SEQUENCE LISTING

<110> ALS THERAPY DEVELOPMENT INSTITUTE

<120> ANTI-CD40L ANTIBODIES AND METHODS FOR TREATING CD40L-RELATED DISEASES OR DISORDERS

<130> 224823-384897

<150> PCT/US2016/016165
<151> 2016-02-02

<150> 62/111,261
<151> 2015-02-03

<160> 25

<170> PatentIn version 3.5

<210> 1
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically Generated Sequence

<400> 1

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


Glu Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Arg Val Ser Ser Ser
            20                  25                  30


Thr Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50                  55                  60


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


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


Glu Ile Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 2

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

<220>
<223> Synthetically Generated Sequence

<400> 2

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

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

Tyr Met Tyr Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn Pro Ser Asn Gly Asp Thr Asn Phe Asn Glu Lys Phe
50 55 60

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

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

Thr Arg Ser Asp Gly Arg Asn Asp Met Asp Ser Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 3
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically Generated Sequence

<400> 3

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

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

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

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

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

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

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

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

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

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
225                 230
```

<210> 4
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically Generated Sequence

<400> 4

```
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala
1               5                  10                  15

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

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

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

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

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

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

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

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

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

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

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
```

210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 5
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically Generated Sequence

<400> 5

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

Glu Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Lys Val Ser Ser Ser
20 25 30

Thr Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60

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

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

Glu Ile Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 6
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically Generated Sequence

<400> 6

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

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

Tyr Met Tyr Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Glu Ile Asn Pro Ser Asn Gly Asp Thr Asn Phe Asn Glu Lys Phe
    50                  55                  60

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

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

Thr Arg Ser Asp Gly Arg Asn Asp Met Asp Ser Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
```

<210> 7
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically Generated Sequence

<400> 7

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

Glu Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Arg Val Ser Ser Ser
            20                  25                  30

Thr Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50                  55                  60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80
```

```
Ser Val Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Trp
                85                  90                  95

Glu Ile Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105                 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        115                 120                 125

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145                 150                 155                 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
            180                 185                 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
        195                 200                 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 8
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically Generated Sequence

<400> 8
gacatcgtgc tgacccagtc ccccgccacc ctgtccgtgt ccccccggcga gagggccacc
60

atctcctgca gggcctccca gagggtgtcc tcctccacct actcctacat gcactggtac
120

cagcagaagc ccggccagcc ccccaagctg ctgatcaagt acgcctccaa cctggagtcc
180

ggcgtgcccg ccaggttctc cggctccggc tccggcaccg acttcaccct gaccatctcc
240

tccgtggagc ccgaggactt cgccacctac tactgccagc actcctggga gatccccccc
300

accttcggcg gcggcaccaa gctggaaatc aaacgtacgg tggctgcacc atctgtcttc
360

atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg
420

aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg
480

ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc
540

agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc
600

acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgttagtga
660

<210> 9
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically Generated Sequence

<400> 9

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

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

Tyr Met Tyr Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn Pro Ser Asn Gly Asp Thr Asn Phe Asn Glu Lys Phe
50 55 60

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

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

Thr Arg Ser Asp Gly Arg Asn Asp Met Asp Ser Trp Gly Gln Gly Thr
100 105 110

```
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

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

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Ser Asp Lys Thr
    210                 215                 220

His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335
```

```
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

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

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 10
<211> 1956
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically Generated Sequence

<400> 10
caggtgcagc tggtgcagtc cggcgccgag gtggtgaagc ccggcgcctc cgtgaagctg
60

tcctgcaagg cctccggcta catcttcacc tcctactaca tgtactgggt gaagcaggcc
120

cccggccagg gcctggagtg gatcggcgag atcaacccct ccaacggcga caccaacttc
180

aacgagaagt tcaagtccaa ggccaccctg accgtggaca agtccgcctc caccgcctac
240

atggagctgt cctccctgag gtccgaggac accgccgtgt actactgcac caggtccgac
300

ggcaggaacg acatggactc ctggggccag ggcaccctgg tgaccgtgtc ctccgctagc
360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca
420

gcagccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac
480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc
540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc
600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttgg tgagaggcca
660

gcacagggag ggagggtgtc tgctggaagc caggctcagc gctcctgcct ggacgcatcc
720

cggctatgca gccccagtcc agggcagcaa ggcaggcccc gtctgcctct tcacccggag
780

gcctctgccc gccccactca tgctcaggga gagggtcttc tggcttttc cccaggctct
840

gggcaggcac aggctaggtg cccctaaccc aggccctgca cacaaagggg caggtgctgg
900

gctcagacct gccaagagcc atatccggga ggaccctgcc cctgacctaa gcccacccca
960

aaggccaaac tctccactcc ctcagctcgg acaccttctc tcctcccaga ttccagtaac
1020

tcccaatctt ctctctgcag agcccaaatc tagtgacaaa actcacacaa gcccaccgag
1080

cccaggtaag ccagcccagg cctcgccctc cagctcaagg cgggacaggt gccctagagt
1140

agcctgcatc cagggacagg ccccagccgg gtgctgacac gtccacctcc atctcttcct
1200

cagcacctga actcctgggg ggatcctcag tcttcctctt ccccccaaaa cccaaggaca
1260

ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg agccacgaag
1320

accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat gccaagacaa
1380

agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc accgtcctgc
1440

accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa gccctcccag
1500

cccccatcga gaaaaccatc tccaaagcca aaggtgggac ccgtggggtg cgagggccac
1560

atggacagag gccggctcgg cccaccctct gccctgagag tgaccgctgt accaacctct
1620

gtccctacag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag
1680

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc
1740

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg
1800

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg
1860

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacaca
1920

cagaagagcc tctccctgtc tccgggtaaa taatga
1956

<210> 11
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically Generated Sequence

<400> 11

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

Glu Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Lys Val Ser Ser Ser
20 25 30

Thr Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60

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

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

Glu Ile Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

```
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        115                 120                 125

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145                 150                 155                 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
            180                 185                 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
        195                 200                 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 12
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically Generated Sequence

<400> 12
gacatcgtgc tgacccagtc ccccgccacc ctgtccgtgt cccccggcga gagggccacc
60

atctcctgca gggcctccca gaaggtgtcc tcctccacct actcctacat gcactggtac
120

cagcagaagc ccggccagcc ccccaagctg ctgatcaagt acgcctccaa cctggagtcc
180

ggcgtgcccg ccaggttctc cggctccggc tccggcaccg acttcaccct gaccatctcc
240

tccgtggagc ccgaggactt cgccacctac tactgccagc actcctggga gatccccccc
300

accttcggcg gcggcaccaa gctggaaatc aaacgtacgg tggctgcacc atctgtcttc
360

atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg
420

aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg
480

ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc
540

agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc
600

acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgttagtga
660

<210> 13
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically Generated Sequence

<400> 13

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

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

Tyr Met Tyr Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn Pro Ser Asn Gly Asp Thr Asn Phe Asn Glu Lys Phe
50 55 60

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

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

Thr Arg Ser Asp Gly Arg Asn Asp Met Asp Ser Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

```
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

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

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Ser Asp Lys Thr
    210                 215                 220

His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365
```

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

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 14
<211> 1956
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically Generated Sequence

<400> 14
caggtgcagc tggtgcagtc cggcgccgag gtggtgaagc ccggcgcctc cgtgaagctg
60

tcctgcaagg cctccggcta catcttcacc tcctactaca tgtactgggt gaagcaggcc
120

cccggccagg gcctggagtg gatcggcgag atcaacccct ccaacggcga caccaacttc
180

aacgagaagt tcaagtccaa ggccaccctg accgtggaca ggtccgcctc caccgcctac
240

atggagctgt cctccctgag gtccgaggac accgccgtgt actactgcac caggtccgac
300

ggcaggaacg acatggactc ctggggccag ggcaccctgg tgaccgtgtc ctccgctagc
360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca
420

gcagccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac
480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc
540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc
600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttgg tgagaggcca
660

gcacagggag ggagggtgtc tgctggaagc caggctcagc gctcctgcct ggacgcatcc
720

cggctatgca gccccagtcc agggcagcaa ggcaggcccc gtctgcctct tcacccggag
780

gcctctgccc gccccactca tgctcaggga gagggtcttc tggcttttc cccaggctct
840

gggcaggcac aggctaggtg cccctaaccc aggccctgca cacaaagggg caggtgctgg
900

gctcagacct gccaagagcc atatccggga ggaccctgcc cctgacctaa gcccacccca
960

aaggccaaac tctccactcc ctcagctcgg acaccttctc tcctcccaga ttccagtaac
1020

tcccaatctt ctctctgcag agcccaaatc tagtgacaaa actcacacaa gcccaccgag
1080

cccaggtaag ccagcccagg cctcgccctc cagctcaagg cgggacaggt gccctagagt
1140

agcctgcatc cagggacagg ccccagccgg gtgctgacac gtccacctcc atctcttcct
1200

cagcacctga actcctgggg ggatcctcag tcttcctctt ccccccaaaa cccaaggaca
1260

ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg agccacgaag
1320

accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat gccaagacaa
1380

agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc accgtcctgc
1440

accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa gccctcccag
1500

cccccatcga gaaaaccatc tccaaagcca aaggtgggac ccgtggggtg cgagggccac
1560

atggacagag gccggctcgg cccaccctct gccctgagag tgaccgctgt accaacctct
1620

gtccctacag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag
1680

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc
1740

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg
1800

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg
1860

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1920

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Met His

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Ser Tyr Tyr Met Tyr
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Ser

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<400> 21

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

Tyr Met Tyr Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Glu Ile Asn Pro Ser Asn Gly Asp Thr Asn Phe Asn Glu Lys Phe
    50                  55                  60

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

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

Thr Arg Ser Asp Gly Arg Asn Asp Met Asp Ser Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

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

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    210                 215                 220
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His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

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

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
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