

8010.W000
SEQUENCE LISTING

<110> Sampath, Prakash
Junghans, Richard P.
Sengupta, Sadhak

<120> METHODS AND COMPOSITIONS FOR TREATING CANCER

<130> 096201-0074/8010.W000

<140> Not yet assigned

<121> Filed herewith

<150> US 62/086346

<151> 2014-12-02

<160> 49

<170> PatentIn version 3.5

<210> 1

<211> 1848

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 1

ggatccgccca ccatgcatcc gctcctcaat cctctcctgt tggcactggg cctcatggcg	60
cttttgttga ccacggtcat tgctctcact tgccttggcg gctttgcctc cccaggccct	120
gtgcctccct ctacagccct caggagagctc attgaggagc tgggtcaacat caccagaac	180
cagaaggctc cgctctgcaa tggcagcatg gtatggagca tcaacctgac agctggcatg	240
tactgtgcag ccctggaatc cctgatcaac gtgtcaggct gcagtgccat cgagaagacc	300
cagaggatgc tgagcggatt ctgcccgcac aaggtctcag ctgggcagtt ttccagcttg	360
catgtccgag acacaaaaat cgaggtggcc cagtttgtaa aggacctgct cttacattta	420
aagaaacttt ttcgcgaggg acagttcaac cctaggaagc ccaccacgac gccagcgccg	480
cgaccaccaa caccggcgcc caccatcgcg tcgcagcccc tgtccctgcg cccagaggcg	540
tgccggccag cggcgggggg cgcagtgcac acgagggggc tggacttcgc ccaattgctc	600
tgctacctgc tggatggaat cctcttcac tcttggtgtca ttctcactgc cttgttcctg	660
agagtgggta acttctgggt gaggagtaag aggagcaggc tcctgcacag tgactacatg	720
aacatgactc cccgccgccc cgggcccacc cgcaagcatt accagcccta tgccccacca	780
cgcgacttcg cagcctatcg ctccacgct aagttcagca ggagcgcaga cgccccgcg	840
taccagcagg gccagaacca gctctataac gagctcaatc taggacgaag agaggagtac	900
gatgttttg acaagagacg tggccgggac cctgagatgg ggggaaagcc gagaaggaag	960
aaccctcagg aaggcctgta caatgaactg cagaaagata agatggcgga ggcctacagt	1020
gagattggga tgaaaggcga gcgccggagg ggcaaggggc acgatggcct ttaccaggg	1080
ctcagtacag ccaccaagga cacctacgac gcccttcaca tgcaggccct gccccctgc	1140
taacagccag cggccgcaga gggcagagga agtcttctaa catgcggtga cgtggaggag	1200

8010.W000

aatccccggcc	ctccatggat	ggacaaagat	tgcgagatga	agcggaccac	actggactcc	1260
cccctggggca	aactggagct	gtctggctgt	gaacaggggc	tgcacgagat	caaactgctg	1320
ggaaagggca	ctagcgccgc	tgatgctgtg	gaagtgccag	ctccagctgc	tgtgctggga	1380
ggacctgagc	cactgatgca	gtgcaccgcc	tggctgaacg	cttacttcca	tcagcctgaa	1440
gccatcgagg	aatttcccg	gcctgccctg	caccatccag	tgttccagca	ggagagtttt	1500
acaaggcagg	tgctgtggaa	gctgctgaaa	gtggtgaagt	tcggggaagt	gatttcctac	1560
cagcagctgg	ctgctctggc	tggaaacca	aaagctgctc	gggccgtggg	aggagctatg	1620
agaggcaatc	cagtgaata	cctgattccc	tgccacaggg	tgggtgtgtg	ctccggagct	1680
gtggggaact	attctggggg	actggccgtg	aaagaatggc	tgctggctca	cgagggacat	1740
aggctgggaa	agcctggcct	gggagggctc	agtggactgg	ctggagcttg	gctgaaggga	1800
gctggagcta	cctcaggaag	cccacctgcc	ggccggaatt	gacggccg		1848

<210> 2

<211> 1848

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 2

ggatccgccca	ccatgcatcc	gctcctcaat	cctctcctgt	tggcactggg	cctcatggcg	60
cttttgttga	ccacggatcat	tgctctcact	tgcttggcg	gctttgcctc	cccaggccct	120
gtgcctccct	ctacagccct	caggtacctc	attgaggagc	tgggtcaacat	caccagaac	180
cagaaggctc	cgctctgcaa	tggcagcatg	gtatggagca	tcaacctgac	agctggcatg	240
tactgtgcag	ccctggaatc	cctgatcaac	gtgtcaggct	gcagtgccat	cgagaagacc	300
cagaggatgc	tgagcggatt	ctgcccgcac	aagggtctcag	ctgggcagtt	ttccagcttg	360
catgtccgag	acacaaaaat	cgaggtggcc	cagtttgtaa	aggacctgct	cttacattta	420
aagaaacttt	ttcgcgaggg	acagttcaac	cctaggaagc	ccaccacgac	gccagcgccg	480
cgaccaccaa	caccggcgcc	caccatcgcg	tcgcagcccc	tgtccctgcg	cccagaggcg	540
tgccggccag	cgccgggggg	cgcagtgcac	acgagggggc	tggacttcgc	ccaattgctc	600
tgctacctgc	tggatggaat	cctcttcac	tatggtgtca	ttctcactgc	cttgttcctg	660
agagtgggta	acttctgggt	gaggagtaag	aggagcaggc	tcctgcacag	tgactacatg	720
aacatgactc	cccgccgcc	cgggccacc	cgcaagcatt	accagcccta	tgccccacca	780
cgcgacttcg	cagcctatcg	ctccacgcgt	aagttcagca	ggagcgcaga	cgcccccgcg	840
taccagcagg	gccagaacca	gctctataac	gagctcaatc	taggacgaag	agaggagtac	900
gatgttttgg	acaagagacg	tggccgggac	cctgagatgg	ggggaaagcc	gagaaggaag	960
aaccctcagg	aaggcctgta	caatgaactg	cagaaagata	agatggcgga	ggcctacagt	1020
gagattggga	tgaaaggcga	gcgccggagg	ggcaaggggc	acgatggcct	ttaccagggg	1080

8010.W000

ctcagtacag	ccaccaagga	cacctacgac	gcccttcaca	tgcaggccct	gccccctcgc	1140
taacagccag	cggccgcaga	gggcagagga	agtcttctaa	catgcggtga	cgtggaggag	1200
aatcccggcc	ctccatggat	ggacaaagat	tgcgagatga	agcggaccac	actggactcc	1260
cccctgggca	aactggagct	gtctggctgt	gaacaggggc	tgcacgagat	caaactgctg	1320
ggaaagggca	ctagcgccgc	tgatgctgtg	gaagtgccag	ctccagctgc	tgtgctggga	1380
ggacctgagc	cactgatgca	gtgcaccgcc	tggctgaacg	cttacttcca	tcagcctgaa	1440
gccatcgagg	aatttcccg	gcctgccctg	caccatccag	tgttccagca	ggagagtttt	1500
acaaggcagg	tgctgtggaa	gctgctgaaa	gtggtgaagt	tcggggaagt	gatttcctac	1560
cagcagctgg	ctgctctggc	tggaaacca	aaagctgctc	gggccgtggg	aggagctatg	1620
agaggcaatc	cagtgaaaat	cctgattccc	tgccacaggg	tgggtgtgtag	ctccggagct	1680
gtggggaact	attctggggg	actggccgtg	aaagaatggc	tgctggctca	cgagggacat	1740
aggctgggaa	agcctggcct	gggagggctc	agtggactgg	ctggagcttg	gctgaaggga	1800
gctggagcta	cctcaggaag	cccacctgcc	ggccggaatt	gacggccg		1848

<210> 3
 <211> 1848
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

ggatccgcca	ccatgcatcc	gctcctcaat	cctctcctgt	tggcactggg	cctcatggcg	60
cttttgttga	ccacggatcc	tgctctcact	tgcttggcg	gctttgcctc	cccaggccct	120
gtgcctccct	ctacagccct	caggaagctc	attgaggagc	tgggtcaacat	caccagaac	180
cagaaggctc	cgctctgcaa	tggcagcatg	gtatggagca	tcaacctgac	agctggcatg	240
tactgtgcag	ccctggaatc	cctgatcaac	gtgtcaggct	gcagtgccat	cgagaagacc	300
cagaggatgc	tgagcggatt	ctgcccgcac	aaggctctcag	ctgggcagtt	ttccagcttg	360
catgtccgag	acacaaaaat	cgagggtggc	cagtttgtaa	aggacctgct	cttacattta	420
aagaaacttt	ttaaggaggg	acagttcaac	cctaggaagc	ccaccacgac	gccagcgccg	480
cgaccaccaa	caccggcgcc	caccatcgcg	tcgcagcccc	tgtccctgcg	cccagaggcg	540
tgccggccag	cggcgggggg	cgcagtgcac	acgagggggc	tggacttcgc	ccaattgctc	600
tgctacctgc	tggatggaat	cctcttcac	tatggtgtca	ttctcactgc	cttgttcctg	660
agagtgggta	acttctgggt	gaggagtaag	aggagcaggc	tcctgcacag	tgactacatg	720
aacatgactc	cccgccgcc	cgggcccacc	cgcaagcatt	accagcccta	tgccccacca	780
cgcgacttcg	cagcctatcg	ctccacgcgt	aagttcagca	ggagcgcaga	cgcccccgcg	840
taccagcagg	gccagaacca	gctctataac	gagctcaatc	taggacgaag	agaggagtac	900
gatgttttgg	acaagagacg	tggccgggac	cctgagatgg	ggggaaagcc	gagaaggaag	960

8010.W000

```

aaccctcagg aaggcctgta caatgaactg cagaaagata agatggcgga ggcctacagt 1020
gagattggga tgaaaggcga gcgccggagg ggcaaggggc acgatggcct ttaccagggg 1080
ctcagtacag ccaccaagga cacctacgac gcccttcaca tgcaggccct gccccctcgc 1140
taacagccag cggccgcaga gggcagagga agtcttctaa catgcggtga cgtggaggag 1200
aatccccggc ctccatggat ggacaaagat tgcgagatga agcggaccac actggactcc 1260
cccctgggca aactggagct gtctggctgt gaacaggggc tgcacgagat caaactgctg 1320
ggaaagggca ctagcgccgc tgatgctgtg gaagtgccag ctccagctgc tgtgctggga 1380
ggacctgagc cactgatgca gtgcaccgcc tggctgaacg cttacttcca tcagcctgaa 1440
gccatcgagg aatttcccg gcctgccctg caccatccag tgttccagca ggagagtttt 1500
acaaggcagg tgctgtggaa gctgctgaaa gtggtgaagt tcggggaagt gatttcctac 1560
cagcagctgg ctgctctggc tggaaccaca aaagctgctc gggccgtggg aggagctatg 1620
agaggcaatc cagtgaaaat cctgattccc tgccacaggg tgggtgtgtag ctccggagct 1680
gtggggaact attctggggg actggccgtg aaagaatggc tgctggctca cgagggacat 1740
aggctgggaa agcctggcct gggaggggtct agtggactgg ctggagcttg gctgaagggg 1800
gctggagcta cctcaggaag cccacctgcc ggccggaatt gacggccg 1848

```

```

<210> 4
<211> 606
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic construct

```

```

<400> 4

```

```

Met His Pro Leu Leu Asn Pro Leu Leu Leu Ala Leu Gly Leu Met Ala
1           5           10           15

```

```

Leu Leu Leu Thr Thr Val Ile Ala Leu Thr Cys Leu Gly Gly Phe Ala
20           25           30

```

```

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
35           40           45

```

```

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
50           55           60

```

```

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
65           70           75           80

```

```

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
85           90           95

```

```

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
100          105          110

```

Phe Ser Ser₁₁₅ Leu His Val Arg Asp₁₂₀ Thr Lys Ile Glu Val₁₂₅ Ala Gln Phe
 Val Lys₁₃₀ Asp Leu Leu Leu His₁₃₅ Leu Lys Lys Leu Phe₁₄₀ Arg Glu Gly Gln
 Phe₁₄₅ Asn Pro Arg Lys Pro₁₅₀ Thr Thr Thr Pro Ala₁₅₅ Pro Arg Pro Pro Thr₁₆₀
 Pro Ala Pro Thr Ile₁₆₅ Ala Ser Gln Pro Leu₁₇₀ Ser Leu Arg Pro Glu₁₇₅ Ala
 Cys Arg Pro Ala₁₈₀ Ala Gly Gly Ala Val₁₈₅ His Thr Arg Gly Leu₁₉₀ Asp Phe
 Ala Gln Leu₁₉₅ Leu Cys Tyr Leu Leu₂₀₀ Asp Gly Ile Leu Phe₂₀₅ Ile Tyr Gly
 Val Ile₂₁₀ Leu Thr Ala Leu Phe₂₁₅ Leu Arg Val Val Thr₂₂₀ Phe Trp Val Arg
 Ser₂₂₅ Lys Arg Ser Arg Leu₂₃₀ Leu His Ser Asp Tyr₂₃₅ Met Asn Met Thr Pro₂₄₀
 Arg Arg Pro Gly Pro₂₄₅ Thr Arg Lys His Tyr₂₅₀ Gln Pro Tyr Ala Pro₂₅₅ Pro
 Arg Asp Phe Ala₂₆₀ Ala Tyr Arg Ser Thr₂₆₅ Arg Lys Phe Ser Arg₂₇₀ Ser Ala
 Asp Ala Pro₂₇₅ Ala Tyr Gln Gln Gly₂₈₀ Gln Asn Gln Leu Tyr₂₈₅ Asn Glu Leu
 Asn Leu₂₉₀ Gly Arg Arg Glu Glu₂₉₅ Tyr Asp Val Leu Asp₃₀₀ Lys Arg Arg Gly
 Arg₃₀₅ Asp Pro Glu Met Gly₃₁₀ Gly Lys Pro Arg Arg₃₁₅ Lys Asn Pro Gln Glu₃₂₀
 Gly Leu Tyr Asn Glu₃₂₅ Leu Gln Lys Asp Lys₃₃₀ Met Ala Glu Ala Tyr₃₃₅ Ser
 Glu Ile Gly Met₃₄₀ Lys Gly Glu Arg Arg₃₄₅ Arg Gly Lys Gly His₃₅₀ Asp Gly
 Leu Tyr Gln₃₅₅ Gly Leu Ser Thr Ala₃₆₀ Thr Lys Asp Thr Tyr₃₆₅ Asp Ala Leu
 His Met₃₇₀ Gln Ala Leu Pro Pro₃₇₅ Arg Gln Pro Ala Ala₃₈₀ Ala Glu Gly Arg

Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met
385 390 395 400

Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu Gly
405 410 415

Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu
420 425 430

Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro
435 440 445

Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Cys Thr Ala Trp
450 455 460

Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val
465 470 475 480

Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln
485 490 495

Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser
500 505 510

Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Lys Ala Ala Arg Ala
515 520 525

Val Gly Gly Ala Met Arg Gly Asn Pro Val Lys Ile Leu Ile Pro Cys
530 535 540

His Arg Val Val Cys Ser Ser Gly Ala Val Gly Asn Tyr Ser Gly Gly
545 550 555 560

Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly
565 570 575

Lys Pro Gly Leu Gly Gly Ser Ser Gly Leu Ala Gly Ala Trp Leu Lys
580 585 590

Gly Ala Gly Ala Thr Ser Gly Ser Pro Pro Ala Gly Arg Asn
595 600 605

<210> 5
<211> 606
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic construct

<400> 5

Met His Pro Leu Leu Asn Pro Leu Leu Leu Ala Leu Gly Leu Met Ala
 1 5 10 15
 Leu Leu Leu Thr Thr Val Ile Ala Leu Thr Cys Leu Gly Gly Phe Ala
 20 25 30
 Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Tyr Leu Ile Glu
 35 40 45
 Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
 50 55 60
 Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
 65 70 75 80
 Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
 85 90 95
 Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
 100 105 110
 Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
 115 120 125
 Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Gln
 130 135 140
 Phe Asn Pro Arg Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
 145 150 155 160
 Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
 165 170 175
 Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
 180 185 190
 Ala Gln Leu Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly
 195 200 205
 Val Ile Leu Thr Ala Leu Phe Leu Arg Val Val Thr Phe Trp Val Arg
 210 215 220
 Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
 225 230 235 240
 Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
 245 250 255
 Arg Asp Phe Ala Ala Tyr Arg Ser Thr Arg Lys Phe Ser Arg Ser Ala
 260 265 270

Asp Ala Pro₂₇₅ Ala Tyr Gln Gln Gly₂₈₀ Gln Asn Gln Leu Tyr₂₈₅ Asn Glu Leu
 Asn Leu₂₉₀ Gly Arg Arg Glu Gly₂₉₅ Tyr Asp Val Leu Asp₃₀₀ Lys Arg Arg Gly
 Arg Asp Pro Glu Met Gly₃₁₀ Gly Lys Pro Arg Arg₃₁₅ Lys Asn Pro Gln Glu₃₂₀
 Gly Leu Tyr Asn Glu₃₂₅ Leu Gln Lys Asp Lys₃₃₀ Met Ala Glu Ala Tyr₃₃₅ Ser
 Glu Ile Gly Met₃₄₀ Lys Gly Glu Arg Arg₃₄₅ Arg Gly Lys Gly His₃₅₀ Asp Gly
 Leu Tyr Gln₃₅₅ Gly Leu Ser Thr Ala₃₆₀ Thr Lys Asp Thr Tyr₃₆₅ Asp Ala Leu
 His Met₃₇₀ Gln Ala Leu Pro Pro₃₇₅ Arg Gln Pro Ala Ala₃₈₀ Ala Glu Gly Arg
 Gly₃₈₅ Ser Leu Leu Thr Cys₃₉₀ Gly Asp Val Glu Glu₃₉₅ Asn Pro Gly Pro Met₄₀₀
 Asp Lys Asp Cys Glu₄₀₅ Met Lys Arg Thr Thr₄₁₀ Leu Asp Ser Pro Leu Gly₄₁₅
 Lys Leu Glu Leu₄₂₀ Ser Gly Cys Glu Gln₄₂₅ Gly Leu His Glu Ile₄₃₀ Lys Leu
 Leu Gly Lys₄₃₅ Gly Thr Ser Ala Ala₄₄₀ Asp Ala Val Glu Val₄₄₅ Pro Ala Pro
 Ala Ala Val Leu Gly Gly Pro₄₅₅ Glu Pro Leu Met Gln₄₆₀ Cys Thr Ala Trp
 Leu Asn Ala Tyr Phe His₄₇₀ Gln Pro Glu Ala Ile₄₇₅ Glu Glu Phe Pro Val₄₈₀
 Pro Ala Leu His His₄₈₅ Pro Val Phe Gln Gln₄₉₀ Glu Ser Phe Thr Arg₄₉₅ Gln
 Val Leu Trp Lys₅₀₀ Leu Leu Lys Val Val₅₀₅ Lys Phe Gly Glu Val₅₁₀ Ile Ser
 Tyr Gln Gln₅₁₅ Leu Ala Ala Leu Ala₅₂₀ Gly Asn Pro Lys Ala₅₂₅ Ala Arg Ala
 Val Gly₅₃₀ Gly Ala Met Arg Gly₅₃₅ Asn Pro Val Lys Ile₅₄₀ Leu Ile Pro Cys

His Arg Val Val Cys Ser Ser Gly Ala Val Gly Asn Tyr Ser Gly Gly
 545 550 555 560

Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly
 565 570 575

Lys Pro Gly Leu Gly Gly Ser Ser Gly Leu Ala Gly Ala Trp Leu Lys
 580 585 590

Gly Ala Gly Ala Thr Ser Gly Ser Pro Pro Ala Gly Arg Asn
 595 600 605

<210> 6

<211> 606

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 6

Met His Pro Leu Leu Asn Pro Leu Leu Leu Ala Leu Gly Leu Met Ala
 1 5 10 15

Leu Leu Leu Thr Thr Val Ile Ala Leu Thr Cys Leu Gly Gly Phe Ala
 20 25 30

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Lys Leu Ile Glu
 35 40 45

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
 50 55 60

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
 65 70 75 80

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
 85 90 95

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
 100 105 110

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

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Lys Glu Gly Gln
 130 135 140

Phe Asn Pro Arg Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
 145 150 155 160

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
 165 170 175

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
 180 185 190
 Ala Gln Leu Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly
 195 200 205
 Val Ile Leu Thr Ala Leu Phe Leu Arg Val Val Thr Phe Trp Val Arg
 210 215 220
 Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
 225 230 235 240
 Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
 245 250 255
 Arg Asp Phe Ala Ala Tyr Arg Ser Thr Arg Lys Phe Ser Arg Ser Ala
 260 265 270
 Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
 275 280 285
 Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
 290 295 300
 Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
 305 310 315 320
 Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
 325 330 335
 Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
 340 345 350
 Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
 355 360 365
 His Met Gln Ala Leu Pro Pro Arg Gln Pro Ala Ala Ala Glu Gly Arg
 370 375 380
 Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met
 385 390 395 400
 Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu Gly
 405 410 415
 Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu
 420 425 430
 Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala Pro
 435 440 445

Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Cys Thr Ala Trp
 450 455 460

Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val
 465 470 475 480

Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln
 485 490 495

Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser
 500 505 510

Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Lys Ala Ala Arg Ala
 515 520 525

Val Gly Gly Ala Met Arg Gly Asn Pro Val Lys Ile Leu Ile Pro Cys
 530 535 540

His Arg Val Val Cys Ser Ser Gly Ala Val Gly Asn Tyr Ser Gly Gly
 545 550 555 560

Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly
 565 570 575

Lys Pro Gly Leu Gly Gly Ser Ser Gly Leu Ala Gly Ala Trp Leu Lys
 580 585 590

Gly Ala Gly Ala Thr Ser Gly Ser Pro Pro Ala Gly Arg Asn
 595 600 605

<210> 7
 <211> 6
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 7
 ggatcc

6

<210> 8
 <211> 6
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 8
 gccacc

6

<210> 9
 <211> 96

<212> DNA
<213> Homo sapiens

<400> 9
atgcatccgc tcctcaatcc tctcctgttg gcactgggcc tcatggcgct tttgttgacc 60
acggtcattg ctctcacttg ccttggcggc tttgcc 96

<210> 10
<211> 342
<212> DNA
<213> Homo sapiens

<400> 10
tccccaggcc ctgtgcctcc ctctacagcc ctcagggagc tcattgagga gctggtcaac 60
atcacccaga accagaaggc tccgctctgc aatggcagca tggataggag catcaacctg 120
acagctggca tgtactgtgc agccctggaa tccctgatca acgtgtcagg ctgcagtgcc 180
atcgagaaga cccagaggat gctgagcgga ttctgcccgc acaaggtctc agctgggcag 240
ttttccagct tgcattgtccg agacaccaa atcgaggtgg cccagtttgt aaaggacctg 300
ctcttacatt taaagaaact ttttcgagag ggacagttca ac 342

<210> 11
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 11
cctagg 6

<210> 12
<211> 135
<212> DNA
<213> Homo sapiens

<400> 12
aagcccacca cgacgccagc gccgcgacca ccaacaccgg cgcccaccat cgcgtcgag 60
cccctgtccc tgcgccaga ggcgtgccgg ccagcggcgg ggggcgcagt gcacacgagg 120
gggctggact tcgcc 135

<210> 13
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 13
caattg 6

<210> 14
<211> 69
<212> DNA

<213> Homo sapiens

<400> 14
ctctgctacc tgctggatgg aatcctcttc atctatggtg tcattctcac tgccttgttc 60
ctgagagtg 69

<210> 15
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 15
gttaac 6

<210> 16
<211> 132
<212> DNA
<213> Homo sapiens

<400> 16
ttctgggtga ggagtaagag gagcaggctc ctgcacagtg actacatgaa catgactccc 60
cgccgccccg ggcccacccg caagcattac cagccctatg ccccaccacg cgacttcgca 120
gcctatcgct cc 132

<210> 17
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 17
acgcgt 6

<210> 18
<211> 330
<212> DNA
<213> Homo sapiens

<400> 18
aagttcagca ggagcgcaga cgcccccgcg taccagcagg gccagaacca gctctataac 60
gagctcaatc taggacgaag agaggagtac gatgttttgg acaagagacg tggccgggac 120
cctgagatgg ggggaaagcc gagaaggaag aaccctcagg aaggcctgta caatgaactg 180
cagaaagata agatggcgga ggcctacagt gagattggga tgaaaggcga gcgccggagg 240
ggcaaggggc acgatggcct ttaccagggt ctcagtacag ccaccaagga cacctacgac 300
gcccttcaca tgcaggccct gccccctcgc 330

<210> 19
<211> 3
<212> DNA
<213> Homo sapiens

<400> 19
taa 3

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

<220>
<223> Synthetic construct

<400> 20
cagccagcgg ccgca 15

<210> 21
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 21
gagggcagag gaagtcttct aacatgcggt gacgtggagg agaatcccgg ccct 54

<210> 22
<211> 621
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 22
atggacaaag attgcgagat gaagcggacc aactggact cccccctggg caaactggag 60
ctgtctggct gtgaacaggg gctgcacgag atcaaactgc tgggaaaggg cactagcgcc 120
gctgatgctg tggaagtgcc agctccagct gctgtgctgg gaggacctga gccactgatg 180
cagtgaccg cctggctgaa cgcttacttc catcagcctg aagccatcga ggaatttccc 240
gtgcctgccc tgcaccatcc agtggtccag caggagagtt ttacaaggca ggtgctgtgg 300
aagctgctga aagtgggtgaa gttcggggaa gtgatttcct accagcagct ggctgctctg 360
gctggaaacc caaaagctgc tcgggccgtg ggaggagcta tgagaggcaa tccagtga 420
atcctgattc cctgccacag ggtggtgtgt agctccggag ctgtggggaa ctattctggg 480
ggactggccg tgaaagaatg gctgctggct cagcaggac ataggctggg aaagcctggc 540
ctgggagggg ttagtgagct ggctggagct tggctgaagg gagctggagc tacctcagga 600
agcccacctg ccggccggaa t 621

<210> 23
<211> 3
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 23
tga 3

<210> 24
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 24
cggccg 6

<210> 25
<211> 32
<212> PRT
<213> Homo sapiens

<400> 25
Met His Pro Leu Leu Asn Pro Leu Leu Leu Ala Leu Gly Leu Met Ala
1 5 10 15

Leu Leu Leu Thr Thr Val Ile Ala Leu Thr Cys Leu Gly Gly Phe Ala
20 25 30

<210> 26
<211> 114
<212> PRT
<213> Homo sapiens

<400> 26
Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Gln
100 105 110

Phe Asn

<210> 27
 <211> 45
 <212> PRT
 <213> Homo sapiens

<400> 27

Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
 1 5 10 15

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
 20 25 30

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
 35 40 45

<210> 28
 <211> 23
 <212> PRT
 <213> Homo sapiens

<400> 28

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 Arg Val
 20

<210> 29
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 29

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
 1 5 10 15

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
 20 25 30

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
 35 40

<210> 30
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 30

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
 1 5 10 15

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 Page 16

20

25

30

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
 35 40 45

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
 50 55 60

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
 65 70 75 80

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
 85 90 95

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 100 105 110

<210> 31
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 31

Gln Pro Ala Ala Ala
 1 5

<210> 32
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 32

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
 1 5 10 15

Gly Pro

<210> 33
 <211> 207
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 33

Met Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu
 1 5 10 15

8010.W000

Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys
20 25 30

Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala
35 40 45

Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Cys Thr Ala
50 55 60

Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro
65 70 75 80

Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg
85 90 95

Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile
100 105 110

Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Lys Ala Ala Arg
115 120 125

Ala Val Gly Gly Ala Met Arg Gly Asn Pro Val Lys Ile Leu Ile Pro
130 135 140

Cys His Arg Val Val Cys Ser Ser Gly Ala Val Gly Asn Tyr Ser Gly
145 150 155 160

Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu
165 170 175

Gly Lys Pro Gly Leu Gly Gly Ser Ser Gly Leu Ala Gly Ala Trp Leu
180 185 190

Lys Gly Ala Gly Ala Thr Ser Gly Ser Pro Pro Ala Gly Arg Asn
195 200 205

<210> 34
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 34
tccccaggcc ctgtgcctcc ctctacagcc ctcaggtacc tcattgagga gctgggtcaac 60
atcaccaga accagaaggc tccgctctgc aatggcagca tggatatggag catcaacctg 120
acagctggca tgtactgtgc agccctggaa tccctgatca acgtgtcagg ctgcagtgcc 180
atcgagaaga cccagaggat gctgagcgga ttctgcccgc acaaggtctc agctgggcag 240
ttttccagct tgcattgtccg agacacaaa atcgaggtgg cccagtttgt aaaggacctg 300

ctcttacatt taaagaaact ttttcgcgag ggacagttca ac

<210> 35
 <211> 342
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 35
 tccccaggcc ctgtgcctcc ctctacagcc ctcaggaagc tcattgagga gctgggtcaac 60
 atcacccaga accagaaggc tccgctctgc aatggcagca tggatatggag catcaacctg 120
 acagctggca tgtactgtgc agccctggaa tccctgatca acgtgtcagg ctgcagtgcc 180
 atcgagaaga cccagaggat gctgagcgga ttctgcccgc acaaggtctc agctgggcag 240
 ttttccagct tgcattgtccg agacaccaa atcgaggtgg cccagtttgt aaaggacctg 300
 ctcttacatt taaagaaact ttttaaggag ggacagttca ac 342

<210> 36
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 36

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Tyr Leu Ile Glu
 1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
 20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
 85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Gln
 100 105 110

Phe Asn

<210> 37

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

<220>
 <223> Synthetic construct

<400> 37

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Lys Leu Ile Glu
 1 5 10 15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
 20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
 35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
 50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
 65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
 85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Lys Glu Gly Gln
 100 105 110

Phe Asn

<210> 38
 <211> 207
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 38

Met Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu
 1 5 10 15

Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys
 20 25 30

Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala
 35 40 45

Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Cys Thr Ala
 50 55 60

Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro
 Page 20

8010.W000

Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile
100 105 110

Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Lys Ala Ala Arg
115 120 125

Ala Val Gly Gly Ala Met Arg Gly Asn Pro Val Pro Ile Leu Ile Pro
130 135 140

Cys His Arg Val Val Cys Ser His Gly Gly Val Gly Asn His Ser Ser
145 150 155 160

Gly Val Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu
165 170 175

Gly Lys Pro Gly Leu Gly Gly Ser Ser Gly Leu Ala Gly Ala Trp Leu
180 185 190

Lys Gly Ala Gly Ala Thr Ser Gly Ser Pro Pro Ala Gly Arg Asn
195 200 205

<210> 40

<211> 207

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic construct

<400> 40

Met Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu
1 5 10 15

Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys
20 25 30

Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala
35 40 45

Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Cys Thr Ala
50 55 60

Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro
65 70 75 80

Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg
85 90 95

Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile
100 105 110

Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Lys Ala Ala Arg

115

120

125

Ala Val Gly Gly Ala Met Arg Gly Asn Pro Val Pro Ile Leu Ile Pro
 130 135 140

Cys His Arg Val Val Tyr Ser Ser Gly Gly Val Gly Asn Phe Ser Gly
 145 150 155 160

Gly Pro Ala Val Arg Glu Trp Leu Leu Ala His Glu Gly His Arg Leu
 165 170 175

Gly Lys Pro Gly Leu Gly Gly Ser Ser Gly Leu Ala Gly Ala Trp Leu
 180 185 190

Lys Gly Ala Gly Ala Thr Ser Gly Ser Pro Pro Ala Gly Arg Asn
 195 200 205

<210> 41
 <211> 207
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 41

Met Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu
 1 5 10 15

Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys
 20 25 30

Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala
 35 40 45

Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Cys Thr Ala
 50 55 60

Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro
 65 70 75 80

Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg
 85 90 95

Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile
 100 105 110

Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Lys Ala Ala Arg
 115 120 125

Ala Val Gly Gly Ala Met Arg Gly Asn Pro Val Pro Ile Leu Ile Pro
 130 135 140

8010.W000

Cys His Arg Val Val Cys Ser Ser Gly Ala Val Gly Thr His Ser Gly
145 150 155 160

Gly Leu Ala Val Lys Glu Trp Leu Leu Ser His Glu Gly His Arg Leu
165 170 175

Gly Lys Pro Gly Leu Gly Gly Ser Ser Gly Leu Ala Gly Ala Trp Leu
180 185 190

Lys Gly Ala Gly Ala Thr Ser Gly Ser Pro Pro Ala Gly Arg Asn
195 200 205

<210> 42
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 42
ccatgg

6

<210> 43
<211> 238
<212> PRT
<213> Homo sapiens

<400> 43

Met Leu Gly Gln Pro Ala Pro Leu Glu Arg Phe Ala Ser Arg Arg Pro
1 5 10 15

Gln Val Leu Ala Val Arg Thr Val Cys Asp Leu Val Leu Gly Lys Met
20 25 30

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

Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys Leu
50 55 60

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

Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Cys Thr Ala Trp
85 90 95

Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro Val
100 105 110

Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg Gln
115 120 125

Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val Ile Ser
 130 135 140

Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Lys Ala Ala Arg Ala
 145 150 155 160

Val Gly Gly Ala Met Arg Gly Asn Pro Val Lys Ile Leu Ile Pro Cys
 165 170 175

His Arg Val Val Cys Ser Ser Gly Ala Val Gly Asn Tyr Ser Gly Gly
 180 185 190

Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg Leu Gly
 195 200 205

Lys Pro Gly Leu Gly Gly Ser Ser Gly Leu Ala Gly Ala Trp Leu Lys
 210 215 220

Gly Ala Gly Ala Thr Ser Gly Ser Pro Pro Ala Gly Arg Asn
 225 230 235

<210> 44
 <211> 380
 <212> PRT
 <213> Homo sapiens

<400> 44

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

Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
 20 25 30

Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
 35 40 45

Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
 50 55 60

Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
 65 70 75 80

Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
 85 90 95

Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
 100 105 110

Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
 115 120 125

Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
 Page 25

130

135

140

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

Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
 165 170 175

Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
 180 185 190

Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
 195 200 205

Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
 210 215 220

Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
 225 230 235 240

Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
 245 250 255

Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
 260 265 270

Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
 275 280 285

Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
 290 295 300

Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
 305 310 315 320

Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
 325 330 335

Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
 340 345 350

Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
 355 360 365

Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
 370 375 380

<210> 45

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 45

Met His Pro Leu Leu Asn Pro Leu Leu Leu Ala Leu Gly Leu Met Ala
 1 5 10 15

Leu Leu Leu Thr Thr Val Ile Ala Leu Thr Cys Leu Gly Gly Phe Ala
 20 25 30

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
 35 40 45

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
 50 55 60

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
 65 70 75 80

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
 85 90 95

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
 100 105 110

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

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Gln
 130 135 140

Phe Asn Pro Arg Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
 145 150 155 160

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
 165 170 175

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
 180 185 190

Ala Gln Leu Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly
 195 200 205

Val Ile Leu Thr Ala Leu Phe Leu Arg Val Val Thr Phe Trp Val Arg
 210 215 220

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
 225 230 235 240

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
 245 250 255

8010.W000

Arg Asp Phe Ala₂₆₀ Ala Tyr Arg Ser Thr₂₆₅ Arg Lys Phe Ser Arg₂₇₀ Ser Ala
 Asp Ala Pro₂₇₅ Ala Tyr Gln Gln Gly₂₈₀ Gln Asn Gln Leu Tyr₂₈₅ Asn Glu Leu
 Asn Leu₂₉₀ Gly Arg Arg Glu Glu₂₉₅ Tyr Asp Val Leu Asp₃₀₀ Lys Arg Arg Gly
 Arg Asp Pro Glu Met Gly₃₁₀ Gly Lys Pro Arg Arg₃₁₅ Lys Asn Pro Gln Glu₃₂₀
 Gly Leu Tyr Asn Glu₃₂₅ Leu Gln Lys Asp Lys₃₃₀ Met Ala Glu Ala Tyr₃₃₅ Ser
 Glu Ile Gly Met₃₄₀ Lys Gly Glu Arg Arg₃₄₅ Arg Gly Lys Gly His₃₅₀ Asp Gly
 Leu Tyr Gln₃₅₅ Gly Leu Ser Thr Ala₃₆₀ Thr Lys Asp Thr Tyr₃₆₅ Asp Ala Leu
 His Met₃₇₀ Gln Ala Leu Pro Pro₃₇₅ Arg Gln Pro Ala Ala₃₈₀ Ala Glu Gly Arg
 Gly₃₈₅ Ser Leu Leu Thr Cys₃₉₀ Gly Asp Val Glu Glu₃₉₅ Asn Pro Gly Pro Pro₄₀₀
 Trp Met Asp Lys Asp₄₀₅ Cys Glu Met Lys Arg₄₁₀ Thr Thr Leu Asp Ser₄₁₅ Pro
 Leu Gly Lys Leu₄₂₀ Glu Leu Ser Gly Cys₄₂₅ Glu Gln Gly Leu His₄₃₀ Glu Ile
 Lys Leu Leu₄₃₅ Gly Lys Gly Thr Ser Ala Ala Asp Ala Val₄₄₅ Glu Val Pro
 Ala Pro₄₅₀ Ala Ala Val Leu Gly₄₅₅ Gly Pro Glu Pro Leu Met Gln Cys Thr
 Ala Trp Leu Asn Ala Tyr₄₇₀ Phe His Gln Pro Glu₄₇₅ Ala Ile Glu Glu Phe₄₈₀
 Pro Val Pro Ala Leu₄₈₅ His His Pro Val Phe₄₉₀ Gln Gln Glu Ser Phe₄₉₅ Thr
 Arg Gln Val Leu₅₀₀ Trp Lys Leu Leu Lys₅₀₅ Val Val Lys Phe Gly₅₁₀ Glu Val
 Ile Ser Tyr₅₁₅ Gln Gln Leu Ala Ala₅₂₀ Leu Ala Gly Asn Pro₅₂₅ Lys Ala Ala

8010.W000

Arg Ala Val Gly Gly Ala Met Arg Gly Asn Pro Val Lys Ile Leu Ile
530 535 540

Pro Cys His Arg Val Val Cys Ser Ser Gly Ala Val Gly Asn Tyr Ser
545 550 555 560

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
565 570 575

Leu Gly Lys Pro Gly Leu Gly Gly Ser Ser Gly Leu Ala Gly Ala Trp
580 585 590

Leu Lys Gly Ala Gly Ala Thr Ser Gly Ser Pro Pro Ala Gly Arg Asn
595 600 605

<210> 46

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 46

Met His Pro Leu Leu Asn Pro Leu Leu Leu Ala Leu Gly Leu Met Ala
1 5 10 15

Leu Leu Leu Thr Thr Val Ile Ala Leu Thr Cys Leu Gly Gly Phe Ala
20 25 30

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

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
50 55 60

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
65 70 75 80

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
85 90 95

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
100 105 110

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

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Gln
130 135 140

Phe Asn Pro Arg Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
Page 29

145					150					155					160
Pro	Ala	Pro	Thr	Ile 165	Ala	Ser	Gln	Pro	Leu 170	Ser	Leu	Arg	Pro	Glu 175	Ala
Cys	Arg	Pro	Ala 180	Ala	Gly	Gly	Ala	Val 185	His	Thr	Arg	Gly	Leu 190	Asp	Phe
Ala	Gln	Leu 195	Leu	Cys	Tyr	Leu	Leu 200	Asp	Gly	Ile	Leu	Phe 205	Ile	Tyr	Gly
Val	Ile 210	Leu	Thr	Ala	Leu	Phe 215	Leu	Arg	Val	Val	Thr 220	Phe	Trp	Val	Arg
Ser 225	Lys	Arg	Ser	Arg	Leu 230	Leu	His	Ser	Asp	Tyr 235	Met	Asn	Met	Thr	Pro 240
Arg	Arg	Pro	Gly	Pro 245	Thr	Arg	Lys	His	Tyr 250	Gln	Pro	Tyr	Ala	Pro 255	Pro
Arg	Asp	Phe	Ala 260	Ala	Tyr	Arg	Ser	Thr 265	Arg	Lys	Phe	Ser	Arg 270	Ser	Ala
Asp	Ala	Pro 275	Ala	Tyr	Gln	Gln	Gly 280	Gln	Asn	Gln	Leu	Tyr 285	Asn	Glu	Leu
Asn	Leu 290	Gly	Arg	Arg	Glu	Glu 295	Tyr	Asp	Val	Leu	Asp 300	Lys	Arg	Arg	Gly
Arg 305	Asp	Pro	Glu	Met	Gly 310	Gly	Lys	Pro	Arg	Arg 315	Lys	Asn	Pro	Gln	Glu 320
Gly	Leu	Tyr	Asn	Glu 325	Leu	Gln	Lys	Asp	Lys 330	Met	Ala	Glu	Ala	Tyr 335	Ser
Glu	Ile	Gly	Met 340	Lys	Gly	Glu	Arg	Arg 345	Arg	Gly	Lys	Gly	His 350	Asp	Gly
Leu	Tyr	Gln 355	Gly	Leu	Ser	Thr	Ala 360	Thr	Lys	Asp	Thr	Tyr 365	Asp	Ala	Leu
His	Met 370	Gln	Ala	Leu	Pro	Pro 375	Arg	Gln	Pro	Ala	Ala 380	Ala	Glu	Gly	Arg
Gly 385	Ser	Leu	Leu	Thr	Cys 390	Gly	Asp	Val	Glu	Glu 395	Asn	Pro	Gly	Pro	Pro 400
Trp	Met	Asp	Lys	Asp 405	Cys	Glu	Met	Lys	Arg 410	Thr	Thr	Leu	Asp	Ser 415	Pro
Leu	Gly	Lys	Leu	Glu	Leu	Ser	Gly	Cys	Glu	Gln	Gly	Leu	His	Glu	Ile

420

425

430

Lys Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro
 435 440 445

Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Cys Thr
 450 455 460

Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
 465 470 475 480

Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
 485 490 495

Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
 500 505 510

Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Lys Ala Ala
 515 520 525

Arg Ala Val Gly Gly Ala Met Arg Gly Asn Pro Val Lys Ile Leu Ile
 530 535 540

Pro Cys His Arg Val Val Cys Ser Ser Gly Ala Val Gly Asn Tyr Ser
 545 550 555 560

Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
 565 570 575

Leu Gly Lys Pro Gly Leu Gly Gly Ser Ser Gly Leu Ala Gly Ala Trp
 580 585 590

Leu Lys Gly Ala Gly Ala Thr Ser Gly Ser Pro Pro Ala Gly Arg Asn
 595 600 605

<210> 47

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 47

Met His Pro Leu Leu Asn Pro Leu Leu Leu Ala Leu Gly Leu Met Ala
 1 5 10 15

Leu Leu Leu Thr Thr Val Ile Ala Leu Thr Cys Leu Gly Gly Phe Ala
 20 25 30

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Lys Leu Ile Glu
 35 40 45

8010.W000

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
 50 55 60
 Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
 65 70 75 80
 Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
 85 90 95
 Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
 100 105 110
 Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
 115 120 125
 Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Lys Glu Gly Gln
 130 135 140
 Phe Asn Pro Arg Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
 145 150 155 160
 Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
 165 170 175
 Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
 180 185 190
 Ala Gln Leu Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly
 195 200 205
 Val Ile Leu Thr Ala Leu Phe Leu Arg Val Val Thr Phe Trp Val Arg
 210 215 220
 Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
 225 230 235 240
 Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
 245 250 255
 Arg Asp Phe Ala Ala Tyr Arg Ser Thr Arg Lys Phe Ser Arg Ser Ala
 260 265 270
 Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
 275 280 285
 Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
 290 295 300
 Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
 305 310 315 320

8010.W000

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
 325 330 335
 Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
 340 345 350
 Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
 355 360 365
 His Met Gln Ala Leu Pro Pro Arg Gln Pro Ala Ala Ala Glu Gly Arg
 370 375 380
 Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Pro
 385 390 395 400
 Trp Met Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro
 405 410 415
 Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile
 420 425 430
 Lys Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro
 435 440 445
 Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Cys Thr
 450 455 460
 Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe
 465 470 475 480
 Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr
 485 490 495
 Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys Phe Gly Glu Val
 500 505 510
 Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn Pro Lys Ala Ala
 515 520 525
 Arg Ala Val Gly Gly Ala Met Arg Gly Asn Pro Val Lys Ile Leu Ile
 530 535 540
 Pro Cys His Arg Val Val Cys Ser Ser Gly Ala Val Gly Asn Tyr Ser
 545 550 555 560
 Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His Glu Gly His Arg
 565 570 575
 Leu Gly Lys Pro Gly Leu Gly Gly Ser Ser Gly Leu Ala Gly Ala Trp
 580 585 590

8010.W000

Leu Lys Gly Ala Gly Ala Thr Ser Gly Ser Pro Pro Ala Gly Arg Asn
 595 600 605

<210> 48
 <211> 621
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 48
 atggacaaag attgcgagat gaagcggacc acactggact cccccctggg caaactggag 60
 ctgtctggct gtgaacaggg gctgcacgag atcaaactgc tgggaaaggg cactagcgcc 120
 gctgatgctg tggaagtgcc agctccagct gctgtgctgg gaggacctga gccactgatg 180
 cagtgcaccg cctggctgaa cgcttacttc catcagcctg aagccatcga ggaatttccc 240
 gtgcctgccc tgcaccatcc agtggtccag caggagagtt ttacaaggca ggtgctgtgg 300
 aagctgctga aagtggtgaa gttcggggaa gtgatttcct accagcagct ggctgctctg 360
 gctggaaacc caaaagctgc tcggggccgtg ggaggagcta tgagaggcaa tccagtgcc 420
 atcctgattc cctgccacag ggtggtgtgt agctccggag ctgtggggaa ctattctggg 480
 ggactggccg tgaaagaatg gctgctggct cacgagggac ataggctggg aaagcctggc 540
 ctgggagggg ttagtggact ggctggagct tggctgaagg gagctggagc tacctcagga 600
 agcccacctg ccggccggaa t 621

<210> 49
 <211> 207
 <212> PRT
 <213> Homo sapiens

<400> 49

Met Asp Lys Asp Cys Glu Met Lys Arg Thr Thr Leu Asp Ser Pro Leu
 1 5 10 15

Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly Leu His Glu Ile Lys
 20 25 30

Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala Val Glu Val Pro Ala
 35 40 45

Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu Met Gln Cys Thr Ala
 50 55 60

Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala Ile Glu Glu Phe Pro
 65 70 75 80

Val Pro Ala Leu His His Pro Val Phe Gln Gln Glu Ser Phe Thr Arg
 85 90 95

Gln Val Leu Trp₁₀₀ Lys Leu Leu Lys Val₁₀₅ Val Lys Phe Gly Glu Val Ile
 Ser Tyr Gln₁₁₅ Gln Leu Ala Ala Leu₁₂₀ Ala Gly Asn Pro Lys₁₂₅ Ala Ala Arg
 Ala Val₁₃₀ Gly Gly Ala Met Arg₁₃₅ Gly Asn Pro Val Pro₁₄₀ Ile Leu Ile Pro
 Cys₁₄₅ His Arg Val Val Cys₁₅₀ Ser Ser Gly Ala Val₁₅₅ Gly Asn Tyr Ser Gly₁₆₀
 Gly Leu Ala Val Lys₁₆₅ Glu Trp Leu Leu Ala₁₇₀ His Glu Gly His Arg₁₇₅ Leu
 Gly Lys Pro Gly₁₈₀ Leu Gly Gly Ser Ser₁₈₅ Gly Leu Ala Gly Ala₁₉₀ Trp Leu
 Lys Gly Ala₁₉₅ Gly Ala Thr Ser Gly₂₀₀ Ser Pro Pro Ala Gly₂₀₅ Arg Asn