SEQUENCE LISTING

<110> The Regents of the University of California

<120> Chimeric Antigen Receptor Modified T-Cells (CAR-T) for the Treatment of Hematological and Solid Tumor Cancers

<130> 048537-623001WO

<150> US 62/824,080
<151> 2019-03-26

<150> US 62/931,103
<151> 2019-11-05

<150> US 62/969,569
<151> 2020-02-03

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<170> PatentIn version 3.5

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Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
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20 25 30

Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile
35 40 45

Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Asp Arg Phe Ser Gly
50 55 60

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

Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 21
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 21

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Pro Arg Phe Ser Gly
    50   55   60

Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Glu Ser
65   70   75   80

Glu Asp Ala Ala Tyr Tyr Phe Cys Gln Gln His Asp Glu Ser Pro Tyr
                85   90   95

Thr Phe Gly Glu Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 22
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 22

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

Lys Gly

<210> 23
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 23

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

Lys Gly

<210> 24
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 24

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

Gly Glu Gly Ser Thr Lys Gly Gly Gly Gly Gly Ser
            20   25

<210> 25
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 25

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

Ala Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
        35   40   45

Ala Ser Ile Ser Arg Gly Gly Thr Thr Tyr Tyr Pro Asp Ser Val Lys
    50   55   60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Arg Asn Ile Leu Tyr Leu
65   70   75   80

Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Gly
                85   90   95

Arg Tyr Asp Tyr Asp Gly Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Ser Val Thr Val Ser Ser
        115

<210> 26
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 26

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1   5   10   15

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

```
Ala Met Ser Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
        35                  40                  45

Gly Ser Ile Ser Arg Gly Gly Thr Thr Tyr Tyr Pro Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Gly
                85                  90                  95

Arg Tyr Asp Tyr Asp Gly Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser
        115
```

<210> 27
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 27

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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ala Phe Thr Ala Tyr
            20                  25                  30

Asn Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ser Phe Asp Pro Tyr Asp Gly Gly Ser Ser Tyr Asn Gln Lys Phe
    50                  55                  60

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

Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Trp Tyr Tyr Phe Asp Tyr Trp Gly His Gly Thr Leu Val
            100                 105                 110
```

Thr Val Ser Ser
115

<210> 28
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 28

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1 5 10

<210> 29
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 29

Val Asp Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1 5 10

<210> 30
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 30

Val Asp Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1 5 10

<210> 31
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 31

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        35   40   45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50   55   60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65   70   75   80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85   90   95

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
        115   120   125

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145   150   155   160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                165   170   175

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
            180   185   190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        195   200   205

Lys Ser Leu Ser Leu Ser Leu Gly Lys Met
    210   215

<210> 32
<211> 68
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 32

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

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
            20   25   30

Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
        35   40   45

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
    50   55   60

Ala Tyr Arg Ser
65

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

<220>
<223> Synthetic construct

<400> 33

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1   5   10   15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
            20   25   30

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
        35   40

<210> 34
<211> 112
<212> PRT
<213> Homo sapiens

<400> 34

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

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20   25   30

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

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

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

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala

85 90 95

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

<210> 35
<211> 2148
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 35
atgggatggt catgtatcat ccttttttcta gtagcaactg caaccggtgt acattccgac 60

atcaagatga cccagtctcc atcttccatg tatgcatctc taggagagag agtcactatc 120

acttgcaagg cgagtccgga cattaatagc tatttaagct ggttccagca gaaaccaggg 180

aaatctccta agaccctgat ctatcgtgca aacagattgg ttgatggggt cccatcaagg 240

ttcagtggcg gtggatctgg gcaagattat tctctcacca tcaacagcct ggagtatgaa 300

gatatgggaa tttattattg tctacagtat gatgaatttc cgtacacgtt cggaggggggg 360

accaagctgg aaatgaaagg ctccacctct ggatccggca agcccggatc tggcgaggga 420

tccaccaagg gcgaagtgaa actagtggag tctgggggag gcttagtgaa gcctggaggg 480

tccctgaaac tctcctgtgc agcctctgga ttcactttca gtagctatgc catgtcttgg 540

gttcgccaga ttccagagaa gaggctggag tgggtcgcat ccattagtcg tggtggtacc 600

acctactatc cagacagtgt gaagggccga ttcaccatct ccagagataa tgtcaggaac 660

atcctgtacc tgcaaatgag cagtctgagg tctgaggaca cggccatgta ttactgtgga 720

agatatgatt acgacgggta ctatgcaatg gactactggg gtcaaggaac ctcagtcacc 780

gtctcctcag agtccaaata tggtccccca tgcccaccat gcccagcacc tgagttcctg 840

gggggaccat cagtcttcct gttcccccca aaacccaagg acactctcat gatctcccgg 900

acccctgagg tcacgtgcgt ggtggtggac gtgagccagg aagaccccga ggtccagttc 960

aactggtacg tggatggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

ttcaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaac 1080

ggcaaggagt acaagtgcaa ggtctccaac aaaggcctcc cgtcctccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagag ccacaggtgt acaccctgcc cccatcccag 1200

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctaccccagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca ggctaaccgt ggacaagagc 1380

aggtggcagg aggggaatgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacacaga agagcctctc cctgtcccta ggtaaaatgt tttgggtgct ggtggtggtt 1500

ggtggagtcc tggcttgcta tagcttgcta gtaacagtgg cctttattat tttctgggtg 1560

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gggcccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 1680

tccaaacggg gcagaaagaa actcctgtat atattcaaac aaccatttat gagaccagta 1740

caaactactc aagaggaaga tggctgtagc tgccgatttc cagaagaaga agaaggagga 1800

tgtgaactga gagtgaagtt cagcaggagc gcagacgccc ccgcgtacca gcagggccag 1860

aaccagctct ataacgagct caatctagga cgaagagagg agtacgatgt tttggacaag 1920

agacgtggcc gggaccctga gatgggggga aagccgagaa ggaagaaccc tcaggaaggc 1980

ctgtacaatg aactgcagaa agataagatg gcggaggcct acagtgagat tgggatgaaa 2040

ggcgagcgcc ggaggggcaa ggggcacgat ggcctttacc agggtctcag tacagccacc 2100

aaggacacct acgacgccct tcacatgcag gccctgcccc ctcgctga 2148

<210> 36
<211> 2154
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 36
atgggatggt catgtatcat ccttttttcta gtagcaactg caaccggtgt acattccgac 60

atccagatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc 120

acttgcaagg cgagtccgga cattaatagc tatttaagct ggtttcagca gaggccaggc 180

caatctccaa ggcgcctaat ttatcgtgca aacagattgg ttgatggggt cccagacagg 240

ttcagtggca gtgggtcagg cactgatttc acactgaaaa tcagcagggt ggaggctgag 300

gatgttggag tttattactg tctacagtat gatgaatttc cgtacacgtt cggccaaggg 360

accaaggtgg aaatcaaagg ctccacctct ggatccggca agcccggatc tggcgaggga 420

tccaccaagg gcgaagtgca gctggtgcag tctggagcag aggtgaaaaa gcccggggag 480

tctctgagga tctcctgtaa gggttctgga ttcactttca gtagctatgc catgtcttgg 540

atcaggcagt ccccatcgag aggccttgag tggctgggtt ccattagtcg tggtggtacc 600

acctactatc cagacagtgt gaagggcaga ttcaccatct ccagagacaa cgccaagaac 660

tcactgtatc tgcaaatgaa cagcctgaga gccgaggaca cggctgtgta ttactgtgga 720

agatatgatt acgacgggta ctatgcaatg gactactggg gccagggaac gctggtcacc 780

gtcagctcag tcgacgagtc caaatatggt cccccatgcc caccatgccc agcacctgag 840

ttcctggggg gaccatcagt cttcctgttc cccccaaaac ccaaggacac tctcatgatc 900

tcccggaccc ctgaggtcac gtgcgtggtg gtggacgtga gccaggaaga ccccgaggtc 960

cagttcaact ggtacgtgga tggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1020

gagcagttca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1080

ctgaacggca aggagtacaa gtgcaaggtc tccaacaaag gcctcccgtc ctccatcgag 1140

aaaaccatct ccaaagccaa agggcagccc cgagagccac aggtgtacac cctgccccca 1200

tcccaggagg agatgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctac 1260

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1320

acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaggct aaccgtggac 1380

aagagcaggt ggcaggaggg gaatgtcttc tcatgctccg tgatgcatga ggctctgcac 1440

aaccactaca cacagaagag cctctccctg tccctaggta aaatgttttg ggtgctggtg 1500

gtggttggtg gagtcctggc ttgctatagc ttgctagtaa cagtggcctt tattattttc 1560

tgggtgagga gtaagaggag caggggcgga cacagtgact acatgaacat gactccccgc 1620

cgccctgggc ccacccgcaa gcattaccag ccctatgccc caccacgcga cttcgcagcc 1680

tatcgctcca aacggggcag aaagaaactc ctgtatatat tcaaacaacc atttatgaga 1740

ccagtacaaa ctactcaaga ggaagatggc tgtagctgcc gatttccaga agaagaagaa 1800

ggaggatgtg aactgagagt gaagttcagc aggagcgcag acgccccgc gtaccagcag 1860

ggccagaacc agctctataa cgagctcaat ctaggacgaa gagaggagta cgatgttttg 1920

gacaagagac gtggccggga ccctgagatg gggggaaagc cgagaaggaa gaaccctcag 1980

gaaggcctgt acaatgaact gcagaaagat aagatggcgg aggcctacag tgagattggg 2040

atgaaaggcg agcgccggag gggcaagggg cacgatggcc tttaccaggg tctcagtaca 2100

gccaccaagg acacctacga cgcccttcac atgcaggccc tgcccctcg ctga 2154

<210> 37
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 37
atgggatggt catgtatcat ccttttttcta gtagcaactg caaccggtgt acattccgat 60

attgtgatga cccagactcc actctccctg cccgtcaccc ctggagagcc ggcctccatc 120

tcctgcaggg caagtaagag cattagcaaa tatttagcct ggtaccagca gaaacctggc 180

caggctccca ggctcctcat ctattctgga tccactttgc aatctgggat cccacctcga 240

ttcagtggca gcgggtatgg aacagatttt accctcacaa ttaataacat agaatctgag 300

gatgctgcat attacttctg tcaacagcat gatgaatccc cgtacacgtt cggcgagggg 360

accaaggtgg aaatcaaagg tggtggtggt agcggctcca cctctggatc cggcaagccc 420

ggatctggcg agggatccac caagggcgga ggaggaggaa gtcaggtgca gctgcaggag 480

tcgggcccag gactggtgaa gccttcacag accctgtccc tcacctgcac tgtctctggt 540

tatgcattca ctgcctacaa catacactgg gtgcgacagg cccctggaca agggcttgag 600

tggatgggtt cttttgatcc ttacgatggt ggtagtagtt acaaccagaa gttcaaggac 660

agactcacca tctccaagga cacctccaaa aaccaggtgg tccttacaat gaccaacatg 720

gaccctgtgg acacagccac gtattactgt gcaagagggt ggtactactt tgactactgg 780

ggccacggaa ccctggtcac cgtctcctca gtcgacgagt ccaaatatgg tcccccatgc 840

ccaccatgcc cagcacctga gttcctgggg ggaccatcag tcttcctgtt cccccaaaa 900

cccaaggaca ctctcatgat ctcccggacc cctgaggtca cgtgcgtggt ggtggacgtg 960

agccaggaag accccgaggt ccagttcaac tggtacgtgg atggcgtgga ggtgcataat 1020

gccaagacaa agccgcggga ggagcagttc aacagcacgt accgtgtggt cagcgtcctc 1080

accgtcctgc accaggactg gctgaacggc aaggagtaca agtgcaaggt ctccaacaaa 1140

ggcctcccgt cctccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagagcca 1200

caggtgtaca ccctgccccc atcccaggag gagatgacca agaaccaggt cagcctgacc 1260

tgcctggtca aaggcttcta ccccagcgac atcgccgtgg agtgggagag caatgggcag 1320

ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1380

tacagcaggc taaccgtgga caagagcagg tggcaggagg ggaatgtctt ctcatgctcc 1440

gtgatgcatg aggctctgca caaccactac acacagaaga gcctctccct gtccctaggt 1500

aaaatgtttt gggtgctggt ggtggttggt ggagtcctgg cttgctatag cttgctagta 1560

acagtggcct ttattatttt ctgggtgagg agtaagagga gcaggggcgg acacagtgac 1620

tacatgaaca tgactccccg ccgccctggg cccacccgca agcattacca gccctatgcc 1680

ccaccacgcg acttcgcagc ctatcgctcc aaacggggca gaaagaaact cctgtatata 1740

ttcaaacaac catttatgag accagtacaa actactcaag aggaagatgg ctgtagctgc 1800

cgatttccag aagaagaaga aggaggatgt gaactgagag tgaagttcag caggagcgca 1860

gacgcccccg cgtaccagca gggccagaac cagctctata acgagctcaa tctaggacga 1920

agagaggagt acgatgtttt ggacaagaga cgtggccggg accctgagat ggggggaaag 1980

ccgagaagga agaaccctca ggaaggcctg tacaatgaac tgcagaaaga taagatggcg 2040

gaggcctaca gtgagattgg gatgaaaggc gagcgccgga ggggcaaggg gcacgatggc 2100

ctttaccagg gtctcagtac agccaccaag gacacctacg acgcccttca catgcaggcc 2160

ctgccccctc gctga 2175

<210> 38

<211> 715
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 38

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

Val His Ser Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr Ala
20 25 30

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

Asn Ser Tyr Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys
50 55 60

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

Phe Ser Gly Gly Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Asn Ser
85 90 95

Leu Glu Tyr Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Glu
100 105 110

Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Met Lys Gly Ser
115 120 125

Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly
130 135 140

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
145 150 155 160

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
165 170 175

Ala Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
180 185 190

Ala Ser Ile Ser Arg Gly Gly Thr Thr Tyr Tyr Pro Asp Ser Val Lys
195 200 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Arg Asn Ile Leu Tyr Leu
210 215 220

```
Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Gly
225                 230                 235                 240


Arg Tyr Asp Tyr Asp Gly Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
                245                 250                 255


Thr Ser Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro
            260                 265                 270


Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
        275                 280                 285


Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    290                 295                 300


Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
305                 310                 315                 320


Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                325                 330                 335


Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            340                 345                 350


Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        355                 360                 365


Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
    370                 375                 380


Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
385                 390                 395                 400


Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                405                 410                 415


Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            420                 425                 430


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


Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
    450                 455                 460


Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
465                 470                 475                 480
```

```
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val
                485                 490                 495

Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr
            500                 505                 510

Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly
        515                 520                 525

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
    530                 535                 540

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
545                 550                 555                 560

Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
                565                 570                 575

Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg
            580                 585                 590

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

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
    610                 615                 620

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
625                 630                 635                 640

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
                645                 650                 655

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
            660                 665                 670

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

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
    690                 695                 700

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
705                 710                 715
```

<210> 39
<211> 717
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 39

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


Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
            20                  25                  30


Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Pro Asp Ile
        35                  40                  45


Asn Ser Tyr Leu Ser Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg
    50                  55                  60


Arg Leu Ile Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Asp Arg
65                  70                  75                  80


Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg
                85                  90                  95


Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Tyr Asp Glu
            100                 105                 110


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


Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly
    130                 135                 140


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


Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Phe Thr Phe Ser Ser Tyr
                165                 170                 175


Ala Met Ser Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
            180                 185                 190


Gly Ser Ile Ser Arg Gly Gly Thr Thr Tyr Tyr Pro Asp Ser Val Lys
        195                 200                 205


Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
    210                 215                 220


Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Gly
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225                 230                 235                 240

Arg Tyr Asp Tyr Asp Gly Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
                245                 250                 255

Thr Leu Val Thr Val Ser Ser Val Asp Glu Ser Lys Tyr Gly Pro Pro
            260                 265                 270

Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe
        275                 280                 285

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    290                 295                 300

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
305                 310                 315                 320

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                325                 330                 335

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
            340                 345                 350

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        355                 360                 365

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
    370                 375                 380

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
385                 390                 395                 400

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                405                 410                 415

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            420                 425                 430

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        435                 440                 445

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
    450                 455                 460

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
465                 470                 475                 480

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe
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                485                 490                 495

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
            500                 505                 510

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
        515                 520                 525

Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
    530                 535                 540

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
545                 550                 555                 560

Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
                565                 570                 575

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
            580                 585                 590

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
        595                 600                 605

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
    610                 615                 620

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
625                 630                 635                 640

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
                645                 650                 655

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
            660                 665                 670

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

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
    690                 695                 700

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
705                 710                 715
```

<210> 40
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 40

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

Val His Ser Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
            20   25   30

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

Ser Lys Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
    50   55   60

Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Pro Arg
65   70   75   80

Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn
                85   90   95

Ile Glu Ser Glu Asp Ala Ala Tyr Tyr Phe Cys Gln Gln His Asp Glu
            100   105   110

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

Gly Gly Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu
    130   135   140

Gly Ser Thr Lys Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Glu
145   150   155   160

Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys
                165   170   175

Thr Val Ser Gly Tyr Ala Phe Thr Ala Tyr Asn Ile His Trp Val Arg
            180   185   190

Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Ser Phe Asp Pro Tyr
        195   200   205

Asp Gly Gly Ser Ser Tyr Asn Gln Lys Phe Lys Asp Arg Leu Thr Ile
    210   215   220

Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr Met Thr Asn Met
225   230   235   240

```
Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Gly Trp Tyr Tyr
                245                 250                 255

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

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
        275                 280                 285

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
    290                 295                 300

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
305                 310                 315                 320

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
                325                 330                 335

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
            340                 345                 350

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
        355                 360                 365

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
    370                 375                 380

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
385                 390                 395                 400

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
                405                 410                 415

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
            420                 425                 430

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
        435                 440                 445

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
    450                 455                 460

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
465                 470                 475                 480

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
                485                 490                 495
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```
Leu Ser Leu Gly Lys Met Phe Trp Val Leu Val Val Val Gly Gly Val
            500                 505                 510

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
        515                 520                 525

Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met
    530                 535                 540

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
545                 550                 555                 560

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys
                565                 570                 575

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
            580                 585                 590

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
        595                 600                 605

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
    610                 615                 620

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
625                 630                 635                 640

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
                645                 650                 655

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
            660                 665                 670

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
        675                 680                 685

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
    690                 695                 700

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
705                 710                 715                 720

Leu Pro Pro Arg
```

<210> 41
<211> 111
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 41

Val Asp Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Leu Pro
1 5 10 15

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
20 25 30

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
35 40 45

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
50 55 60

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
65 70 75 80

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
85 90 95

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
100 105 110

<210> 42
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 42

Val Asp Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
1 5 10 15

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

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

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
50 55 60

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

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


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


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


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


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


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


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


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


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


Leu Ser Leu Ser Leu Gly Lys
225                 230


<210>  43
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic construct

<400>  43

Lys Ser Ile Ser Lys Tyr
1               5


<210>  44
<211>  3
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic construct

<400>  44
```

Ser Gly Ser
1

<210> 45
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 45

Gln Gln His Asp Glu Ser Pro Tyr
1 5

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 46

Gly Tyr Ala Phe Thr Ala Tyr Asn
1 5

<210> 47
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 47

Phe Asp Pro Tyr Asp Gly Gly Ser
1 5

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 48

Gly Trp Tyr Tyr Phe Asp Tyr
1 5

<210> 49
<211> 6
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 49

Pro Asp Ile Asn Ser Tyr
1 5

<210> 50
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 50

Arg Ala Asn
1

<210> 51
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 51

Leu Gln Tyr Asp Glu Phe Pro Tyr Thr
1 5

<210> 52
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 52

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 53
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 53

Ile Ser Arg Gly Gly Thr Thr

1 5

<210> 54
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 54

Tyr Asp Tyr Asp Gly Tyr Tyr Ala Met Asp Tyr
1 5 10

<210> 55
<211> 937
<212> PRT
<213> Homo sapiens

<400> 55

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

Leu Ala Ala Leu Leu Leu Ala Ala Arg Gly Ala Ala Ala Gln Glu Thr
20 25 30

Glu Leu Ser Val Ser Ala Glu Leu Val Pro Thr Ser Ser Trp Asn Ile
35 40 45

Ser Ser Glu Leu Asn Lys Asp Ser Tyr Leu Thr Leu Asp Glu Pro Met
50 55 60

Asn Asn Ile Thr Thr Ser Leu Gly Gln Thr Ala Glu Leu His Cys Lys
65 70 75 80

Val Ser Gly Asn Pro Pro Pro Thr Ile Arg Trp Phe Lys Asn Asp Ala
85 90 95

Pro Val Val Gln Glu Pro Arg Arg Leu Ser Phe Arg Ser Thr Ile Tyr
100 105 110

Gly Ser Arg Leu Arg Ile Arg Asn Leu Asp Thr Thr Asp Thr Gly Tyr
115 120 125

Phe Gln Cys Val Ala Thr Asn Gly Lys Glu Val Val Ser Ser Thr Gly
130 135 140

Val Leu Phe Val Lys Phe Gly Pro Pro Pro Thr Ala Ser Pro Gly Tyr
145 150 155 160

```
Ser Asp Glu Tyr Glu Glu Asp Gly Phe Cys Gln Pro Tyr Arg Gly Ile
                165                 170                 175

Ala Cys Ala Arg Phe Ile Gly Asn Arg Thr Val Tyr Met Glu Ser Leu
            180                 185                 190

His Met Gln Gly Glu Ile Glu Asn Gln Ile Thr Ala Ala Phe Thr Met
        195                 200                 205

Ile Gly Thr Ser Ser His Leu Ser Asp Lys Cys Ser Gln Phe Ala Ile
    210                 215                 220

Pro Ser Leu Cys His Tyr Ala Phe Pro Tyr Cys Asp Glu Thr Ser Ser
225                 230                 235                 240

Val Pro Lys Pro Arg Asp Leu Cys Arg Asp Glu Cys Glu Ile Leu Glu
                245                 250                 255

Asn Val Leu Cys Gln Thr Glu Tyr Ile Phe Ala Arg Ser Asn Pro Met
            260                 265                 270

Ile Leu Met Arg Leu Lys Leu Pro Asn Cys Glu Asp Leu Pro Gln Pro
        275                 280                 285

Glu Ser Pro Glu Ala Ala Asn Cys Ile Arg Ile Gly Ile Pro Met Ala
    290                 295                 300

Asp Pro Ile Asn Lys Asn His Lys Cys Tyr Asn Ser Thr Gly Val Asp
305                 310                 315                 320

Tyr Arg Gly Thr Val Ser Val Thr Lys Ser Gly Arg Gln Cys Gln Pro
                325                 330                 335

Trp Asn Ser Gln Tyr Pro His Thr His Thr Phe Thr Ala Leu Arg Phe
            340                 345                 350

Pro Glu Leu Asn Gly Gly His Ser Tyr Cys Arg Asn Pro Gly Asn Gln
        355                 360                 365

Lys Glu Ala Pro Trp Cys Phe Thr Leu Asp Glu Asn Phe Lys Ser Asp
    370                 375                 380

Leu Cys Asp Ile Pro Ala Cys Asp Ser Lys Asp Ser Lys Glu Lys Asn
385                 390                 395                 400

Lys Met Glu Ile Leu Tyr Ile Leu Val Pro Ser Val Ala Ile Pro Leu
                405                 410                 415
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```
Ala Ile Ala Leu Leu Phe Phe Phe Ile Cys Val Cys Arg Asn Asn Gln
            420                 425                 430

Lys Ser Ser Ser Ala Pro Val Gln Arg Gln Pro Lys His Val Arg Gly
        435                 440                 445

Gln Asn Val Glu Met Ser Met Leu Asn Ala Tyr Lys Pro Lys Ser Lys
    450                 455                 460

Ala Lys Glu Leu Pro Leu Ser Ala Val Arg Phe Met Glu Glu Leu Gly
465                 470                 475                 480

Glu Cys Ala Phe Gly Lys Ile Tyr Lys Gly His Leu Tyr Leu Pro Gly
                485                 490                 495

Met Asp His Ala Gln Leu Val Ala Ile Lys Thr Leu Lys Asp Tyr Asn
            500                 505                 510

Asn Pro Gln Gln Trp Met Glu Phe Gln Gln Glu Ala Ser Leu Met Ala
        515                 520                 525

Glu Leu His His Pro Asn Ile Val Cys Leu Leu Gly Ala Val Thr Gln
    530                 535                 540

Glu Gln Pro Val Cys Met Leu Phe Glu Tyr Ile Asn Gln Gly Asp Leu
545                 550                 555                 560

His Glu Phe Leu Ile Met Arg Ser Pro His Ser Asp Val Gly Cys Ser
                565                 570                 575

Ser Asp Glu Asp Gly Thr Val Lys Ser Ser Leu Asp His Gly Asp Phe
            580                 585                 590

Leu His Ile Ala Ile Gln Ile Ala Ala Gly Met Glu Tyr Leu Ser Ser
        595                 600                 605

His Phe Phe Val His Lys Asp Leu Ala Ala Arg Asn Ile Leu Ile Gly
    610                 615                 620

Glu Gln Leu His Val Lys Ile Ser Asp Leu Gly Leu Ser Arg Glu Ile
625                 630                 635                 640

Tyr Ser Ala Asp Tyr Tyr Arg Val Gln Ser Lys Ser Leu Leu Pro Ile
                645                 650                 655

Arg Trp Met Pro Pro Glu Ala Ile Met Tyr Gly Lys Phe Ser Ser Asp
            660                 665                 670
```

```
Ser Asp Ile Trp Ser Phe Gly Val Val Leu Trp Glu Ile Phe Ser Phe
        675                 680                 685

Gly Leu Gln Pro Tyr Tyr Gly Phe Ser Asn Gln Glu Val Ile Glu Met
    690                 695                 700

Val Arg Lys Arg Gln Leu Leu Pro Cys Ser Glu Asp Cys Pro Pro Arg
705                 710                 715                 720

Met Tyr Ser Leu Met Thr Glu Cys Trp Asn Glu Ile Pro Ser Arg Arg
                725                 730                 735

Pro Arg Phe Lys Asp Ile His Val Arg Leu Arg Ser Trp Glu Gly Leu
            740                 745                 750

Ser Ser His Thr Ser Ser Thr Thr Pro Ser Gly Gly Asn Ala Thr Thr
        755                 760                 765

Gln Thr Thr Ser Leu Ser Ala Ser Pro Val Ser Asn Leu Ser Asn Pro
    770                 775                 780

Arg Tyr Pro Asn Tyr Met Phe Pro Ser Gln Gly Ile Thr Pro Gln Gly
785                 790                 795                 800

Gln Ile Ala Gly Phe Ile Gly Pro Pro Ile Pro Gln Asn Gln Arg Phe
                805                 810                 815

Ile Pro Ile Asn Gly Tyr Pro Ile Pro Pro Gly Tyr Ala Ala Phe Pro
            820                 825                 830

Ala Ala His Tyr Gln Pro Thr Gly Pro Pro Arg Val Ile Gln His Cys
        835                 840                 845

Pro Pro Pro Lys Ser Arg Ser Pro Ser Ser Ala Ser Gly Ser Thr Ser
    850                 855                 860

Thr Gly His Val Thr Ser Leu Pro Ser Ser Gly Ser Asn Gln Glu Ala
865                 870                 875                 880

Asn Ile Pro Leu Leu Pro His Met Ser Ile Pro Asn His Pro Gly Gly
                885                 890                 895

Met Gly Ile Thr Val Phe Gly Asn Lys Ser Gln Lys Pro Tyr Lys Ile
            900                 905                 910

Asp Ser Lys Gln Ala Ser Leu Leu Gly Asp Ala Asn Ile His Gly His
        915                 920                 925
```

Thr Glu Ser Met Ile Ser Ala Glu Leu
    930   935

<210> 56
<211> 21
<212> PRT
<213> Homo sapiens

<400> 56

Val Ala Thr Asn Gly Lys Glu Val Val Ser Ser Thr Gly Val Leu Phe
1   5   10   15

Val Lys Phe Gly Pro
            20

<210> 57
<211> 15
<212> PRT
<213> Homo sapiens

<400> 57

Glu Val Val Ser Ser Thr Gly Val Leu Phe Val Lys Phe Gly Pro
1   5   10   15