

SEQUENCE LISTING

<110> THE BOARD OF REGENTS OF THE UNIVERSITY OF TEXAS SYSTEM

<120> SUICIDE GENE

<130> UTFC.P1151W0

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<150> 62/791,464

<151> 2019-01-11

<150> 62/773,372

<151> 2018-11-30

<150> 62/769,405

<151> 2018-11-19

<160> 59

<170> PatentIn version 3.5

<210> 1

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

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Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
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Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Arg Ser Ser Ser
65 70 75 80

Arg Thr Pro Ser Asp Lys Val Ala His Val Val Ala Asn Pro Gln Ala
85 90 95

Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala
100 105 110

Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly
115 120 125

Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro
130 135 140

Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser
145 150 155 160

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

Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile
180 185 190

Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala
195 200 205

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

Tyr Phe Gly Ile Ile Ala Leu
225 230

<210> 2

<211> 696

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 2

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gtggcaggcg ccaccacgct cttctgcctg ctgcactttg gagtgatcgg cccccagagg      180
gaagagttcc ccagggacct ctctctaata agccctctgg cccaggcaag atcatcttct      240
cgaaccccga gtgacaaggc agcccatgtt gtagcaaacc ctcaagctga ggggcagctc      300
cagtggctga accgccgggc caatgccctc ctggccaatg gcgtggagct gagagataac      360
cagctgggtg tgccatcaga gggcctgtac ctcatctact cccaggctcct cttcaagggc      420
caaggctgcc cctccacca tgtgtcctc acccacacca tcagccgcat cgccgtctcc      480
taccagacca aggtcaacct cctctctgcc atcaagagcc cctgccagag ggagaccca      540
gagggggctg aggccaagcc ctggtatgag cccatctatc tgggaggggt cttccagctg      600
gagaagggtg accgactcag cgctgagatc aatcgggccg actatctcga ctttgccgag      660
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<210> 3

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 3

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Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
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Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20          25          30
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Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Ala His Val Val
65 70 75 80

Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala
85 90 95

Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val
100 105 110

Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys
115 120 125

Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser
130 135 140

Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile
145 150 155 160

Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro
165 170 175

Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly
180 185 190

Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala
195 200 205

Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
210 215 220

<210> 4
<211> 663

<212> DNA
<213> Artificial Sequence

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

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gccaatggcg tggagctgag agataaccag ctggtgggtg catcagaggg cctgtacctc 360
atctactccc aggtcctctt caagggcca ggctgcccct ccacccatgt gtcctcacc 420
cacaccatca gccgcatcgc cgtctcctac cagaccaagg tcaacctcct ctctgccatc 480
aagagcccct gccagagggga gacccagag ggggctgagg ccaagccctg gtatgagccc 540
atctatctgg gaggggtctt ccagctggag aagggtgacc gactcagcgc tgagatcaat 600
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<210> 5
<211> 231
<212> PRT
<213> Artificial Sequence

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

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

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe

20

25

30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
 35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
 50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Arg Ser Ser Ser
 65 70 75 80

Arg Thr Pro Ser Asp Lys Pro Ala His Val Val Ala Asn Pro Gln Ala
 85 90 95

Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala
 100 105 110

Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly
 115 120 125

Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro
 130 135 140

Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser
 145 150 155 160

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

Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile
 180 185 190

Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala
 195 200 205

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

Tyr Phe Gly Ile Ile Ala Leu
225 230

<210> 6
<211> 696
<212> DNA
<213> Artificial Sequence

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

<400> 6
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gtggcaggcg ccaccacgct cttctgcctg ctgcactttg gagtgatcgg cccccagagg 180
gaagagttcc ccagggacct ctctctaata agccctctgg cccaggcaag atcatcttct 240
cgaaccccgga gtgacaagcc tgcccatgtt gtagcaaacc ctcaagctga ggggcagctc 300
cagtggctga accgccgggc caatgccctc ctggccaatg gcgtggagct gagagataac 360
cagctggtgg tgccatcaga gggcctgtac ctcatctact cccaggtcct cttcaagggc 420
caaggctgcc cctccacca tgtgtcctc acccacacca tcagccgcat cgccgtctcc 480
taccagacca aggtcaacct cctctctgcc atcaagagcc cctgccagag ggagacccca 540
gagggggctg aggccaagcc ctggtatgag cccatctatc tgggaggggt cttccagctg 600
gagaagggtg accgactcag cgctgagatc aatcggcccg actatctcga ctttgccgag 660
tctgggcagg tctacttttg gatcattgcc ctgtcg 696

<210> 7
<211> 233
<212> PRT
<213> Homo sapiens

<400> 7
Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
65 70 75 80

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
85 90 95

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
100 105 110

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
115 120 125

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
130 135 140

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
145 150 155 160

Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
165 170 175

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
180 185 190

Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
195 200 205

Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly

210

215

220

Gln Val Tyr Phe Gly Ile Ile Ala Leu
 225 230

<210> 8

<211> 157

<212> PRT

<213> Homo sapiens

<400> 8

Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
 1 5 10 15

Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
 20 25 30

Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
 35 40 45

Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
 50 55 60

Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
 65 70 75 80

Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
 85 90 95

Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
 100 105 110

Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
 115 120 125

Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
 130 135 140

Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu

145

150

155

<210> 9

<211> 113

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
DAP12 sequence"

<400> 9

Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Leu Pro Leu Leu
1 5 10 15

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala Gln Ala Gln Ser Asp
20 25 30

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met
35 40 45

Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
50 55 60

Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg
65 70 75 80

Lys Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly
85 90 95

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

Lys

<210> 10

<211> 342

<212> DNA

<213> Unknown

<220>
 <221> source
 <223> /note="Description of Unknown:
 DAP12 sequence"

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 ggcgtgctgg cagggatcgt gatgggagac ctgggtgctga cagtgtcat tgccctggcc 180
 gtgtacttcc tgggccggct ggtccctcgg gggcgagggg ctgcggaggc agcgacccgg 240
 aaacagcgta tctactgagac cgagtcgcct tatcaggagc tccagggtca gaggtcggat 300
 gtctacagcg acctcaacac acagaggccg tattacaaat ga 342

<210> 11
 <211> 182
 <212> PRT
 <213> Unknown

<220>
 <221> source
 <223> /note="Description of Unknown:
 CD28 sequence"

<400> 11
 Lys Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
 1 5 10 15
 Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
 20 25 30
 Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
 35 40 45
 Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
 50 55 60
 Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
 65 70 75 80

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
85 90 95

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
100 105 110

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
115 120 125

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
130 135 140

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
145 150 155 160

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
165 170 175

Ala Leu Pro Pro Arg Gly
180

<210> 12
<211> 209
<212> DNA
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
CD28 sequence"

<400> 12
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ggcctttatt attttctggg tgaggagtaa gaggagcagg ctctgcaca gtgactacat 120
gaacatgact ccccgccgcc ccgggcccac ccgcaagcat taccagccct atgccccacc 180
acgcgacttc gcagcctatc gctcacgcg 209

<210> 13

<211> 247
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
IgG1 hinge sequence"

<400> 13
Ser Tyr Val Thr Val Ser Ser Gln Asp Pro Ala Glu Pro Lys Ser Pro
1 5 10 15

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
20 25 30

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
35 40 45

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
50 55 60

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
65 70 75 80

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
85 90 95

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
100 105 110

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
115 120 125

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

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
165 170 175

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
180 185 190

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
195 200 205

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
210 215 220

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
225 230 235 240

Pro Gly Lys Lys Asp Pro Lys
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<210> 14
<211> 734
<212> DNA
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
IgG1 hinge sequence"

<400> 14
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aaaacccaag gacaccctca tgatctcccg gaccctgag gtcacatgcg tggtggtgga 180
cgtgagccac gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca 240
taatgccaag acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt 300
cctcaccgtc ctgcaccagg actggctgaa tggcaaggag tacaagtgca aggtctccaa 360
caaagccctc ccagcccca tcgagaaaac catctccaaa gccaaagggc agccccgaga 420
accacaggtg tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct 480

gacctgcctg gtcaaaggct tctatcccag cgacatcgcc gtggagtggg agagcaatgg	540
gcaaccggag aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt	600
cctctacagc aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg	660
ctccgtgatg catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc	720
gggtaaaaaa gatc	734

<210> 15

<211> 9764

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 15

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cccgactatg gtgtaagctg gattcgccag cctccacgaa agggctctgga gtggctggga	3240
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atcaaggaca actccaagag ccaagttttc ttaaaaatga acagtctgca aactgatgac	3360
acagccattt actactgtgc caaacattat tactacgggtg gtagctatgc tatggactac	3420
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gtatgagtat tcaacatttc cgtgtcgccc ttattccctt ttttgcgga ttttgccttc	7080
ctgtttttgc tcaccagaa acgctgggtga aagtaaaaga tgctgaagat cagttgggtg	7140
cacgagtggg ttacatcgaa ctggatctca acagcggtaa gatccttgag agttttcgcc	7200

ccgaagaacg ttttccaatg atgagcactt ttaaagttct gctatgtggc gcggtattat	7260
cccgtattga cgccgggcaa gagcaactcg gtcgccgcat acactattct cagaatgact	7320
tggttgagta ctcaccagtc acagaaaagc atcttacgga tggcatgaca gtaagagaat	7380
tatgcagtgc tgccataacc atgagtgata acactgcggc caacttactt ctgacaacga	7440
tcggaggacc gaaggagcta accgcttttt tgcacaacat gggggatcat gtaactcgcc	7500
ttgatcgttg ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt gacaccacga	7560
tgctttagc aatggcaaca acgttgcgca aactattaac tggcgaacta cttactctag	7620
cttcccggca acaattaata gactggatgg aggcggataa agttgcagga ccacttctgc	7680
gctcggccct tccggctggc tggtttattg ctgataaatc tggagccggt gagcgtgggt	7740
ctcgcggtat cattgcagca ctggggccag atggtaagcc ctcccgtatc gtagttatct	7800
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cctcactgat taagcattgg taactgtcag accaagtta ctcatatata ctttagattg	7920
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tcaaaggatc ttcttgagat cttttttttc tgcgcgtaat ctgctgcttg caaacaaaaa	8100
aaccaccgct accagcggtg gtttgtttgc cggatcaaga gctaccaact ctttttccga	8160
aggtaactgg cttcagcaga gcgcagatac caaatactgt tcttctagtg tagccgtagt	8220
taggccacca cttcaagaac tctgtagcac cgctacata cctcgctctg ctaatcctgt	8280
taccagtggc tgctgccagt ggcgataagt cgtgtcttac cgggttggac tcaagacgat	8340
agttaccgga taaggcgcag cggtcgggct gaacgggggg ttcgtgcaca cagcccagct	8400
tggagcgaac gacctacacc gaactgagat acctacagcg tgagctatga gaaagcgcca	8460
cgcttcccga agggagaaaag gcggacaggc atccggtaag cggcagggtc ggaacaggag	8520
agcgcacgag ggagcttcca gggggaaacg cctggatatc ttatagtcct gtcgggtttc	8580
gccacctctg acttgagcgt cgatttttgt gatgctcgtc aggggggcgg agcctatgga	8640
aaaacgccag caacgcggcc tttttacggt tcctggcctt ttgctggcct tttgctcaca	8700

tggtctttcc tgcgttatcc cctgattctg tggataaccg tattaccgcc tttgagtgag	8760
ctgataccgc tcgccgcagc cgaacgaccg agcgcagcga gtcagtgagc gaggaagcgg	8820
aagagcgcgc aatacgcaaa ccgcctctcc ccgcgcgttg gccgattcat taatgcagct	8880
ggcacgacag gtttcccgac tggaaagcgg gcagtgcgcg caacgcaatt aatgtgagtt	8940
agctcactca ttaggcaccc caggctttac actttatgct tccggctcgt atgttgtgtg	9000
gaattgtgag cggataacaa tttcacacag gaaacagcta tgaccatgat tacgccaagc	9060
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tctatgccct agggggcggg gggaagctaa gccagctttt tttaacattt aaaatgttaa	9180
ttccatttta aatgcacaga tgtttttatt tcataagggt ttcaatgtgc atgaatgctg	9240
caatattcct gttaccaaag ctagtataaa taaaaataga taaacgtgga aattacttag	9300
agtttctgtc attaacgttt ccttcctcag ttgacaacat aaatgcgctg ctgagcaagc	9360
cagtttgcac ctgtcaggat caatttccca ttatgccagt catattaatt actagtcaat	9420
tagttgattt ttatttttga catatacatg tg	9452

<210> 17
 <211> 33
 <212> PRT
 <213> Homo sapiens

<400> 17
 Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
 1 5 10 15

 Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
 20 25 30

Leu

<210> 18
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 18
Ser Thr Glu Ser
1

<210> 19
<211> 21
<212> PRT
<213> Homo sapiens

<400> 19
Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe Cys Leu Leu
1 5 10 15

His Phe Gly Val Ile
20

<210> 20
<211> 20
<212> PRT
<213> Homo sapiens

<400> 20
Gly Pro Gln Arg Glu Glu Phe Pro Arg Asp Leu Ser Leu Ile Ser Pro
1 5 10 15

Leu Ala Gln Ala
20

<210> 21
<211> 13
<212> PRT
<213> Homo sapiens

<400> 21
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val
1 5 10

<210> 22
<211> 662
<212> DNA
<213> Artificial Sequence

<220>

<221> source

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

<400> 22

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acaggggggc cccagggtc caggcggtgc ttgttcctca gcctcttctc cttcctgac      120
gtggcaggcg ccaccacgct cttctgcctg ctgcactttg gagtgatcgg cccccagagg      180
gaagagttcc ccagggacct ctctctaata agccctctgg cccaggcagc ccatgttgta      240
gcaaaccctc aagctgaggg gcagctccag tggctgaacc gccgggcca tgccctcctg      300
gccaatggcg tggagctgag agataaccag ctggtggtgc catcagaggg cctgtacctc      360
atctactccc aggtcctctt caagggccaa ggctgcccct ccacccatgt gtcctcacc      420
cacaccatca gccgcatcgc cgtctcctac cagaccaagg tcaacctcct ctctgccatc      480
aagagcccct gccagaggga gaccccagag ggggctgagg ccaagccctg gtatgagccc      540
atctatctgg gaggggtctt ccagctggag aagggtgacc gactcagcgc tgagatcaat      600
cggcccgact atctcgactt tgccgagtct gggcagggtct actttgggat cattgccctg      660
cg                                                                                   662
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<210> 23

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 23

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Met Ser Thr Glu Met His Pro Gly Arg Gly Ser Trp His Glu Glu Ala
1           5           10          15
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Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20          25          30
```

```
Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
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35

40

45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
 50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
 65 70 75 80

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
 85 90 95

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
 100 105 110

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
 115 120 125

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
 130 135 140

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
 145 150 155 160

Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
 165 170 175

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
 180 185 190

Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
 195 200 205

Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
 210 215 220

Gln Val Tyr Phe Gly Ile Ile Ala Leu
 225 230

<210> 24
<211> 663
<212> DNA
<213> Artificial Sequence

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

<400> 24
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gtggcaggcg ccaccacgct cttctgcctg ctgcactttg gaggatcgg cccccagagg 180
gaagagttcc ccagggacct ctctctaata agccctctgg cccaggcagc ccatgttgta 240
gcaaaccctc aagctgaggg gcagctccag tggctgaacc gccgggcca tgccctcctg 300
gccaatggcg tggagctgag agataaccag ctgggtggtgc catcagaggg cctgtacctc 360
atctactccc aggtcctctt caagggccaa ggctgcccct ccacccatgt gtcctcacc 420
cacaccatca gccgcatcgc cgtctccac cagaccaagg tcaacctcct ctctgccatc 480
aagagcccct gccagaggga gacccagag ggggctgagg ccaagccctg gtatgagccc 540
atctatctgg gaggggtctt ccagctggag aagggtgacc gactcagcg tgagatcaat 600
cgccccgact atctcgactt tgccgagtct gggcagggtct actttgggat cattgccctg 660
tcg 663

<210> 25
<211> 220
<212> PRT
<213> Artificial Sequence

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

<400> 25
Met Ser Thr Glu Ser Lys Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Ala His Val Val
65 70 75 80

Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala
85 90 95

Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val
100 105 110

Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys
115 120 125

Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser
130 135 140

Arg Ile Ala Val Ser His Gln Thr Lys Val Asn Leu Leu Ser Ala Ile
145 150 155 160

Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro
165 170 175

Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly
180 185 190

Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala
195 200 205

Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu
210						215					220

<210> 26
 <211> 663
 <212> DNA
 <213> Artificial Sequence

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

<400> 26
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 gtggcaggcg ccaccacgct cttcttcctg ctgcactttg gactgatcgg cccccagagg 180
 gaagagttcc ccagggacct ctctctaata agccctctgg cccaggcagc ccatgttgta 240
 gcaaaccctc aagctgaggg gcagctccag tggctgaacc gccgggcaa tgccctcctg 300
 gccaatggcg tggagctgag agataaccag ctggtgggtg catcagaggg cctgtacctc 360
 atctactccc aggtcctctt caagggccaa ggctgcccct ccacccatgt gtcctcacc 420
 cacaccatca gccgcatcgc cgtctcctac cagaccaagg tcaacctcct cttcgccatc 480
 aagagcccct gccagaggga gaccccagag ggggctgagg ccaagccctg gtatgagccc 540
 atctatctgg gaggggtcct ccagctggag aagggtgacc gactcagcgc tgagatcaat 600
 cggcccgact atctcgactt tgccgagtct gggcagggtc actttgggat cattgccctg 660
 tcg 663

<210> 27
 <211> 220
 <212> PRT
 <213> Artificial Sequence

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

<400> 27

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

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Phe Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Ala His Val Val
65 70 75 80

Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala
85 90 95

Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val
100 105 110

Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys
115 120 125

Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser
130 135 140

Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Phe Ala Ile
145 150 155 160

Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro
165 170 175

Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly
180 185 190

Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala

195

200

205

Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
210 215 220

<210> 28

<211> 663

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 28

atgagcactg aaagcatgat ccgggacgtg gagctggccg aggaggcgct cccaagaag 60
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gtggcaggcg ccaccacgct cttctgcctg ctgcactttg gagtgatcgg ccccagagg 180
gaagagttcc ccagggacct ctctctaata agccctctgg cccaggcagc ccatgttgta 240
gcaaaccctc aagctgaggg gcagctccag tggctgaacc gccgggcca tgccctcctg 300
gccaatggcg tggagctgag agataaccag ctggtggtgc catcagaggg cctgtacctc 360
atctactccc aggtcctctt caagggccaa ggctgcccct ccacccatgt gtcctcacc 420
cacaccatca gccgcatcgc cgtctcctac cagaccaagg tcaacctcct ctctgccatc 480
aagagcccct gccagaggga gaccccagag ggggctgagg ccaagccctg gtatgagccc 540
atctatctgg gaggggtctt ccagctggag aagggtgacc gactcatcgc tgagatcaat 600
cggcccgact atctcgactt tgccgagtat gggcaggtct actttgggat cattgccctg 660
tcg 663

<210> 29

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 29

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

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Ala His Val Val
65 70 75 80

Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala
85 90 95

Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val
100 105 110

Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys
115 120 125

Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser
130 135 140

Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile
145 150 155 160

Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro
165 170 175

Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly
180 185 190

Asp Arg Leu Ile Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala
195 200 205

Glu Tyr Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
210 215 220

<210> 30
<211> 663
<212> DNA
<213> Artificial Sequence

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

<400> 30
atgagcactg aaagcatgat ccgggacgtg gagctggccg aggaggcgct cccaagaag 60
acaggggggc cccagggtc caggcggcgtg ttgttcctca gcctcttctc cttcctgac 120
gtggcaggcg ccaccacgct cttctgcctg ctgcactttg gagtgatcgg cccccagagg 180
gaagagttcc ccagggtacgt ctctctaata agccctctgg cccaggcagc ccatgttgta 240
gcaaaccctc aagctgaggg gcagctccag tggctgaacc gccgggcca tgccctcctg 300
gccaatggcg tggagctgag agataaccag ctggtgggtgc catcagaggg cctgtacctc 360
atctactccc aggtcctctt caagggtcca ggctgccccct ccacccatgt gtcctcacc 420
cacaccatca gccgcatcgc cgtctcctac cagaccaagg tcaacctcct ctctgccatc 480
aagagccccct gccagagggg gacccagag ggggctgagg ccaagccctg gtatgagccc 540
atctatctgg gaggggtctt ccagctggag aagggtgacc gactcagcgc tgagatcaat 600
cggcccgact atctctactt tgccgagtct gggcagggtct actttgggat cattgccctg 660
tcg 663

<210> 31
<211> 220
<212> PRT
<213> Artificial Sequence

<220>

<221> source

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

<400> 31

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

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Ala His Val Val
65 70 75 80

Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala
85 90 95

Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val
100 105 110

Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys
115 120 125

Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser
130 135 140

Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile
145 150 155 160

Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro
165 170 175

Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly
180 185 190

Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Tyr Phe Ala
195 200 205

Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
210 215 220

<210> 32

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 32

atgagcactg aaagcatgat ccgggacgtg gagctggccg aggaggcgct cccaagaag 60
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gtggcaggcg ccaccacgct cttctgcctg ctgcactttg gaggatcggt ccccgagg 180
gaagagttcc ccagggacct ctctctaata agccctctgc aggcagccca tgttgtagca 240
aaccctcaag ctgaggggca gctccagtgg ctgaaccgcc gggccaatgc ctcctggcc 300
aatggcgtgg agctgagaga taaccagctg gtggtgccat cagagggcct gtacctcatc 360
tactcccagg tcctcttcaa gggccaaggc tgcccctcca cccatgtgct ctcacccac 420
accatcagcc gcatcgccgt ctctaccag accaagggtc acctcctctc tgccatcaag 480
agcccctgcc agaggggagac cccagagggg gctgaggcca agccctggta tgagcccatc 540
tatctgggag gggctcttca gctggagaag ggtgaccgac tcagcgctga gatcaatcgg 600
cccgactatc tctactttgc cgagtctggg cagggtctact ttgggatcat tgccctgtcg 660

<210> 33

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 33

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

Leu	Pro	Lys	Lys	Thr	Gly	Gly	Pro	Gln	Gly	Ser	Arg	Arg	Cys	Leu	Phe
			20					25					30		

Leu	Ser	Leu	Phe	Ser	Phe	Leu	Ile	Val	Ala	Gly	Ala	Thr	Thr	Leu	Phe
		35					40						45		

Cys	Leu	Leu	His	Phe	Gly	Val	Ile	Gly	Pro	Gln	Arg	Glu	Glu	Phe	Pro
	50					55					60				

Arg	Asp	Leu	Ser	Leu	Ile	Ser	Pro	Leu	Ala	Gln	Ala	His	Val	Val	Ala
65					70					75					80

Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	Arg	Ala	Asn
				85					90					95	

Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu	Val	Val
			100					105					110		

Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe	Lys	Gly
		115					120					125			

Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	Ile	Ser	Arg
	130					135					140				

Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	Ala	Ile	Lys
145					150					155					160

Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	Lys	Pro	Trp
				165					170					175	

Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp
180 185 190

Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Tyr Phe Ala Glu
195 200 205

Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
210 215

<210> 34

<211> 671

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 34

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cgctcccca gaagacaggg gggccccagg gctccaggcg gtgcttggtc ctcagcctct	120
tctccttcct gatcgtggca ggcgccacca cgctcttctt cctgctgcac tttggagtga	180
tcggcccca gaggggaagag ttccccaggg acctctctct aatcagccct ctggcagccc	240
atgttgtagc aaacctcaa gctgaggggc agctccagtg gctgaaccgc cgggccaatg	300
ccctcctggc caatggcgtg gagctgagag ataaccagct ggtggtgcca tcagagggcc	360
tgtacctcat ctactcccag gtcctcttca agggccaagg ctgcccctcc acccatgtgc	420
tcctcaccca caccatcagc cgcacgccc tctcccacca gaccaaggtc aacctcctct	480
tcgcatcaa gagcccctgc cagagggaga cccagaggg ggctgaggcc aagccctggt	540
atgagcccat ctatctggga ggggtcttcc agctggagaa gggtgaccga ctcatcgctg	600
agatcaatcg gcccactat ctctactttg ccgagtatgg gcaggcttac tttgggatca	660
ttgccctgtc g	671

<210> 35
<211> 219
<212> PRT
<213> Artificial Sequence

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

<400> 35
Met Ser Thr Glu Met His Pro Gly Arg Gly Ser Trp His Glu Glu Ala
1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Phe Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala His Val Val Ala
65 70 75 80

Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn
85 90 95

Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val
100 105 110

Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly
115 120 125

Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg
130 135 140

Ile Ala Val Ser His Gln Thr Lys Val Asn Leu Leu Phe Ala Ile Lys
145 150 155 160

Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp
165 170 175

Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp
180 185 190

Arg Leu Ile Ala Glu Ile Asn Arg Pro Asp Tyr Leu Tyr Phe Ala Glu
195 200 205

Tyr Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
210 215

<210> 36

<211> 1131

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 36

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

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Arg Ser Ser Ser
65 70 75 80

Arg Thr Pro Ser Asp Lys Val Ala His Val Val Ala Asn Pro Gln Ala
85 90 95

Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala
100 105 110

Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly
115 120 125

Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro
130 135 140

Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser
145 150 155 160

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

Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile
180 185 190

Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala
195 200 205

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

Tyr Phe Gly Ile Ile Ala Leu Ser Arg Ala Glu Gly Arg Gly Ser Leu
225 230 235 240

Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Phe Gly
245 250 255

Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly Val Gln Cys Ser
260 265 270

Arg Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu
275 280 285

Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys
290 295 300

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu
305 310 315 320

Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser
325 330 335

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu
340 345 350

Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
355 360 365

Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg Gly Gly Gly
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
385 390 395 400

Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Ala Pro Ser
405 410 415

Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp
420 425 430

Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp
435 440 445

Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu
450 455 460

Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe
465 470 475 480

Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys
485 490 495

Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly
500 505 510

Gln Gly Thr Thr Val Thr Val Ser Ser Tyr Val Thr Val Ser Ser Gln
515 520 525

Asp Pro Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro
530 535 540

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
545 550 555 560

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
565 570 575

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

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
595 600 605

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
610 615 620

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
625 630 635 640

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
645 650 655

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
660 665 670

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
675 680 685

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
690 695 700

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
705 710 715 720

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
725 730 735

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
740 745 750

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp Pro Lys Phe
755 760 765

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
770 775 780

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
785 790 795 800

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
805 810 815

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
820 825 830

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
835 840 845

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
850 855 860

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
865 870 875 880

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
885 890 895

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
900 905 910

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
915 920 925

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
930 935 940

Pro Pro Arg Gly Pro Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala
945 950 955 960

Gly Asp Val Glu Ser Asn Pro Gly Pro Met Arg Ile Ser Lys Pro His
965 970 975

Leu Arg Ser Ile Ser Ile Gln Cys Tyr Leu Cys Leu Leu Leu Asn Ser
980 985 990

His Phe Leu Thr Glu Ala Gly Ile His Val Phe Ile Leu Gly Cys Phe
995 1000 1005

Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile
1010 1015 1020

Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
1025 1030 1035

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
1040 1045 1050

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser
1055 1060 1065

Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu
1070 1075 1080

Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
1085 1090 1095

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
1100 1105 1110

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile
1115 1120 1125

Asn Thr Ser
1130

<210> 37
<211> 1138
<212> PRT
<213> Artificial Sequence

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

<400> 37
Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Arg Ser Ser Ser
65 70 75 80

Arg Thr Pro Ser Asp Lys Val Ala His Val Val Ala Asn Pro Gln Ala
85 90 95

Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala
100 105 110

Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly
115 120 125

Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro
130 135 140

Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser
145 150 155 160

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

Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile
180 185 190

Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala
195 200 205

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

Tyr Phe Gly Ile Ile Ala Leu Ser Arg Ala Glu Gly Arg Gly Ser Leu
225 230 235 240

Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Phe Gly
245 250 255

Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly Val Gln Cys Ser
260 265 270

Arg Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu
275 280 285

Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys

290

295

300

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu
 305 310 315 320

Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser
 325 330 335

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu
 340 345 350

Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
 355 360 365

Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg Gly Gly Gly
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 385 390 395 400

Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Ala Pro Ser
 405 410 415

Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp
 420 425 430

Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp
 435 440 445

Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu
 450 455 460

Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe
 465 470 475 480

Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys
 485 490 495

Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly
500 505 510

Gln Gly Thr Thr Val Thr Val Ser Ser Tyr Val Thr Val Ser Ser Gln
515 520 525

Asp Pro Ala Glu Pro Lys Ser Pro Asp Lys Thr His Thr Cys Pro Pro
530 535 540

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
545 550 555 560

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
565 570 575

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

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
595 600 605

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
610 615 620

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
625 630 635 640

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
645 650 655

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
660 665 670

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
675 680 685

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

690

695

700

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 705 710 715 720

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 725 730 735

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 740 745 750

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Lys Asp Pro Lys Phe
 755 760 765

Trp Gly Val Leu Ala Gly Ile Val Met Gly Asp Leu Val Leu Thr Val
 770 775 780

Leu Ile Ala Leu Ala Val Tyr Phe Leu Gly Arg Leu Val Pro Arg Gly
 785 790 795 800

Arg Gly Ala Ala Glu Ala Ala Thr Arg Lys Gln Arg Ile Thr Glu Thr
 805 810 815

Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg Ser Asp Val Tyr Ser
 820 825 830

Asp Leu Asn Thr Gln Arg Pro Tyr Tyr Lys Arg Val Lys Phe Ser Arg
 835 840 845

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
 850 855 860

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

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
 885 890 895

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
900 905 910

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
915 920 925

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
930 935 940

Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Pro Gln Cys Thr Asn
945 950 955 960

Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro
965 970 975

Met Arg Ile Ser Lys Pro His Leu Arg Ser Ile Ser Ile Gln Cys Tyr
980 985 990

Leu Cys Leu Leu Leu Asn Ser His Phe Leu Thr Glu Ala Gly Ile His
995 1000 1005

Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu
1010 1015 1020

Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp
1025 1030 1035

Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser
1040 1045 1050

Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu
1055 1060 1065

Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
1070 1075 1080

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu

1085

1090

1095

Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu
 1100 1105 1110

Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val
 1115 1120 1125

His Ile Val Gln Met Phe Ile Asn Thr Ser
 1130 1135

<210> 38

<211> 673

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 38

tcgagtcgag atgagcactg aaagcatgat ccgggacgtg gagctggccg aggaggcgct	60
ccccaagaag acaggggggc cccagggctc caggcgggtgc ttgttcctca gcctcttctc	120
cttcctgatc gtggcaggcg ccaccacgct cttctgcctg ctgcactttg gagtgatcgg	180
ccccagagg gaagagttcc ccagggacct ctctctaatac agccctctgc aggcagccca	240
tgttgtagca aaccctcaag ctgaggggca gctccagtgg ctgaaccgcc gggccaatgc	300
cctcctggcc aatggcgtgg agctgagaga taaccagctg gtggtgcat cagagggcct	360
gtacctcatc tactcccagg tcctcttcaa gggccaaggc tgcccctcca cccatgtgct	420
cctcaccac accatcagcc gcatcgccgt ctctaccag accaaggta acctcctctc	480
tgccatcaag agcccctgcc agaggagac cccagagggg gctgaggcca agccctggta	540
tgagcccatc tatctgggag gggctttcca gctggagaag ggtgaccgac tcagcgctga	600
gatcaatcgg cccgactatc tcgactttgc cgagtctggg caggtctact ttgggatcat	660
tgccctgtcg tcg	673

<210> 39
<211> 219
<212> PRT
<213> Artificial Sequence

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

<400> 39
Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Gln Ala Ala His Val Val Ala
65 70 75 80

Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn
85 90 95

Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val
100 105 110

Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly
115 120 125

Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg
130 135 140

Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys
145 150 155 160

Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp
165 170 175

Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp
180 185 190

Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu
195 200 205

Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
210 215

<210> 40

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 40

atgagcactg aaatgcatcc cggaagggggg tcctggcacg aggaggcgct cccaagaag	60
acagggggggc cccagggtct caggcggtgc ttgttcctca gcctcttctc cttcctgac	120
gtggcaggcg ccaccacgct cttcttcctg ctgcactttg gaggatcg cccagagg	180
gaagagttcc ccagggacct ctctctaata agccctctgg cccatgttgt agcaaaccct	240
caagctgagg ggcagctcca gtggctgaac cgccgggcca atgccctcct ggccaatggc	300
gtggagctga gagataacca gctgggtggtg ccatcagagg gcctgtacct catctactcc	360
caggctctct tcaagggcca aggctgcccc tccacccatg tgctcctcac ccacaccatc	420
agccgcatcg cgtctccca ccagaccaag gtcaacctcc tcttcgcat caagagcccc	480
tgccagaggg agaccccaga gggggctgag gccaagccct ggtatgagcc catctatctg	540
ggaggggtct tccagctgga gaagggtgac cgactcatcg ctgagatcaa tcggcccgac	600
tatctctact ttgccgagta tgggcagggtc tactttggga tcattgccct gtcg	654

<210> 41

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 41

Met Ser Thr Glu Met His Pro Gly Arg Gly Ser Trp His Glu Glu Ala
1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Phe Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala His Val Val Ala Asn Pro
65 70 75 80

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
85 90 95

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
100 105 110

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
115 120 125

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
130 135 140

Val Ser His Gln Thr Lys Val Asn Leu Leu Phe Ala Ile Lys Ser Pro

145 150 155 160

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
 165 170 175

Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
 180 185 190

Ile Ala Glu Ile Asn Arg Pro Asp Tyr Leu Tyr Phe Ala Glu Tyr Gly
 195 200 205

Gln Val Tyr Phe Gly Ile Ile Ala Leu Ser
 210 215

<210> 42
<211> 33
<212> DNA
<213> Artificial Sequence

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

<400> 42
tcgagaagat gatctgactg cctgggccag agg 33

<210> 43
<211> 30
<212> DNA
<213> Artificial Sequence

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

<400> 43
tcgagaagat gatcttgcct gggccagagg 30

<210> 44
<211> 12
<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 44

tgatcttgcc tg

12

<210> 45

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 45

tacaacatgg gctacaggct tgcactcgg ggt

33

<210> 46

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 46

tacaacatgg gctaccttgt cactcggggt

30

<210> 47

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 47

ggctaccttg tc

12

<210> 48

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<400> 48

caggcagtca gatcatcttc tcgaaccccg agtgacaagc ctgtagcc

48

<210> 49

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 49

Gln Ala Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala
1 5 10 15

<210> 50

<211> 220

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
TNF alpha sequence"

<400> 50

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

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Ala His Val Val
65 70 75 80

Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala
85 90 95

Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val
100 105 110

Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys
115 120 125

Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser
130 135 140

Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile
145 150 155 160

Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro
165 170 175

Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly
180 185 190

Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala
195 200 205

Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
210 215 220

<210> 51

<211> 233
<212> PRT
<213> Homo sapiens

<400> 51

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

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
65 70 75 80

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
85 90 95

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
100 105 110

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
115 120 125

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
130 135 140

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
145 150 155 160

Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
165 170 175

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu

180

185

190

Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
 195 200 205

Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
 210 215 220

Gln Val Tyr Phe Gly Ile Ile Ala Leu
 225 230

<210> 52

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<220>

<221> misc_feature

<222> (214)..(219)

<223> /note="This region may or may not be present"

<400> 52

atgagcactg aaatgcatcc cggaaggggg tcctggcacg aggaggcgct cccaagaag 60

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gtggcaggcg ccaccacgct cttcttcctg ctgcactttg gagtgatcgg ccccagagg 180

gaagagttcc ccagggacct ctctctaata agccctctgg ccgcagccca tgtttagca 240

aaccctcaag ctgaggggca gctccagtgg ctgaaccgcc gggccaatgc ctcctggcc 300

aatggcgtgg agctgagaga taaccagctg gtggtgcat cagagggcct gtacctcatc 360

tactcccagg tcctcttcaa gggccaaggc tgccctcca cccatgtgct ctcaccac 420

accatcagcc gcatcgccgt ctcccaccag accaagggtca acctcctctt cgccatcaag 480

agcccctgcc agaggagac cccagagggg gctgaggcca agccctggta tgagcccatc 540

tatctgggag gggctcttcca gctggagaag ggtgaccgac tcatcgctga gatcaatcgg	600
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<210> 53
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<220>
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<220>
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 <223> /note="This region may or may not be present"

<400> 53
 Met Ser Thr Glu Met His Pro Gly Arg Gly Ser Trp His Glu Glu Ala
 1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
 20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
 35 40 45

Phe Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
 50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala His Val Val Ala
 65 70 75 80

Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn
 85 90 95

Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val
 100 105 110

Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly
115 120 125

Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg
130 135 140

Ile Ala Val Ser His Gln Thr Lys Val Asn Leu Leu Phe Ala Ile Lys
145 150 155 160

Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp
165 170 175

Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp
180 185 190

Arg Leu Ile Ala Glu Ile Asn Arg Pro Asp Tyr Leu Tyr Phe Ala Glu
195 200 205

Tyr Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Ser
210 215 220

<210> 54

<211> 56

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
monkey TNF alpha sequence"

<400> 54

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

Leu Pro Arg Lys Thr Ala Gly Pro Gln Gly Ser Arg Arg Cys Trp Phe
20 25 30

Leu Ser Leu Phe Ser Phe Leu Leu Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile
50 55

<210> 55
<211> 56
<212> PRT
<213> Sus sp.

<400> 55
Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1 5 10 15

Leu Ala Lys Lys Ala Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Cys
20 25 30

Leu Ser Leu Phe Ser Phe Leu Leu Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Glu Val Ile
50 55

<210> 56
<211> 56
<212> PRT
<213> Mus sp.

<400> 56
Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1 5 10 15

Leu Pro Gln Lys Met Gly Gly Phe Gln Asn Ser Arg Arg Cys Leu Cys
20 25 30

Leu Ser Leu Phe Ser Phe Leu Leu Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu Asn Phe Gly Val Ile
50 55

<210> 57

<211> 56

<212> PRT

<213> *Oryctolagus* sp.

<400> 57

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

Leu Pro Lys Lys Ala Gly Gly Pro Gln Gly Ser Lys Arg Cys Leu Cys
20 25 30

Leu Ser Leu Phe Ser Phe Leu Leu Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Arg Val Ile
50 55

<210> 58

<211> 56

<212> PRT

<213> *Capra* sp.

<400> 58

Met Ser Thr Lys Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Val
1 5 10 15

Leu Ser Lys Lys Ala Gly Gly Pro Gln Gly Ser Arg Ser Cys Trp Cys
20 25 30

Leu Ser Leu Phe Ser Phe Leu Leu Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile
50 55

<210> 59

<211> 56

<212> PRT

<213> *Ovis* sp.

<400> 59

Met Ser Thr Lys Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Val

1

5

10

15

Leu Ser Asn Lys Ala Gly Gly Pro Gln Gly Ser Arg Ser Cys Trp Cys
20 25 30

Leu Ser Leu Phe Ser Phe Leu Leu Val Ala Gly Ala Thr Thr Leu Phe
35 40 45

Cys Leu Leu His Phe Gly Val Ile
50 55