgtgtccag cgagagcaag tacggccctc cctgcccccc ttgccctgcc 840
cccagattcc tgggcggacc cagcgtgttc ctgttcccc ccaagcccaa ggacaccctg 900
atgatcagcc ggacccccga ggtgacctgt gtggtggtgg acgtgtcca ggaggacccc 960
gaggtccagt tcaactggta cgtggacggc gtggaggtgc acaacgcaa gaccaagccc 1020
cgggaggagc agttcaatag cacctaccgg gtggtgtccg tgctgaccgt gctgcaccag 1080
gactggctga acggcaagga atacaagtgt aaggtgtcca acaaggcct gccagcagc 1140
atcgagaaaa ccatcagcaa ggccaagggc cagcctcggg agccccaggt gtacaccctg 1200

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ccccctagcc aagaggagat gaccaagaat caggtgtccc tgacctgcct ggtgaagggc 1260
ttctacccca gcgacatcgc cgtgggagtgg gagagcaacg gccagcccga gaacaactac 1320
aagaccaccc cccctgtgct ggacagcgac ggcagcttct tcctgtacag caggctgacc 1380
gtggacaaga gccggtggca ggagggcaac gtcttttagct gctccgtgat gcacgaggcc 1440
ctgcacaacc actacacca gaagagcctg tccctgagcc tgggcaagat gttctgggtg 1500
ctggtcgtgg tgggtggcgt gctggcctgc tacagcctgc tggtgacagt ggccttcac 1560
atcttttggg tgaggagcaa gcggagcaga ggcggccaca gcgactacat gaacatgacc 1620
ccccggaggc ctggccccac ccggaagcac taccagccct acgcccctcc cagggacttc 1680
gccgcctacc ggagccgggt gaagttcagc cggagcgccg acgcccctgc ctaccagcag 1740
ggccagaacc agctgtacaa cgagctgaac ctgggcccga gggaggagta cgacgtgctg 1800
gacaagcgga gaggccggga ccctgagatg ggcggcaagc cccggagaaa gaaccctcag 1860
gagggcctgt ataacgaact gcagaaagac aagatggccg aggcctacag cgagatcggc 1920
atgaagggcg agcggcggag gggcaagggc cacgacggcc tgtaccaggg cctgagcacc 1980
gccaccaagg atacctacga cgccctgcac atgcaggccc tgccccccag a 2031

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<210> 176
 <211> 677
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 176
 Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
 1 5 10 15

Ala Phe Leu Leu Ile Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser
 20 25 30

Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser
 35 40 45

Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly
 50 55 60

Thr Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val
65 70 75 80

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

Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln
100 105 110

Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
115 120 125

Thr Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser
130 135 140

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

Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu
165 170 175

Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu
180 185 190

Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser
195 200 205

Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln
210 215 220

Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr
225 230 235 240

Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr
245 250 255

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Glu Ser Lys Tyr Gly
260 265 270

Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
275 280 285

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
290 295 300

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
305 310 315 320

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
325 330 335

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
340 345 350

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
355 360 365

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
370 375 380

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
385 390 395 400

Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
405 410 415

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
420 425 430

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
435 440 445

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
450 455 460

Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
465 470 475 480

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
485 490 495

Met Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
500 505 510

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
515 520 525

Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
530 535 540

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
545 550 555 560

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
565 570 575

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
580 585 590

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
595 600 605

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
610 615 620

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
625 630 635 640

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
645 650 655

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
660 665 670

Ala Leu Pro Pro Arg
675

<210> 177

<211> 1131

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 177

aactgggtga atgtgatcag cgacctgaag aagatcgagg atctgatcca gagcatgcac	60
attgatgcca ccctgtacac agaattctgat gtgcacccta gctgtaaagt gaccgccatg	120
aagtgttttc tgctggagct gcaggtgatt tctctggaaa gcggagatgc ctctatccac	180
gacacagtgg agaattctgat catcctggcc aacaatagcc tgagcagcaa tggcaatgtg	240
acagagtctg gctgtaagga gtgtgaggag ctggaggaga agaacatcaa ggagtttctg	300
cagagctttg tgcacatcgt gcagatgttc atcaatacaa gctctggcgg aggatctgga	360
ggaggcggat ctggaggagg aggcagtgga ggcggaggat ctggcggagg atctctgcag	420
attacatgcc ctctccaat gtctgtggag caccgccgata tttgggtgaa gtcctacagc	480
ctgtacagca gagagagata catctgcaac agcggcttta agagaaaggc cggcacctct	540
tctctgacag agtgcgtgct gaataaggcc acaaattgtgg cccactggac aacacctagc	600
ctgaagtgca ttagagatcc tgccctggtc caccagaggc ctgcccctcc atctacagtg	660
acaacagccg gagtgcacc tcagcctgaa tctctgagcc cttctggaaa agaacctgcc	720
gccagctctc ctagctctaa taataccgcc gccacaacag ccgccattgt gcctggatct	780
cagctgatgc ctagcaagtc tcctagcaca ggcacaacag agatcagcag ccacgaatct	840
tctcacggaa caccttctca gaccaccgcc aagaattggg agctgacagc ctctgcctct	900
caccagcctc caggagtgtg tcctcagggc cactctgata caacagtggc catcagcaca	960
tctacagtgc tgctgtgtgg actgtctgcc gtgtctctgc tggcctgtta cctgaagtct	1020
agacagacac ctctctggc ctctgtggag atggaggcca tggaagccct gcctgtgaca	1080
tggggaacaa gcagcagaga tgaggacctg gagaattgtt ctcaccacct g	1131

<210> 178

<211> 377

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 178

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
1 5 10 15

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

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
35 40 45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
50 55 60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
85 90 95

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
100 105 110

Thr Ser Ser 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 Ser Leu Gln Ile Thr Cys Pro
130 135 140

Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser
145 150 155 160

Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys
165 170 175

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

Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp Pro Ala
195 200 205

Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val Thr Thr Ala Gly

210

215

220

Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly Lys Glu Pro Ala
 225 230 235 240

Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr Thr Ala Ala Ile
 245 250 255

Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro Ser Thr Gly Thr
 260 265 270

Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr Pro Ser Gln Thr
 275 280 285

Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser His Gln Pro Pro
 290 295 300

Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr Val Ala Ile Ser Thr
 305 310 315 320

Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val Ser Leu Leu Ala Cys
 325 330 335

Tyr Leu Lys Ser Arg Gln Thr Pro Pro Leu Ala Ser Val Glu Met Glu
 340 345 350

Ala Met Glu Ala Leu Pro Val Thr Trp Gly Thr Ser Ser Arg Asp Glu
 355 360 365

Asp Leu Glu Asn Cys Ser His His Leu
 370 375

<210> 179

<211> 841

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 179

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly

1	5	10	15
Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr	20	25	30
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile	35	40	45
Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly	50	55	60
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln	65	70	75
Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr	85	90	95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly	100	105	110
Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys	115	120	125
Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser	130	135	140
Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser	145	150	155
Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile	165	170	175
Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu	180	185	190
Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn	195	200	205
Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr	210	215	220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240

Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
245 250 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
260 265 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
275 280 285

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
290 295 300

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
305 310 315 320

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
325 330 335

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
340 345 350

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
355 360 365

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
370 375 380

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
385 390 395 400

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
405 410 415

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
420 425 430

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly

435

440

445

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
 450 455 460

Leu Pro Pro Arg Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
 465 470 475 480

Glu Glu Asn Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu
 485 490 495

Leu Met Leu Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly
 500 505 510

Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn
 515 520 525

Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile
 530 535 540

Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu
 545 550 555 560

Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly
 565 570 575

Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala
 580 585 590

Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln
 595 600 605

Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg
 610 615 620

Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys
 625 630 635 640

Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr
 645 650 655

Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys
660 665 670

Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys
675 680 685

Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg
690 695 700

Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg
705 710 715 720

Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu
725 730 735

Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys
740 745 750

Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys
755 760 765

Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala
770 775 780

Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly
785 790 795 800

Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile
805 810 815

Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu Leu Leu Val
820 825 830

Val Ala Leu Gly Ile Gly Leu Phe Met
835 840

<210> 180

<211> 750

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 180

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn

195

200

205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
 210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
 225 230 235 240

Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
 245 250 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
 260 265 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
 275 280 285

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
 290 295 300

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
 305 310 315 320

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
 325 330 335

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
 340 345 350

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
 355 360 365

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
 370 375 380

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
 385 390 395 400

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
 405 410 415

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
420 425 430

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
435 440 445

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
450 455 460

Leu Pro Pro Arg Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
465 470 475 480

Glu Glu Asn Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu
485 490 495

Leu Met Leu Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly
500 505 510

Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn
515 520 525

Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile
530 535 540

Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu
545 550 555 560

Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly
565 570 575

Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala
580 585 590

Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln
595 600 605

Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg
610 615 620

Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys

625		630		635		640									
Asn	Leu	Cys	Tyr	Ala	Asn	Thr	Ile	Asn	Trp	Lys	Lys	Leu	Phe	Gly	Thr
				645					650					655	
Ser	Gly	Gln	Lys	Thr	Lys	Ile	Ile	Ser	Asn	Arg	Gly	Glu	Asn	Ser	Cys
			660					665					670		
Lys	Ala	Thr	Gly	Gln	Val	Cys	His	Ala	Leu	Cys	Ser	Pro	Glu	Gly	Cys
		675					680					685			
Trp	Gly	Pro	Glu	Pro	Arg	Asp	Cys	Val	Ser	Gly	Gly	Gly	Gly	Ser	Gly
	690					695					700				
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Phe	Trp
705					710					715					720
Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val
				725					730					735	
Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser		
		740						745					750		

<210> 181
 <211> 2814
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 181	
gacatccaaa tgacacagac aaccagcagc ctctctgcc	60
gtctgggaga tcgtgtgacc	
atcagttgta gaggctcaca agatatttcc aaatacctaa	120
actggtatca gcaaaaacca	
gatggtacag tgaagttact gatctaccat actagccgtc	180
ttcattccgg tgtgccttct	
cgcttttagcg ggtctggatc aggaacagat tacagtctca	240
ccatcagcaa cctcgaacaa	
gaagatatag ctacctattt ctgccagcag ggtaacactt	300
tgccatatac ctccggagga	
ggcacaaaac tggagatcac tggttctacc agtggagcg	360
gcaagcctgg ctccggtgaa	
ggaagtacca aaggcgaagt gaagctgcaa gagtcaggtc	420
caggtttggt agctcccagc	

caatccctat ctgttacctg tacagtgtct ggtgtgtcac ttccagatta tggcgtgtca	480
tggataaggc agccccacg aaaaggcctg gaatggttgg gggatgatctg gggatctgag	540
accacctact acaacagcgc cctgaaaagt cggctcacca tcatcaaaga caactccaag	600
tcacaagtgt ttcttaagat gaactcactt cagaccgacg acacagccat atactactgt	660
gctaaacatt actactatgg cggtagctat gccatggatt actgggggtca aggtactagt	720
gtgacagtat catctgaatc aaagtatggc ccaccctgcc ccccttgtcc cgctcctgag	780
ttcctgggtg gtccctccgt attcctgttt ccacctaagc caaaagacac tctcatgac	840
agcagaacac ctgaggtgac atgcgtcgta gttgatgtta gccaggagga ccccgaaagt	900
caatttaact ggtacgtaga cgggtgtggaa gtgcataacg caaagaccaa gccacgtgaa	960
gagcagttta actccaccta ccgagtggtg tctgtgtctca cagtcttaca tcaagattgg	1020
ctgaacggaa aagagtataa atgtaaagta tccaataagg gccttccctc tagcatcgaa	1080
aagactatct ccaaagccaa gggacagcca cgcgaaccac aggtgtatac tttacctcct	1140
tctcaagaag agatgaccaa gaaccaagta tctctgacgt gtttggtgaa ggggttctac	1200
ccctctgaca tcgcagtgga atgggaatca aacggtaac ctgagaacaa ttacaaaacc	1260
acccacctg tgctggatag cgacggcagc ttctttctgt atagcaggct cacagtggat	1320
aaaagtcggt ggcaggaagg aaacgtatth agttgcagtg tgatgcacga ggccctccat	1380
aaccattata cccagaagtc actctcactt agtctgggta agatgttctg ggtgctcgtg	1440
gtcgtaggtg gagtgtctggc ttgctactcc ctcttagtga ccgtggcttt tatcatcttc	1500
tgggtacgtt ccaaaaagtc ccgtggtggc cattcagatt acatgaatat gacccccaga	1560
cgaccaggcc caacaaggaa gcattatcaa ccttacgccc ctccccgaga ttttgcagct	1620
tatcgaagta gggatgaagtt cagccggtct gctgacgctc ctgcatacca gcaaggtcag	1680
aatcagttat acaatgagct aaatctagga cgacgcgaag aatatgatgt gctggacaaa	1740
cgacgtggca gggaccctga aatgggtggc aagccaagaa ggaagaaccc acaagagggt	1800
ctgtacaacg agttgcagaa agacaagatg gcagaggcct actccgagat cggaatgaaa	1860
ggagagaggc ggaggggtaa aggacatgac ggtctttacc agggcctgag cacagctact	1920
aaagatacct acgacgccct ccacatgcag gctttgcccc cacgagctac caattttagt	1980
ctgttgaaac aagctggaga tgtcgaggaa aatccaggcc caatgcgact tcctgctcaa	2040

ctgctgggtc tgctcatgct gtgggttcct ggaagcagtg gccgaaaggt ctgcaacggc 2100
 atcggtatcg gcgaatttaa ggatagtcta tctatcaacg ctaccaatat taagcatttt 2160
 aagaactgca cgtctatttc cggcgacttg cacatcctcc ctgttgcatc tcgggggtgat 2220
 agtttcaccc ataccccccc tctcgatcca caagaactgg acattcttaa aaccgttaaa 2280
 gaaataacag gttttctcct catccaggca tggcccgaga ataggacaga tcttcacgca 2340
 tttgaaaacc tcgaaatcat cagagggagg accaaacagc atggtcagtt tagtctcgca 2400
 gtggtgtctc tgaacatcac ttctttaggg cttcgatcac ttaaggaaat ctctgacggt 2460
 gatgtaatca tcagcggtaa caagaacctg tgctacgcta acacgatcaa ctggaagaag 2520
 ctgtttggca caagcggcca gaaaaccaag atcattagta ataggggcga gaatagctgt 2580
 aaagcaaccg ggcaagtgtg tcacgctctg tgttctcccg agggatgttg gggacctgaa 2640
 ccaagagact gcgttagtgg aggggggggc tctggtggcg gaggatctgg cggaggcgga 2700
 agcggaggcg gggggagctt ctgggtgctc gtggtcgtag gaggggtgct ggcctgttac 2760
 tctctactcg taactgttgc tttcatcata ttctgggtcc gaagtaagcg tagc 2814

<210> 182

<211> 938

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 182

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240

Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
245 250 255

Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
260 265 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
275 280 285

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
290 295 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305 310 315 320

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
325 330 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
340 345 350

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
355 360 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
370 375 380

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385 390 395 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
405 410 415

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
420 425 430

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
435 440 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
450 455 460

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val Leu Val
465 470 475 480

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
485 490 495

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser
500 505 510

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
515 520 525

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
530 535 540

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
545 550 555 560

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
565 570 575

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
580 585 590

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
595 600 605

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
610 615 620

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
625 630 635 640

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala
645 650 655

Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro
660 665 670

Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp
675 680 685

Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
690 695 700

Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
705 710 715 720

Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
725 730 735

Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
740 745 750

Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
755 760 765

Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
770 775 780

Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala
785 790 795 800

Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
805 810 815

Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
820 825 830

Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys
835 840 845

Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
850 855 860

Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu
865 870 875 880

Pro Arg Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
885 890 895

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe Trp Val Leu Val Val
900 905 910

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
915 920 925

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
930 935

<210> 183

<211> 959

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 183

Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro
1 5 10 15

Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe
20 25 30

Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn
35 40 45

Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg
50 55 60

Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp
65 70 75 80

Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala
85 90 95

Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile
100 105 110

Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val
115 120 125

Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser
130 135 140

Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn
145 150 155 160

Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys
165 170 175

Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val
180 185 190

Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg
195 200 205

Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly
225 230 235 240

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
245 250 255

Phe Trp Val Arg Ser Lys Arg Ser Ala Thr Asn Phe Ser Leu Leu Lys
260 265 270

Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val
275 280 285

Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro
290 295 300

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
305 310 315 320

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
325 330 335

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
340 345 350

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
355 360 365

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
370 375 380

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
385 390 395 400

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
405 410 415

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
420 425 430

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
435 440 445

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
450 455 460

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
465 470 475 480

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
485 490 495

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
500 505 510

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
515 520 525

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
530 535 540

Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
545 550 555 560

Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
565 570 575

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
580 585 590

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
595 600 605

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
610 615 620

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
625 630 635 640

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
645 650 655

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
660 665 670

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
675 680 685

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
690 695 700

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
705 710 715 720

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
725 730 735

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
740 745 750

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
755 760 765

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val Leu Val
770 775 780

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
785 790 795 800

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser
805 810 815

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
820 825 830

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
835 840 845

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
850 855 860

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
865 870 875 880

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
885 890 895

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
900 905 910

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
915 920 925

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
930 935 940

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
945 950 955

<210> 184

<211> 763

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 184

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240

Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro
245 250 255

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
260 265 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
275 280 285

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
290 295 300

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
305 310 315 320

Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
325 330 335

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
340 345 350

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
355 360 365

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
370 375 380

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
385 390 395 400

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
405 410 415

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
420 425 430

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
435 440 445

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
450 455 460

Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Lys Arg Ser Gly Ser
465 470 475 480

Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn
485 490 495

Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu
500 505 510

Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile
515 520 525

Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His
530 535 540

Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val
545 550 555 560

Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln
565 570 575

Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu
580 585 590

Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn
595 600 605

Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu
610 615 620

Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys
625 630 635 640

Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys
645 650 655

Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln
660 665 670

Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr
675 680 685

Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro
690 695 700

Glu Pro Arg Asp Cys Val Ser Gly Gly Gly Ser Gly Gly Gly Gly
705 710 715 720

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe Trp Val Leu Val
725 730 735

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
740 745 750

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
755 760

<210> 185

<211> 2553

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 185

gacatacaga tgactcagac aacaagtagc ttgtccgcat ccctgggcga tagagtgacc	60
atcagttgtc gagcatccca agatatatcc aagtacttaa actggtatca gcagaagcca	120
gatggcaccg tcaagctgct aatctaccac acaagtaggc tccacagcgg agtgcctagc	180
cgatttctctg gttctggttc tggcacagac tattccctaa ccatcagcaa cctggagcaa	240
gaggacattg caacatattt ttgccagcag ggcaacacac tgccatatac ctttggaggc	300
gggaccaagc tggaaatcac cggtagtacg agtggttctg gaaaacctgg ttctggcgaa	360
ggtagtacta aaggagaggt gaaacttcaa gagagtggcc ctggcttggt ggcccccttct	420
caaagtttga gcgtgacctg cacagtaagt ggcgtcagcc tgccagatta cggagtcagt	480
tggattcgcc agcctccaag gaagggcctt gaatggctgg gcgtaatctg ggggtccgaa	540
accacctatt acaactccgc acttaagagc cgtttaacca tcatcaaaga caacagcaag	600

agtcaggtct ttctcaaaat gaatagtctg caaacggacg acaccgctat ctactattgt	660
gccaagcact actactatgg tggctcctac gctatggatt actggggaca aggaacaagc	720
gtgacagtgt caagtactac cacacctgct ccccgctctc caacccccgc tcctactatt	780
gccagtcaac cactgtctct taggccccgag gcatgtaggc cagcagcagg cggggctgtg	840
cataccccgag gtctcgactt cgcctgcgac atatatatct gggccccctct ggctggcact	900
tgtgggggtcc tcctcctgag tctcgtgatc actctgtatt gtaaactgtg gcgaaagaag	960
ctcctttaca tcttcaagca acccttcatg aggctgtac agaccacgca ggaggaggac	1020
gggtgtagtt gccgattccc cgaagaggaa gaaggcggtt gcgagcttcg agtgaaattc	1080
agtaggagtg ctgacgcacc agcatataag cagggccaga accaattata caacgagctg	1140
aacctcggac gaaggggaaga gtatgatgtg ctggataagc gcagaggccg tgatccagaa	1200
atgggcggca aacctcgtcg gaaaaatcca caagaggggc tatacaacga attgcagaaa	1260
gacaaaatgg cagaggccta ttctgaaatc ggcatgaagg gcgaacgacg aagaggtaag	1320
ggtcatgacg gcctgtatca aggtctctct accgccacaa aggacactta cgatgcttta	1380
cacatgcagg ctctccctcc cagacaatgc accaactacg ctctattgaa gttggcagga	1440
gatgtggaat ccaacccccg tcctatgcgt ctacctgcc agctgcttgg gctcctgatg	1500
ctgtgggtcc ccggcagcag tggtagaaaa gtatgtaacg gcataggtat cggatgaattt	1560
aaggactcac taagcatcaa cgccacaaac atcaagcact ttaagaactg tacctctatt	1620
agcggagact tacacatcct gccagtcgca tttcgaggag acagtttcac ccacactcca	1680
cctctcgatc cttaggaatt agacattctt aaaacagtta aggaaatcac tggatttctt	1740
cttatccagg cctggccaga aaatagaaca gacctgcacg ctttcgagaa cttgaaata	1800
atacagggca ggaccaaaca gcatggccaa tttagtttgg ctgtagtctc cttgaacatc	1860
acttcccttg gcctaaggtc tttgaaggaa atcagtgcg gagacgtgat tatcagcggg	1920
aacaagaacc tctgttacgc aaacacaatc aactggaaga agctcttttg caccagcggc	1980
cagaagacaa agatcatttc taaccgagga gagaacagtt gtaaggcaac aggacaagtg	2040
tgccacgctt tgtgcagccc cgagggatgt tggggctctg agccacgtga ttgtgtctct	2100
tgccggaacg tcagcagagg tagagaatgt gtggataagt gcaacctcct ggaaggggag	2160
cctcgtgagt tcgtggagaa ctccgaatgt atccagtgtc atccagaatg cctgccccag	2220

gccatgaaca taacatgtac aggacgcggc ccagacaact gcatacagtg cgcccactac 2280
attgatggcc cccattgcgt aaagacttgt cctgctggag tcatgggcga aaataacacc 2340
ctgggtgtgga agtacgccga cgctggccat gtatgtcatc tgtgtcatcc taattgcacc 2400
tatggctgca ctggccccgg ccttgaagga tgccccggcg gtggaggagg aggctctttc 2460
tgggtcctcg tggtgggtggg aggcgtgctg gcctgctatt ccttgctggt cacggtcgcc 2520
ttcattatatt tctgggtgag atctaaaaga agc 2553

<210> 186

<211> 851

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 186

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240

Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
245 250 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
260 265 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
275 280 285

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
290 295 300

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
305 310 315 320

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
325 330 335

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly

340

345

350

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
 355 360 365

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
 370 375 380

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
 385 390 395 400

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
 405 410 415

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
 420 425 430

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
 435 440 445

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
 450 455 460

Leu Pro Pro Arg Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly
 465 470 475 480

Asp Val Glu Ser Asn Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu
 485 490 495

Gly Leu Leu Met Leu Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys
 500 505 510

Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala
 515 520 525

Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu
 530 535 540

His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro
 545 550 555 560

Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile
565 570 575

Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu
580 585 590

His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His
595 600 605

Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly
610 615 620

Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly
625 630 635 640

Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe
645 650 655

Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn
660 665 670

Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu
675 680 685

Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn Val
690 695 700

Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly Glu
705 710 715 720

Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro Glu
725 730 735

Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp
740 745 750

Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val Lys
755 760 765

Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp Lys

770

775

780

Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys Thr
 785 790 795 800

Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Gly Gly Gly Gly
 805 810 815

Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
 820 825 830

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
 835 840 845

Lys Arg Ser
 850

<210> 187

<211> 761

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 187

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr

85

90

95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
 100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
 115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
 130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
 145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
 165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
 180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
 195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
 210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
 225 230 235 240

Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro
 245 250 255

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
 260 265 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
 275 280 285

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
 290 295 300

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
305 310 315 320

Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
325 330 335

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
340 345 350

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
355 360 365

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
370 375 380

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
385 390 395 400

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
405 410 415

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
420 425 430

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
435 440 445

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
450 455 460

Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Lys Arg Ser Gly Ser
465 470 475 480

Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn
485 490 495

Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu
500 505 510

Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile

515

520

525

Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His
 530 535 540

Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val
 545 550 555 560

Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln
 565 570 575

Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu
 580 585 590

Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn
 595 600 605

Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu
 610 615 620

Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys
 625 630 635 640

Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys
 645 650 655

Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln
 660 665 670

Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr
 675 680 685

Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro
 690 695 700

Glu Pro Arg Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 705 710 715 720

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Thr Leu Ile
 725 730 735

Ile Phe Gly Val Met Ala Gly Val Ile Gly Thr Ile Leu Leu Ile Ser
740 745 750

Tyr Gly Ile Arg Arg Gly Gly Gly Ser
755 760

<210> 188

<211> 750

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 188

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240

Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
245 250 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
260 265 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
275 280 285

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
290 295 300

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
305 310 315 320

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
325 330 335

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
340 345 350

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala

355

360

365

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
 370 375 380

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
 385 390 395 400

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
 405 410 415

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
 420 425 430

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
 435 440 445

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
 450 455 460

Leu Pro Pro Arg Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly
 465 470 475 480

Asp Val Glu Ser Asn Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu
 485 490 495

Gly Leu Leu Met Leu Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys
 500 505 510

Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala
 515 520 525

Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu
 530 535 540

His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro
 545 550 555 560

Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile
 565 570 575

Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu
580 585 590

His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His
595 600 605

Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly
610 615 620

Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly
625 630 635 640

Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe
645 650 655

Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn
660 665 670

Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu
675 680 685

Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Gly Gly Gly Gly
690 695 700

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
705 710 715 720

Glu Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile Gly Thr
725 730 735

Ile Leu Leu Ile Ser Tyr Gly Ile Arg Arg Gly Gly Gly Ser
740 745 750

<210> 189

<211> 758

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 189

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr

210

215

220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
 225 230 235 240

Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro
 245 250 255

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
 260 265 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
 275 280 285

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
 290 295 300

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
 305 310 315 320

Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
 325 330 335

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
 340 345 350

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
 355 360 365

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
 370 375 380

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
 385 390 395 400

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
 405 410 415

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
 420 425 430

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
435 440 445

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
450 455 460

Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Lys Arg Ser Gly Ser
465 470 475 480

Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn
485 490 495

Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu
500 505 510

Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile
515 520 525

Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His
530 535 540

Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val
545 550 555 560

Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln
565 570 575

Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu
580 585 590

Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn
595 600 605

Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu
610 615 620

Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys
625 630 635 640

Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys

645

650

655

Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln
 660 665 670

Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr
 675 680 685

Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro
 690 695 700

Glu Pro Arg Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 705 710 715 720

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Thr Leu Ile Ile
 725 730 735

Phe Gly Val Met Ala Gly Val Ile Gly Thr Ile Leu Leu Ile Ser Tyr
 740 745 750

Gly Ile Gly Gly Gly Ser
 755

<210> 190

<211> 747

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 190

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240

Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
245 250 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
260 265 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
275 280 285

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
290 295 300

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
305 310 315 320

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
325 330 335

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
340 345 350

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
355 360 365

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
370 375 380

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
385 390 395 400

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
405 410 415

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
420 425 430

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
435 440 445

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
450 455 460

Leu Pro Pro Arg Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly
465 470 475 480

Asp Val Glu Ser Asn Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu

485

490

495

Gly Leu Leu Met Leu Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys
 500 505 510

Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala
 515 520 525

Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu
 530 535 540

His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro
 545 550 555 560

Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile
 565 570 575

Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu
 580 585 590

His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His
 595 600 605

Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly
 610 615 620

Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly
 625 630 635 640

Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe
 645 650 655

Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn
 660 665 670

Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu
 675 680 685

Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Gly Gly Gly Gly
 690 695 700

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
705 710 715 720

Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile Gly Thr Ile
725 730 735

Leu Leu Ile Ser Tyr Gly Ile Gly Gly Gly Ser
740 745

<210> 191

<211> 758

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 191

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240

Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro
245 250 255

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
260 265 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
275 280 285

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
290 295 300

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
305 310 315 320

Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
325 330 335

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro

340

345

350

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
 355 360 365

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
 370 375 380

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
 385 390 395 400

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
 405 410 415

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
 420 425 430

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
 435 440 445

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
 450 455 460

Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Lys Arg Ser Gly Ser
 465 470 475 480

Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn
 485 490 495

Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu
 500 505 510

Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile
 515 520 525

Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His
 530 535 540

Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val
 545 550 555 560

Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln
565 570 575

Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu
580 585 590

Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn
595 600 605

Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu
610 615 620

Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys
625 630 635 640

Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys
645 650 655

Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln
660 665 670

Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr
675 680 685

Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro
690 695 700

Glu Pro Arg Asp Cys Val Ser Gly Gly Gly Ser Gly Gly Gly Gly
705 710 715 720

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Thr Leu Ile Ile
725 730 735

Phe Gly Val Met Ala Gly Val Ile Gly Thr Ile Leu Leu Ala Leu Leu
740 745 750

Ile Trp Gly Gly Gly Ser
755

<211> 747
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 192

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu

180

185

190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
 195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
 210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
 225 230 235 240

Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
 245 250 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
 260 265 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
 275 280 285

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
 290 295 300

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
 305 310 315 320

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
 325 330 335

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
 340 345 350

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
 355 360 365

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
 370 375 380

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
 385 390 395 400

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
405 410 415

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
420 425 430

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
435 440 445

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
450 455 460

Leu Pro Pro Arg Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly
465 470 475 480

Asp Val Glu Ser Asn Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu
485 490 495

Gly Leu Leu Met Leu Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys
500 505 510

Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala
515 520 525

Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu
530 535 540

His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro
545 550 555 560

Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile
565 570 575

Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu
580 585 590

His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His
595 600 605

Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly

610

615

620

Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly
 625 630 635 640

Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe
 645 650 655

Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn
 660 665 670

Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu
 675 680 685

Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Gly Gly Gly Gly
 690 695 700

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 705 710 715 720

Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile Gly Thr Ile
 725 730 735

Leu Leu Ala Leu Leu Ile Trp Gly Gly Gly Ser
 740 745

<210> 193

<211> 666

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 193

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
 1 5 10 15

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

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln

35

40

45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
 50 55 60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
 65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
 85 90 95

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
 100 105 110

Thr Ser Ser 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 Ser Leu Gln Ile Thr Cys Pro
 130 135 140

Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser
 145 150 155 160

Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys
 165 170 175

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

Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp Pro Ala
 195 200 205

Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val Thr Thr Ala Gly
 210 215 220

Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly Lys Glu Pro Ala
 225 230 235 240

Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr Thr Ala Ala Ile
 245 250 255

Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro Ser Thr Gly Thr
260 265 270

Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr Pro Ser Gln Thr
275 280 285

Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser His Gln Pro Pro
290 295 300

Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr Val Ala Ile Ser Thr
305 310 315 320

Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val Ser Leu Leu Ala Cys
325 330 335

Tyr Leu Lys Ser Arg Gln Thr Pro Pro Leu Ala Ser Val Glu Met Glu
340 345 350

Ala Met Glu Ala Leu Pro Val Thr Trp Gly Thr Ser Ser Arg Asp Glu
355 360 365

Asp Leu Glu Asn Cys Ser His His Leu Arg Ala Lys Arg Gly Ser Gly
370 375 380

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
385 390 395 400

Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp
405 410 415

Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
420 425 430

Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
435 440 445

Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
450 455 460

Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu

465		470		475		480									
Leu	Asp	Ile	Leu	Lys	Thr	Val	Lys	Glu	Ile	Thr	Gly	Phe	Leu	Leu	Ile
			485					490						495	
Gln	Ala	Trp	Pro	Glu	Asn	Arg	Thr	Asp	Leu	His	Ala	Phe	Glu	Asn	Leu
			500					505					510		
Glu	Ile	Ile	Arg	Gly	Arg	Thr	Lys	Gln	His	Gly	Gln	Phe	Ser	Leu	Ala
		515					520					525			
Val	Val	Ser	Leu	Asn	Ile	Thr	Ser	Leu	Gly	Leu	Arg	Ser	Leu	Lys	Glu
	530					535					540				
Ile	Ser	Asp	Gly	Asp	Val	Ile	Ile	Ser	Gly	Asn	Lys	Asn	Leu	Cys	Tyr
545					550					555					560
Ala	Asn	Thr	Ile	Asn	Trp	Lys	Lys	Leu	Phe	Gly	Thr	Ser	Gly	Gln	Lys
				565					570					575	
Thr	Lys	Ile	Ile	Ser	Asn	Arg	Gly	Glu	Asn	Ser	Cys	Lys	Ala	Thr	Gly
			580					585					590		
Gln	Val	Cys	His	Ala	Leu	Cys	Ser	Pro	Glu	Gly	Cys	Trp	Gly	Pro	Glu
		595					600					605			
Pro	Arg	Asp	Cys	Val	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	610					615					620				
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Phe	Trp	Val	Leu	Val	Val
625					630					635				640	
Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala	Phe
				645					650					655	
Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser						
			660					665							

<210> 194
 <211> 971
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 194

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240

Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
245 250 255

Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
260 265 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
275 280 285

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
290 295 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305 310 315 320

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
325 330 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
340 345 350

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
355 360 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
370 375 380

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385 390 395 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

405

410

415

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 420 425 430

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
 435 440 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 450 455 460

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val Leu Val
 465 470 475 480

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
 485 490 495

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser
 500 505 510

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
 515 520 525

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
 530 535 540

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
 545 550 555 560

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
 565 570 575

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
 580 585 590

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
 595 600 605

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
 610 615 620

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
625 630 635 640

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala
645 650 655

Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro
660 665 670

Gly Pro Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala
675 680 685

Glu Pro Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu
690 695 700

Phe Arg Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met
705 710 715 720

Arg Glu Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe
725 730 735

His Ile Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala
740 745 750

Pro Ile Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr
755 760 765

Ile Ile Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys
770 775 780

Cys Leu Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala
785 790 795 800

Ala Ile Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys
805 810 815

Ile Ser His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His
820 825 830

Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu

835

840

845

Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe
 850 855 860

Leu Gly Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu
 865 870 875 880

Val Ile Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg
 885 890 895

Pro Lys Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln
 900 905 910

Thr Ile Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser
 915 920 925

Gln Pro Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu
 930 935 940

Glu Glu Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln
 945 950 955 960

Glu Ser Ser Pro Ile Glu Asn Asp Ser Ser Pro
 965 970

<210> 195

<211> 937

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 195

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile

35

40

45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
 100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
 115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
 130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
 145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
 165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
 180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
 195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
 210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
 225 230 235 240

Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
 245 250 255

Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
260 265 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
275 280 285

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
290 295 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305 310 315 320

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
325 330 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
340 345 350

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
355 360 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
370 375 380

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385 390 395 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
405 410 415

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
420 425 430

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
435 440 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
450 455 460

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val Leu Val

465		470		475		480									
Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu	Leu	Val	Thr	Val	Ala
				485					490					495	
Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys	Arg	Ser	Arg	Gly	Gly	His	Ser
			500					505					510		
Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His
		515					520					525			
Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg
	530					535					540				
Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln
545					550					555					560
Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp
				565					570					575	
Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro
			580					585					590		
Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp
		595					600					605			
Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg
	610					615					620				
Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr
625					630					635					640
Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg	Ala
				645					650					655	
Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro
			660					665					670		
Gly	Pro	Met	Thr	Thr	Pro	Arg	Asn	Ser	Val	Asn	Gly	Thr	Phe	Pro	Ala
		675					680					685			

Glu Pro Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu
690 695 700

Phe Arg Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met
705 710 715 720

Arg Glu Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe
725 730 735

His Ile Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala
740 745 750

Pro Ile Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr
755 760 765

Ile Ile Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys
770 775 780

Cys Leu Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala
785 790 795 800

Ala Ile Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys
805 810 815

Ile Ser His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His
820 825 830

Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu
835 840 845

Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe
850 855 860

Leu Gly Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu
865 870 875 880

Val Ile Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg
885 890 895

Pro Lys Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln

900

905

910

Thr Ile Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser
 915 920 925

Gln Pro Lys Asn Glu Glu Asp Ile Glu
 930 935

<210> 196

<211> 888

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 196

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
 100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
 115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser

130

135

140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
 145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
 165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
 180 185 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
 195 200 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
 210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
 225 230 235 240

Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
 245 250 255

Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 260 265 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 275 280 285

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
 290 295 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 305 310 315 320

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 325 330 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 340 345 350

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
355 360 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
370 375 380

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385 390 395 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
405 410 415

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
420 425 430

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
435 440 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
450 455 460

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val Leu Val
465 470 475 480

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
485 490 495

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser
500 505 510

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
515 520 525

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
530 535 540

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
545 550 555 560

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp

565

570

575

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
 580 585 590

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
 595 600 605

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
 610 615 620

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
 625 630 635 640

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala
 645 650 655

Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro
 660 665 670

Gly Pro Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala
 675 680 685

Glu Pro Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu
 690 695 700

Phe Arg Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met
 705 710 715 720

Arg Glu Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe
 725 730 735

His Ile Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala
 740 745 750

Pro Ile Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr
 755 760 765

Ile Ile Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys
 770 775 780

Cys Leu Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala
785 790 795 800

Ala Ile Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys
805 810 815

Ile Ser His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His
820 825 830

Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu
835 840 845

Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe
850 855 860

Leu Gly Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu
865 870 875 880

Val Ile Ala Gly Ile Val Glu Asn
885

<210> 197

<211> 848

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 197

Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
20 25 30

Ser Ser Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly
35 40 45

Glu Gly Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser
50 55 60

Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
65 70 75 80

Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser
85 90 95

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
100 105 110

Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Pro Phe Trp
115 120 125

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
130 135 140

Thr Val Ala Phe Ile Ile Phe Trp Val Ala Thr Asn Phe Ser Leu Leu
145 150 155 160

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro
165 170 175

Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg
180 185 190

Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu
195 200 205

Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys
210 215 220

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

Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser
245 250 255

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu
260 265 270

Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro

275

280

285

Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser
 290 295 300

Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val
 305 310 315 320

Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu
 325 330 335

Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val
 340 345 350

Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val
 355 360 365

Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg
 370 375 380

Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met
 385 390 395 400

Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His
 405 410 415

Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
 420 425 430

Ser Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
 435 440 445

Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 450 455 460

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 465 470 475 480

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
 485 490 495

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
500 505 510

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
515 520 525

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
530 535 540

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
545 550 555 560

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
565 570 575

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
580 585 590

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
595 600 605

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
610 615 620

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
625 630 635 640

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
645 650 655

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val Leu
660 665 670

Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val
675 680 685

Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His
690 695 700

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys

705		710		715		720
His	Tyr	Gln	Pro	Tyr	Ala	Pro
		725				
			Pro	Pro	Arg	Asp
					730	
				Phe	Ala	Ala
						Tyr
						Arg
						Ser
						735
Arg	Val	Lys	Phe	Ser	Arg	Ser
		740				
						Ala
						Asp
						745
						Ala
						Pro
						Ala
						Tyr
						Gln
						Gln
						Gly
						750
Gln	Asn	Gln	Leu	Tyr	Asn	Glu
		755				
						Leu
						Asn
						760
						Leu
						Gly
						Arg
						Arg
						Glu
						Glu
						Tyr
						765
Asp	Val	Leu	Asp	Lys	Arg	Arg
						Gly
						775
						Gly
						Arg
						Asp
						780
						Pro
						Glu
						Met
						Gly
						Gly
						Lys
						770
Pro	Arg	Arg	Lys	Asn	Pro	Gln
						Glu
						Gly
						Leu
						Tyr
						Asn
						Glu
						Leu
						Gln
						Lys
						785
						790
						795
						800
Asp	Lys	Met	Ala	Glu	Ala	Tyr
						Ser
						Glu
						Ile
						Gly
						Met
						Lys
						Gly
						Glu
						Arg
						805
						810
						815
Arg	Arg	Gly	Lys	Gly	His	Asp
						Gly
						Leu
						Tyr
						Gln
						Gly
						Leu
						Ser
						Thr
						Ala
						820
						825
						830
Thr	Lys	Asp	Thr	Tyr	Asp	Ala
						Leu
						His
						Met
						Gln
						Ala
						Leu
						Pro
						Pro
						Arg
						835
						840
						845
<210>	198					
<211>	910					
<212>	PRT					
<213>	Artificial Sequence					
<220>						
<223>	Description of Artificial Sequence: Synthetic					
	polypeptide					
<400>	198					
Met	Arg	Leu	Pro	Ala	Gln	Leu
						Leu
						Gly
						Leu
						Leu
						Met
						Leu
						Trp
						Val
						Pro
1						5
						10
						15
Gly	Ser	Ser	Gly	Arg	Cys	Ala
						Tyr
						Gly
						Tyr
						Tyr
						Gln
						Asp
						Glu
						Thr
						Thr
						20
						25
						30
Gly	Arg	Cys	Glu	Ala	Cys	Arg
						Val
						Cys
						Glu
						Ala
						Gly
						Ser
						Gly
						Leu
						Val

35

40

45

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

Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys
 65 70 75 80

Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp
 85 90 95

Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser
 100 105 110

Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro
 115 120 125

Glu Ala Pro Pro Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val
 130 135 140

Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr
 145 150 155 160

Thr Asp Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 165 170 175

Gly Ser Gly Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly
 180 185 190

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
 195 200 205

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

Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr
 225 230 235 240

Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asp
 245 250 255

Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
260 265 270

Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
275 280 285

Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr
290 295 300

His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
305 310 315 320

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu
325 330 335

Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
340 345 350

Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly Ser
355 360 365

Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys Leu
370 375 380

Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val
385 390 395 400

Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp
405 410 415

Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp
420 425 430

Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr
435 440 445

Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser
450 455 460

Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr

465		470		475		480
Tyr Gly Gly Ser	Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val					
	485		490			495
Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro						
	500		505			510
Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys						
	515		520			525
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val						
	530		535			540
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr						
545		550		555		560
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu						
	565		570			575
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His						
	580		585			590
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys						
	595		600			605
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln						
	610		615			620
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met						
625		630		635		640
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro						
	645		650			655
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn						
	660		665			670
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu						
	675		680			685

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
690 695 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705 710 715 720

Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val Leu Val Val
725 730 735

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
740 745 750

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp
755 760 765

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
770 775 780

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
785 790 795 800

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
805 810 815

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
820 825 830

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
835 840 845

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
850 855 860

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
865 870 875 880

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
885 890 895

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg

900

905

910

<210> 199

<211> 513

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 199

```

cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct      60
acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg      120
gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat      180
attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac      240
aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat      300
ggtcagtttt ctcttgagtg cgtcagcctg aacataacat ccttgggatt acgctccctc      360
aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttggt ctatgcaaat      420
acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaact tataagcaac      480
agaggtgaaa acagctgcaa ggccacaggc cag                                     513

```

<210> 200

<211> 171

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 200

```

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1           5           10          15

```

```

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
          20          25          30

```

```

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
          35          40          45

```

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln
165 170

<210> 201

<211> 423

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 201

gtctgccatg ccttgtgctc ccccaggggc tgctggggcc cggagcccag ggactgcgtc 60

tcttgccgga atgtcagccg aggcagggaa tgcgtggaca agtgcaacct tctggagggt 120

gagccaaggg agtttgtgga gaactctgag tgcatacagt gccaccaga gtgcctgcct 180

caggccatga acatcacctg cacaggacgg ggaccagaca actgtatcca gtgtgcccac 240

tacattgacg gccccactg cgtcaagacc tgcccggcag gagtcatggg agaaaacaac 300

accctggtct ggaagtacgc agacgccggc catgtgtgcc acctgtgcca tccaaactgc 360

acctacggat gcactgggcc aggtcttgaa ggctgtccaa cgaatgggcc taagatcccg 420
tcc 423

<210> 202
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 202
Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
1 5 10 15

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val
20 25 30

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
35 40 45

Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn
50 55 60

Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His
65 70 75 80

Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val Met
85 90 95

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

Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly
115 120 125

Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile Pro Ser
130 135 140

<210> 203
<211> 21
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 203

Val	Cys	His	Ala	Leu	Cys	Ser	Pro	Glu	Gly	Cys	Trp	Gly	Pro	Glu	Pro
1				5					10					15	

Arg	Asp	Cys	Val	Ser
			20	

<210> 204

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 204

Val	Cys	His	Ala	Leu	Cys	Ser	Pro	Glu	Gly	Cys	Trp	Gly	Pro	Glu	Pro
1				5					10					15	

Arg	Asp	Cys	Val	Ser	Cys	Arg	Asn	Val	Ser	Arg	Gly	Arg	Glu	Cys	Val
			20					25					30		

Asp	Lys
-----	-----

<210> 205

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 205

Val	Cys	His	Ala	Leu	Cys	Ser	Pro	Glu	Gly	Cys	Trp	Gly	Pro	Glu	Pro
1				5					10					15	

Arg	Asp	Cys	Val	Ser	Cys	Arg	Asn	Val	Ser	Arg	Gly	Arg	Glu	Cys	Val
			20					25					30		

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
35 40 45

Ser Glu Cys Ile Gln
50

<210> 206

<211> 77

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 206

Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
1 5 10 15

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val
20 25 30

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
35 40 45

Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn
50 55 60

Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln
65 70 75

<210> 207

<211> 90

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 207

Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
1 5 10 15

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val

20

25

30

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
 35 40 45

Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn
 50 55 60

Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His
 65 70 75 80

Tyr Ile Asp Gly Pro His Cys Val Lys Thr
 85 90

<210> 208

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 208

Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
 1 5 10 15

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val
 20 25 30

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
 35 40 45

Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn
 50 55 60

Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His
 65 70 75 80

Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val Met
 85 90 95

Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val

100

105

110

Cys His Leu
115

<210> 209

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 209

Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
1 5 10 15

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val
20 25 30

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
35 40 45

Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn
50 55 60

Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His
65 70 75 80

Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val Met
85 90 95

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

Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly
115 120 125

Leu Glu Gly Cys Pro
130

<210> 210

<211> 312
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 210

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser

180

185

190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
 195 200 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
 210 215 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
 225 230 235 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
 245 250 255

His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
 260 265 270

Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His
 275 280 285

Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro
 290 295 300

Thr Asn Gly Pro Lys Ile Pro Ser
 305 310

<210> 211

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 211

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
 1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
 20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe

35

40

45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
 50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
 65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
 85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
 115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
 130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
 145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
 165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
 180 185 190

<210> 212

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 212

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
 1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile

20

25

30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
 35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
 50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
 65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
 85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
 115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
 130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
 145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
 165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
 180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys
 195 200 205

<210> 213

<211> 224

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 213

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
195 200 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
210 215 220

<210> 214

<211> 248

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 214

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
195 200 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
210 215 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225 230 235 240

Arg Gly Pro Asp Asn Cys Ile Gln
245

<210> 215

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 215

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
195 200 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
210 215 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225 230 235 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
245 250 255

His Cys Val Lys Thr
260

<210> 216

<211> 286

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 216

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu

195

200

205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
 210 215 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
 225 230 235 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
 245 250 255

His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
 260 265 270

Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu
 275 280 285

<210> 217

<211> 304

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 217

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
 1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
 20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
 35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
 50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
 65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg

85

90

95

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

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
 115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
 130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
 145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
 165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
 180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
 195 200 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
 210 215 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
 225 230 235 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
 245 250 255

His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
 260 265 270

Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His
 275 280 285

Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro
 290 295 300

<210> 218
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 218
Lys Ile Ser His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala
1 5 10 15

His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser
20 25 30

Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser
35 40 45

<210> 219
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 219
Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys
1 5 10 15

Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser
20 25

<210> 220
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 220
Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr
1 5 10 15

Cys

<210> 221
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 221
Gly Gly Gly Gly Ser
1 5

<210> 222
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> This sequence may encompass 1-5 "Gly Gly Gly Gly Ser"
repeating units

<400> 222
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
20 25

<210> 223
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 223

Ser Gly Gly Gly Gly Ser
1 5

<210> 224
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 224
Gly Gly Gly Ser
1

<210> 225
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 225
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1 5 10

<210> 226
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 226
Ser 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 Ser Leu Gln
20 25

<210> 227
<211> 25
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 227

Arg	Ala	Lys	Arg	Gly	Ser	Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr	Cys
1				5					10					15	

Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro
			20				25	

<210> 228

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 228

Arg	Ala	Lys	Arg	Ser	Gly	Ser	Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr
1				5					10					15	

Cys	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro
				20				25	

<210> 229

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (2)..(2)

<223> Val or Ile

<220>

<221> MOD_RES

<222> (4)..(4)

<223> Any amino acid

<400> 229

Asp Xaa Glu Xaa Asn Pro Gly Pro

<210> 230
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 230
Arg Ala Lys Arg
1

<210> 231
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 231
agagctaaga gg 12

<210> 232
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 232
cgtgcaaagc gt 12

<210> 233
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 233
Arg Ala Lys Arg Ala Pro Val Lys Gln Thr Leu Asn Phe Asp Leu Leu

1 5 10 15

Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25

<210> 234
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 234
agagccaaga gggcaccggt gaaacagact ttgaattttg accttctgaa gttggcagga 60
gacgttgagt ccaaccctgg gccc 84

<210> 235
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 235
Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
20

<210> 236
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 236
ggaagcggag ctactaactt cagcctgctg aagcaggctg gagacgtgga ggagaaccct 60
ggacct 66

<210> 237
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 237
Arg Ala Lys Arg Ala Pro Val Lys Gln Gly Ser Gly Ala Thr Asn Phe
1 5 10 15

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

<210> 238
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 238
cgtgcaaagc gtgcaccggt gaaacaggga agcggagcta ctaacttcag cctgctgaag 60
caggctggag acgtggagga gaaccctgga cct 93

<210> 239
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> This sequence may encompass 2-5 "Xaa Pro"
repeating units

<400> 239
Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro
1 5 10

<210> 240
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MISC_FEATURE
<222> (2)..(26)
<223> This region may encompass 2-5 "Glu Ala Ala Ala Lys"
repeating units

<400> 240
Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
20 25