SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.
Jamie Orengo
Jeanne Allinne
Andrew Murphy
George Yancopoulos

<120> Methods of Treating Inflammatory Conditions

<130> 10142WO01

<150> 62/428,634

<151> 2016-12-01

<150> 62/473,738

<151> 2017-03-30

<150> 62/567,318

<151> 2017-10-03

<160> 356

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 1
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cgtctggatt caccttcagt agttatggca tgcattgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagaaa taaatactat 180
acagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatgg acagcctgag agccgaggac acggctgtgt attactgtgc gagagagagg 300
tatatcagca gctattatgg ggggttcgac ccctggggcc agggagccct ggtcaccgtc 360
tcctca 366

<210> 2
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 2
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Val Ile Trp Tyr Asp Gly Arg Asn Lys Tyr Tyr Thr Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Glu Arg Tyr Ile Ser Ser Tyr Tyr Gly Gly Phe Asp Pro Trp
            100   105   110
Gly Gln Gly Ala Leu Val Thr Val Ser Ser
        115   120

<210> 3
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 3
ggattcacct tcagtagtta tggc   24

<210> 4
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 4
Gly Phe Thr Phe Ser Ser Tyr Gly
 1   5

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 5
atatggtatg atggaagaaa taaa 24

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

<220>
<223> Synthetic

<400> 6
Ile Trp Tyr Asp Gly Arg Asn Lys
1 5

<210> 7
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 7
gcgagagaga ggtatatcag cagctattat ggggggttcg acccc 45

<210> 8
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 8
Ala Arg Glu Arg Tyr Ile Ser Ser Tyr Tyr Gly Gly Phe Asp Pro
1 5 10 15

<210> 9
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 9
gacatccaga tgacccagtc tccatcctcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggtattagt agttggttag cctggtatca gcagaaacca 120
gggaaagccc ctaaggtcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttacta ttgtcaacag gctaacagtt tcccattcac tttcggccct 300

gggaccaaac tggatatcaa g 321

<210> 10
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 10
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe
                85   90   95
Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys
            100   105

<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 11
cagggtatta gtagttgg 18

<210> 12
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 12
Gln Gly Ile Ser Ser Trp
 1   5

<210> 13
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 13
gctgcatcc 9

<210> 14
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 14
Ala Ala Ser
1

<210> 15
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 15
caacaggcta acagtttccc attcact 27

<210> 16
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 16
Gln Gln Ala Asn Ser Phe Pro Phe Thr
1 5

<210> 17
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 17
gaggtgcagc tgttggagtc tgggggagac ttggtacagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt attagtggta gtggaagtag cacagactac 180
gcagactccg tgaagggccg gttcaccatt tccagagaca attccaggga cacgctgcat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaacgttc 300
tactacttct acggtttgga cgtctggggc caagggacca cggtcaccgt ctcctca 357

<210> 18
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 18
Glu Val Gln Leu Leu Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Val Ile Ser Gly Ser Gly Ser Ser Thr Asp Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asp Thr Leu His
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Thr Phe Tyr Tyr Phe Tyr Gly Leu Asp Val Trp Gly Gln Gly
            100   105   110
Thr Thr Val Thr Val Ser Ser
        115

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 19
ggattcacct tcagcagcta tgcc 24

<210> 20
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 20
Gly Phe Thr Phe Ser Ser Tyr Ala
 1   5

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 21
attagtggta gtggaagtag caca 24

<210> 22
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 22
Ile Ser Gly Ser Gly Ser Ser Thr
1 5

<210> 23
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 23
gcgaaaacgt tctactactt ctacggtttg gacgtc 36

<210> 24
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 24
Ala Lys Thr Phe Tyr Tyr Phe Tyr Gly Leu Asp Val
1 5 10

<210> 25
<211> 321
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 25
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctttaagaga cagagtcacc 60
atcacttgcc gggcgagtca gggcattagc aattatttag cctggtatca gcagaaacca 120
gggaaagttc ctaaggtcct aatctatgct gcatccactt tgcaatcagg ggtcccatct 180
cggttcagtg gcagtggatc tgggacagtt ttcactctca ccatcagcag cctgcagact 240
gaagatgttg caacttatta ctgtcaaaag tatagcagtg ccccattcac tttcggccct 300
gggaccaaag tggatatcaa a 321

<210> 26
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 26
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Arg
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Val Leu Ile
        35   40   45
Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Val Phe Thr Leu Thr Ile Ser Ser Leu Gln Thr
65   70   75   80
Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Ser Ser Ala Pro Phe
                85   90   95
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 27
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 27
cagggcatta gcaattat 18

<210> 28
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 28

Gln Gly Ile Ser Asn Tyr
 1   5

<210> 29
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 29
gctgcatcc   9

<210> 30
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 30
Ala Ala Ser
 1

<210> 31
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 31
caaaagtata gcagtgcccc attcact   27

<210> 32
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 32
Gln Lys Tyr Ser Ser Ala Pro Phe Thr
 1   5

<210> 33
<211> 351
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 33
caggtgcttc tggtacagtc tggggctgag gtgaagaagc ctggggccac agtgaaggtc 60
tcctgcaagg cttctggatc cactttcacc ggctactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcaacccta acaatggtgg cacaaactat 180
gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggaattga gcaggctgag atctgacgac acggccgtat attactgtgc gagagagttg 300
cggtataact ggaagtcctg gggccaggga accctggtca ccgtctcctc a 351

<210> 34
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 34
Gln Val Leu Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Thr Val Lys Val Ser Cys Lys Ala Ser Gly Ser Thr Phe Thr Gly Tyr
            20   25   30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Trp Ile Asn Pro Asn Asn Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50   55   60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Glu Leu Arg Tyr Asn Trp Lys Ser Trp Gly Gln Gly Thr Leu
            100   105   110
Val Thr Val Ser Ser
        115

<210> 35
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 35
ggatccactt tcaccggcta ctat 24

<210> 36
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 36
Gly Ser Thr Phe Thr Gly Tyr Tyr
 1   5

<210> 37
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 37
atcaacccta acaatggtgg caca   24

<210> 38
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 38
Ile Asn Pro Asn Asn Gly Gly Thr
 1   5

<210> 39
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 39
gcgagagagt tgcggtataa ctggaagtcc   30

<210> 40
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 40
Ala Arg Glu Leu Arg Tyr Asn Trp Lys Ser
 1   5   10

<210> 41
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 41
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagtcacc 60
ctctcctgca gggccagtca gagtgttggc aggccctact tagcctggta ccaacagata 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tgacatccca 180
gacaggttca gtggcaatgg gtctgggaca gacttcactc tcaccatcag tagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatgata attcccctta tacttttggc 300
caggggacca ggctggagat caaa 324

<210> 42
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 42
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Arg Pro
            20   25   30
Tyr Leu Ala Trp Tyr Gln Gln Ile Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro Asp Arg Phe Ser
    50   55   60
Gly Asn Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Asn Ser Pro
                85   90   95
Tyr Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100   105

<210> 43
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 43
cagagtgttg gcaggcccta c 21

<210> 44

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

<220>
<223> Synthetic

<400> 44
Gln Ser Val Gly Arg Pro Tyr
 1   5

<210> 45
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 45
ggtgcatcc   9

<210> 46
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 46
Gly Ala Ser
 1

<210> 47
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 47
cagcagtatg ataattcccc ttatact   27

<210> 48
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 48
Gln Gln Tyr Asp Asn Ser Pro Tyr Thr
 1   5

<210> 49
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 49
gaggtgcagc tggtggagtc tgggggaggc ttggtacaac ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttaga agctttgcca tgagctgggt ccgccaggct 120
ccagggaagg ggctggaatt ggtctcagat ctcaggacta gtggtggtag tacatactac 180
gcagactccg tgaagggccg gctcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaagccac 300
tatagcacca gctggttcgg gggctttgac tactggggcc agggaaccct ggtcactgtc 360
tcctca   366

<210> 50
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 50
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Phe
            20   25   30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Leu Val
        35   40   45
Ser Asp Leu Arg Thr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Leu Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Ser His Tyr Ser Thr Ser Trp Phe Gly Gly Phe Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 51
ggattcacct ttagaagctt tgcc 24

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

<220>
<223> Synthetic

<400> 52
Gly Phe Thr Phe Arg Ser Phe Ala
1 5

<210> 53
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 53
ctcaggacta gtggtggtag taca 24

<210> 54
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 54
Leu Arg Thr Ser Gly Gly Ser Thr
1 5

<210> 55
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 55
gcgaaaagcc actatagcac cagctggttc gggggctttg actac 45

<210> 56
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 56
Ala Lys Ser His Tyr Ser Thr Ser Trp Phe Gly Gly Phe Asp Tyr
 1   5   10   15

<210> 57
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 57
gacatccaga tgacccagtc tccatcttcc gtgtctgctt ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggttttagc agctggttag cctggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcaccaa cctgcagcct 240
gaagattttg caacttacta ttgtcaacag gctaacagtt tccctctcac tttcggcgga 300
gggaccaagg tggagatcaa a   321

<210> 58
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 58
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Phe Ser Ser Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Leu
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 59
<211> 18
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 59
cagggtttta gcagctgg 18

<210> 60
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 60
Gln Gly Phe Ser Ser Trp
 1   5

<210> 61
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 61
gctgcatcc 9

<210> 62
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 62
Ala Ala Ser
 1

<210> 63
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 63
caacaggcta acagtttccc tctcact 27

<210> 64
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 64
Gln Gln Ala Asn Ser Phe Pro Leu Thr
 1   5

<210> 65
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 65
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt cacgtttagc agctatgtca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcaagt attagtggta atggtggtag cacaaactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgttt 240
ctggaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaatcactg 300
ggaactacca cgacttttt ggggtttgac tattggggcc agggaaccct ggtcaccgtc 360
tcctca   366

<210> 66
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 66
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Val Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Gly Asn Gly Gly Ser Thr Asn Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65   70   75   80
Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Ser Leu Gly Thr Thr Thr Thr Phe Leu Gly Phe Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 67
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 67
ggattcacgt ttagcagcta tgtc 24

<210> 68
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 68
Gly Phe Thr Phe Ser Ser Tyr Val
1 5

<210> 69
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 69
attagtggta atggtggtag caca 24

<210> 70
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 70
Ile Ser Gly Asn Gly Gly Ser Thr
1 5

<210> 71
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 71
gcgaaatcac tgggaactac cacgactttt ttggggtttg actat 45

<210> 72
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 72
Ala Lys Ser Leu Gly Thr Thr Thr Thr Phe Leu Gly Phe Asp Tyr
1 5 10 15

<210> 73
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 73
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggtattagc agctggttag cctggtatca gcagaaacca 120
gggaaagccc ctaaactcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacatat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttacta ttgtcaacag gctaacagtt tccctctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 74
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 74
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Tyr Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Leu
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 75
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 75
cagggtatta gcagctgg 18

<210> 76
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 76
Gln Gly Ile Ser Ser Trp
1 5

<210> 77
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 77
gctgcatcc 9

<210> 78
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 78
Ala Ala Ser
1

<210> 79

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 79
caacaggcta acagtttccc tctcact 27

<210> 80
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 80
Gln Gln Ala Asn Ser Phe Pro Leu Thr
 1 5

<210> 81
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 81
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagt agttattact ggagctggat ccggcagccc 120
ccagggaagg gactggagtt gattgggtat atttattaca gtgggagcac caattataac 180
ccctccctca agagtcgagt caccatatct gtagacacgt ccaagaacca cttctccctg 240
aagctgagct ctgtgaccgc tgcggacacg gccgtatatt actgtgcgag atcccagtat 300
accagtagtt ggtacggttc ttttgatatc tggggccaag ggacaatggt caccgtctct 360
tca 363

<210> 82
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 82
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
 20 25 30
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Leu Ile
 35 40 45

```
Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
    50                  55                  60
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn His Phe Ser Leu
65                  70                  75                  80
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95
Arg Ser Gln Tyr Thr Ser Ser Trp Tyr Gly Ser Phe Asp Ile Trp Gly
            100                 105                 110
Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120
```

<210> 83
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 83
ggtggctcca tcagtagtta ttac 24

<210> 84
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 84
```
Gly Gly Ser Ile Ser Ser Tyr Tyr
 1               5
```

<210> 85
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 85
atttattaca gtgggagcac c 21

<210> 86
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 86
Ile Tyr Tyr Ser Gly Ser Thr
 1   5

<210> 87
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 87
gcgagatccc agtataccag tagttggtac ggttcttttg atatc   45

<210> 88
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 88
Ala Arg Ser Gln Tyr Thr Ser Ser Trp Tyr Gly Ser Phe Asp Ile
 1   5   10   15

<210> 89
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 89
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggtattagc acctggttag cctggtttca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccactt tacaaggtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggccagaa ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttacta ttgtcaacag gctaacagtt tcccgtggac gttcggccaa 300
gggaccaagg tggaaatcaa a   321

<210> 90
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 90
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly

```
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Trp
            20                  25                  30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Ser Thr Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Pro Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Trp
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 91
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 91
cagggtatta gcacctgg 18

<210> 92
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 92
```
Gln Gly Ile Ser Thr Trp
 1               5
```

<210> 93
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 93
gctgcatcc 9

<210> 94
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 94
Ala Ala Ser
 1

<210> 95
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 95
caacaggcta acagtttccc gtggacg 27

<210> 96
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 96
Gln Gln Ala Asn Ser Phe Pro Trp Thr
 1 5

<210> 97
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 97
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cctctggtta cacctttaac agctatggta tcagctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcagctccc acaatggtaa cagtcactat 180
gtacagaagt tccagggcag agtctccatg accacagaca catccacgag tacagcctac 240
atggaactga ggagccttag atctgacgac acggccgtgt attactgtgc gagacactcg 300
tataccacca gctggtacgg gggttttgac tattggggcc agggaaccct ggtcaccgtc 360
tcctca 366

<210> 98
<211> 122
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 98
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Ser Tyr
            20   25   30
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Trp Ile Ser Ser His Asn Gly Asn Ser His Tyr Val Gln Lys Phe
    50   55   60
Gln Gly Arg Val Ser Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg His Ser Tyr Thr Thr Ser Trp Tyr Gly Gly Phe Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 99
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 99
ggttacacct ttaacagcta tggt   24

<210> 100
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 100
Gly Tyr Thr Phe Asn Ser Tyr Gly
 1   5

<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 101
atcagctccc acaatggtaa cagt   24

<210> 102
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 102
Ile Ser Ser His Asn Gly Asn Ser
 1   5

<210> 103
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 103
gcgagacact cgtataccac cagctggtac gggggttttg actat   45

<210> 104
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 104
Ala Arg His Ser Tyr Thr Thr Ser Trp Tyr Gly Gly Phe Asp Tyr
 1   5   10   15

<210> 105
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 105
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggttttagc agctggttag cctggtatca gcagaaacca 120
gggaaagccc ctcagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggtcagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttacta ttgtcaacag gctaacagtt tccctctcac tttcggcgga 300
gggaccaagg tggagatcaa a   321

<210> 106

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

<220>
<223> Synthetic

<400> 106
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Phe Ser Ser Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Ser Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Leu
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 107
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 107
cagggtttta gcagctgg   18

<210> 108
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 108
Gln Gly Phe Ser Ser Trp
 1   5

<210> 109
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 109
gctgcatcc 9

<210> 110
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 110
Ala Ala Ser
 1

<210> 111
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 111
caacaggcta acagtttccc tctcact 27

<210> 112
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 112
Gln Gln Ala Asn Ser Phe Pro Leu Thr
 1   5

<210> 113
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 113
gaggtgcagc tggtggagtc cgggggaggc ttggttcagc cgggggggtc cctgagactc 60
tcctgtgcag cctctggaat caccttgagc agctatggca tgagctgggt ccgccaggct 120
ccagggaagg gactggagtg ggtcgcatcc atttttggta gtggtggtgg cccatactac 180
gcagactccg tgaagggccg gttcaccatg tccagagaca attccaagaa cacgctgtat 240
ttgcaaatga acagcctgag agccgaggac acggccgtat attattgtgc gaaagatcga 300

tacagtggga gctactacgg aggttttgac tactggggcc ggggaaccct ggtcaccgtc 360
tcctca 366

<210> 114
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 114
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Thr Leu Ser Ser Tyr
            20   25   30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Ser Ile Phe Gly Ser Gly Gly Gly Pro Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Met Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Asp Arg Tyr Ser Gly Ser Tyr Tyr Gly Gly Phe Asp Tyr Trp
            100   105   110
Gly Arg Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 115
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 115
ggaatcacct tgagcagcta tggc 24

<210> 116
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 116
Gly Ile Thr Leu Ser Ser Tyr Gly
 1   5

<210> 117

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

<220>
<223> Synthetic

<400> 117
attttggta gtggtggtgg ccca 24

<210> 118
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 118
Ile Phe Gly Ser Gly Gly Gly Pro
1 5

<210> 119
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 119
gcgaaagatc gatacagtgg gagctactac ggaggttttg actac 45

<210> 120
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 120
Ala Lys Asp Arg Tyr Ser Gly Ser Tyr Tyr Gly Gly Phe Asp Tyr
1 5 10 15

<210> 121
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 121
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggtattacc agctggttag cctggtatca gcagaaacca 120
gggaaagccc ctacactcct gatctatgct gcatccagtt tgcaaactgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaacattttg caacttacta ttgtcaacag gctaacagtt tccctcctac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 122
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 122
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Thr Ser Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Thr Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu His Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Pro
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 123
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 123
cagggtatta ccagctgg 18

<210> 124
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 124
Gln Gly Ile Thr Ser Trp
 1   5

<210> 125
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 125
gctgcatcc 9

<210> 126
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 126
Ala Ala Ser
 1

<210> 127
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 127
caacaggcta acagtttccc tcctact 27

<210> 128
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 128
Gln Gln Ala Asn Ser Phe Pro Pro Thr
 1   5

<210> 129
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 129
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctaagactc 60
tcctgtgcag cctctggatt cacctttagc agttatgcct tgacctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctctttt attagtggta gtggtggtag gccattctac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa catgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccatat attactgtgc gaagtccctg 300
tataccacca gctggtacgg ggggttcgac tcctggggcc agggaaccct ggtcaccgtc 360
tcctca 366

<210> 130
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 130
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Ala Leu Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Phe Ile Ser Gly Ser Gly Gly Arg Pro Phe Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys
                85   90   95
Ala Lys Ser Leu Tyr Thr Thr Ser Trp Tyr Gly Gly Phe Asp Ser Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 131
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 131
ggattcacct ttagcagtta tgcc 24

<210> 132
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 132
Gly Phe Thr Phe Ser Ser Tyr Ala
 1   5

<210> 133
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 133
attagtggta gtggtggtag gcca   24

<210> 134
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 134
Ile Ser Gly Ser Gly Gly Arg Pro
 1   5

<210> 135
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 135
gcgaagtccc tgtataccac cagctggtac ggggggttcg actcc   45

<210> 136
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 136
Ala Lys Ser Leu Tyr Thr Thr Ser Trp Tyr Gly Gly Phe Asp Ser
 1   5   10   15

<210> 137
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 137
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggtgtcgtc agctggttag cctggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ttgtcaacag tctaacagtt tccctttcac tctcggccct 300
gggaccaaag tggatatcaa a 321

<210> 138
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 138
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Val Val Ser Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Ser Phe Pro Phe
                85   90   95
Thr Leu Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 139
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 139
cagggtgtcg tcagctgg 18

<210> 140
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 140
Gln Gly Val Val Ser Trp
 1   5

<210> 141
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 141
gctgcatcc   9

<210> 142
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 142
Ala Ala Ser
 1

<210> 143
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 143
caacagtcta acagtttccc tttc   24

<210> 144
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 144

```
Gln Gln Ser Asn Ser Phe Pro Phe
 1               5


<210> 145
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 145
caggtgcagc tggtgcagtc tggggctgaa gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc ggccactata tgtactggat gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat 180
gcacagaagt ttcaggacag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gagagggaga 300
tatggcagta gctggtacgg ggggtttgag tactggggcc agggaaccct ggtcaccgtc 360
tcctca                                                          366

<210> 146
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 146
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly His
            20                  25                  30
Tyr Met Tyr Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60
Gln Asp Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Gly Arg Tyr Gly Ser Ser Trp Tyr Gly Gly Phe Glu Tyr Trp
            100                 105                 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 147
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic
```

<400> 147
ggatacacct tcaccggcca ctat 24

<210> 148
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 148
Gly Tyr Thr Phe Thr Gly His Tyr
1 5

<210> 149
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 149
atcaacccta acagtggtgg caca 24

<210> 150
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 150
Ile Asn Pro Asn Ser Gly Gly Thr
1 5

<210> 151
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 151
gcgagaggga gatatggcag tagctggtac ggggggtttg agtac 45

<210> 152
<211> 15
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 152
Ala Arg Gly Arg Tyr Gly Ser Ser Trp Tyr Gly Gly Phe Glu Tyr
 1   5   10   15

<210> 153
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 153
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgttggaga cagagtcacc 60
atcacttgtc gggcgagtca gggtattacc agctggttag cctggtatca gcagaaacca 120
gggaaagccc ctaacctcct gatctatgct gcagccagtt tacaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacggat ttcactctca ccatcagcag cctgcagcct 240
gaagacttta caacttacta ttgtcaacag gcttacagtc tccctctcac tttcggcgga 300
gggaccaagg tggagatcaa a   321

<210> 154
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 154
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Thr Ser Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35   40   45
Tyr Ala Ala Ala Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Thr Thr Tyr Tyr Cys Gln Gln Ala Tyr Ser Leu Pro Leu
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 155
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 155
cagggtatta ccagctgg 18

<210> 156
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 156
Gln Gly Ile Thr Ser Trp
 1   5

<210> 157
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 157
gctgcagcc 9

<210> 158
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 158
Ala Ala Ala
 1

<210> 159
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 159
caacaggctt acagtctccc tctcact 27

<210> 160
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 160
Gln Gln Ala Tyr Ser Leu Pro Leu Thr
 1   5

<210> 161
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 161
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agctatggct tgcactgggt ccgccagtct 120
ccaggcaagg ggctggaatg ggtggcactt atatcatatg acggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag acctgaggac acggctggat atttctgtgc gaaatcccta 300
tatacaacca gctggtacgg gggctttgac tattggggcc agggaaccct ggtcaccgtc 360
tcctca   366

<210> 162
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 162
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Gly Leu His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Gly Tyr Phe Cys
                85   90   95
Ala Lys Ser Leu Tyr Thr Thr Ser Trp Tyr Gly Gly Phe Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 163
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 163
ggattcacct tcagtagcta tggc 24

<210> 164
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 164
Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 165
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 165
atatcatatg acggaagtaa taaa 24

<210> 166
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 166
Ile Ser Tyr Asp Gly Ser Asn Lys
1 5

<210> 167
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 167
gcgaaatccc tatatacaac cagctggtac gggggctttg actat 45

<210> 168
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 168
Ala Lys Ser Leu Tyr Thr Thr Ser Trp Tyr Gly Gly Phe Asp Tyr
 1 5 10 15

<210> 169
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 169
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggtattaga agctggttag cctggtatca gcaaaaacca 120
gggaaagccc ctaacctcct gatctatgct gcgtccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttacta ttgtcaacag gctaacagtt tccctcccac tttcggccct 300
gggaccaaag tggatatcaa a 321

<210> 170
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 170
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Ser Trp
            20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Pro

85 90 95
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 171
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 171
cagggtatta gaagctgg 18

<210> 172
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 172
Gln Gly Ile Arg Ser Trp
1 5

<210> 173
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 173
gctgcgtcc 9

<210> 174
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 174
Ala Ala Ser
1

<210> 175
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 175
caacaggcta acagtttccc tcccact 27

<210> 176
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 176
Gln Gln Ala Asn Ser Phe Pro Pro Thr
1 5

<210> 177
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 177
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60
tcctgtgcag cctctgggtt caccttcagc aactatgcca tgacctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcaact atcagtggca gtggtgataa cacatactac 180
gcagactccg tgcagggccg gttcaccatc tccagaggcc attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaacctacg 300
tatagcagaa gctggtacgg tgcttttgat ttctggggcc aagggacaat ggtcaccgtc 360
tcttca 366

<210> 178
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 178
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30
Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Thr Ile Ser Gly Ser Gly Asp Asn Thr Tyr Tyr Ala Asp Ser Val

```
    50                  55                  60
Gln Gly Arg Phe Thr Ile Ser Arg Gly His Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Lys Pro Thr Tyr Ser Arg Ser Trp Tyr Gly Ala Phe Asp Phe Trp
            100                 105                 110
Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120
```

<210> 179
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 179
gggttcacct tcagcaacta tgcc 24

<210> 180
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 180
```
Gly Phe Thr Phe Ser Asn Tyr Ala
 1               5
```

<210> 181
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 181
atcagtggca gtggtgataa caca 24

<210> 182
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 182

Ile Ser Gly Ser Gly Asp Asn Thr
 1   5

<210> 183
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 183
gcgaaaccta cgtatagcag aagctggtac ggtgcttttg atttc   45

<210> 184
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 184
Ala Lys Pro Thr Tyr Ser Arg Ser Trp Tyr Gly Ala Phe Asp Phe
 1   5   10   15

<210> 185
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 185
gacatccaga tgacccagtc tccatcctcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggtattagc agctggttag cctggtatca gcagaaaccg 120
gggaaagccc ctcaactcct gatctatgct gcatccagat tgcaaagtgg ggtcccatca 180
aggttctggg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttacta ttgtcaacag gctaacaatt tcccattcac tttcggccct 300
gggaccaaag tggatatcaa a   321

<210> 186
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 186
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1   5   10   15

```
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Trp Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Asn Phe Pro Phe
                85                  90                  95
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105
```

<210> 187
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 187
cagggtatta gcagctgg 18

<210> 188
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 188
Gln Gly Ile Ser Ser Trp
 1   5

<210> 189
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 189
gctgcatcc 9

<210> 190
<211> 3
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 190
Ala Ala Ser
 1

<210> 191
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 191
caacaggcta acaatttccc attcact 27

<210> 192
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 192
Gln Gln Ala Asn Asn Phe Pro Phe Thr
 1   5

<210> 193
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 193
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggtta cacctttacc agttatggta tcagctgggt gcgacaggcc 120
cctggacaag gccttgagtg gatgggatgg atccgcgctt acaatggtta cacaaactat 180
gcacagaagt ttcagggcag agtcaccatg accacagaca catccacgaa caccgcctac 240
atggagctga ggaccctgaa ttctgacgat acggccgttt attactgtgc gagagatcga 300
tatagtggga gcttccacgg taactttgac tactggggcc agggaaccct ggtcaccgtc 360
tcctca 366

<210> 194
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 194
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Trp Ile Arg Ala Tyr Asn Gly Tyr Thr Asn Tyr Ala Gln Lys Phe
    50   55   60
Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Asn Thr Ala Tyr
65   70   75   80
Met Glu Leu Arg Thr Leu Asn Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Asp Arg Tyr Ser Gly Ser Phe His Gly Asn Phe Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 195
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 195
ggttacacct ttaccagtta tggt   24

<210> 196
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 196
Gly Tyr Thr Phe Thr Ser Tyr Gly
 1   5

<210> 197
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 197
atccgcgctt acaatggtta caca   24

<210> 198
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 198
Ile Arg Ala Tyr Asn Gly Tyr Thr
 1   5

<210> 199
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 199
gcgagagatc gatatagtgg gagcttccac ggtaactttg actac   45

<210> 200
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 200
Ala Arg Asp Arg Tyr Ser Gly Ser Phe His Gly Asn Phe Asp Tyr
 1   5   10   15

<210> 201
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 201
gacatccaga tgacccagtc tccatcttcc gtgtctgcgt ctgtaggaga cagagtgacc 60
atcacttgtc gggcgagtca gggtattttc agctggttag cctggtatca gcagaaacca 120
gggaaagccc ctaaggtcct aatctatgct gcatccaatt tggaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttacta ttgtcaacag gctaacagtt taccgctcac tttcggcgga 300
gggaccaagg tggagatcaa a   321

<210> 202
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 202
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Phe Ser Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
        35   40   45
Tyr Ala Ala Ser Asn Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Leu Pro Leu
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 203
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 203
cagggtattt tcagctgg   18

<210> 204
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 204
Gln Gly Ile Phe Ser Trp
 1   5

<210> 205
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 205
gctgcatcc 9

<210> 206
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 206
Ala Ala Ser
 1

<210> 207
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 207
caacaggcta acagtttacc gctcact 27

<210> 208
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 208
Gln Gln Ala Asn Ser Leu Pro Leu Thr
 1 5

<210> 209
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 209
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt acctattcta tgcactgggt ccgccaggct 120
ccagggaagg gactggaata tgtttcaact attaataata atggggatac cacatattat 180
gcagactctg tgaagggcag attcaccatc tccagagaca attccaagaa cacgctgtat 240
cttcaactgg gcagcctgag acctgaggac atggctgtgt attactgtgc gagacagacg 300
tataccagca gctggtacgg ggggttcgac tcctggggcc agggaaccct ggtcaccgtc 360

tcctca 366

<210> 210
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 210
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
            20   25   30
Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val
        35   40   45
Ser Thr Ile Asn Asn Asn Gly Asp Thr Thr Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Leu Gly Ser Leu Arg Pro Glu Asp Met Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gln Thr Tyr Thr Ser Ser Trp Tyr Gly Gly Phe Asp Ser Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

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

<220>
<223> Synthetic

<400> 211
ggattcacct tcagtaccta ttct 24

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

<220>
<223> Synthetic

<400> 212
Gly Phe Thr Phe Ser Thr Tyr Ser
 1   5

<210> 213
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 213
attaataata atggggatac caca 24

<210> 214
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 214
Ile Asn Asn Asn Gly Asp Thr Thr
1 5

<210> 215
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 215
gcgagacaga cgtataccag cagctggtac ggggggttcg actcc 45

<210> 216
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 216
Ala Arg Gln Thr Tyr Thr Ser Ser Trp Tyr Gly Gly Phe Asp Ser
1 5 10 15

<210> 217
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 217

gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggcga cagagtcacc 60
atcacttgtc gggcgagtca gggtattacc agctggttag cctggtatca gcagaaacca 120
gggaaagccc ctaaactcct gatctatgct gcatccaatt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcaccag cctgcagcct 240
gaggattttg caacttacta ttgtcaacag gctaacagtc tcccattcac tttcggccct 300
gggaccaaag tggatatcaa a 321

<210> 218
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 218
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Thr Ser Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Leu Pro Phe
                85   90   95
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 219
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 219
cagggtatta ccagctgg 18

<210> 220
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 220
Gln Gly Ile Thr Ser Trp
 1   5

<210> 221
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 221
gctgcatcc 9

<210> 222
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 222
Ala Ala Ser
1

<210> 223
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 223
caacaggcta acagtctccc attcact 27

<210> 224
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 224
Gln Gln Ala Asn Ser Leu Pro Phe Thr
1 5

<210> 225
<211> 366
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 225
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt cacccttagc agctatgcca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggcag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa ctcgctgtat 240
ctgcaattga acagcctgag agccgaggac acggccgtat attactgtgc gaagacgctg 300
tatactacca gctggtacgg gggcttccag cactggggcc agggcaccct ggtcactgtc 360
tcctca 366

<210> 226
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 226
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Ser Tyr
            20   25   30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr
65   70   75   80
Leu Gln Leu Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Thr Leu Tyr Thr Thr Ser Trp Tyr Gly Gly Phe Gln His Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 227
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 227
ggattcaccc ttagcagcta tgcc 24

<210> 228
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 228
Gly Phe Thr Leu Ser Ser Tyr Ala
 1   5

<210> 229
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 229
attagtggta gtggtggcag caca   24

<210> 230
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 230
Ile Ser Gly Ser Gly Gly Ser Thr
 1   5

<210> 231
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 231
gcgaagacgc tgtatactac cagctggtac gggggcttcc agcac   45

<210> 232
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 232
Ala Lys Thr Leu Tyr Thr Thr Ser Trp Tyr Gly Gly Phe Gln His
 1   5   10   15

<210> 233
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 233
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctataggaga cagagtcacc 60
atcacttgtc gggcgagtca gggaatcagc agttggttag cctggtatca gcagaaacca 120
gggaaagtcc ctaagctcct gatctatgct gcgtcctctt tgcaaagtgg gttcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagtag cctgcagccc 240
gaagattttg caacttacta ttgtcaacag actcacagtt tcccgtggac ggtcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 234
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 234
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Ile Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Phe Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr His Ser Phe Pro Trp
                85   90   95
Thr Val Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 235
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 235
cagggaatca gcagttgg 18

<210> 236
<211> 6
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 236
Gln Gly Ile Ser Ser Trp
 1   5

<210> 237
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 237
gctgcgtcc   9

<210> 238
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 238
Ala Ala Ser
 1

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 239
caacagactc acagtttccc gtgg   24

<210> 240
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 240
Gln Gln Thr His Ser Phe Pro Trp

1 5

<210> 241
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 241
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt cacccttagg agctatttca tgacctgggt ccgccaggtt 120
ccagggaagg ggctggaggg ggtctcagct attagtggca ttagtggtgg cacatactac 180
acagactccg ttaagggccg gttcaccatc tccagagaca attccaagaa cacgctgttt 240
ctgcaaatga acagcctgag agccgaggac acggccgtat atttctgtgc gagaacggtg 300
tatagtagta gttactacgg gggcttccag cactggggcc agggcaccct ggtcaccgtc 360
tcctca 366

<210> 242
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 242
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Arg Ser Tyr
20 25 30
Phe Met Thr Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Gly Val
35 40 45
Ser Ala Ile Ser Gly Ile Ser Gly Gly Thr Tyr Tyr Thr Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95
Ala Arg Thr Val Tyr Ser Ser Ser Tyr Tyr Gly Gly Phe Gln His Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 243
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 243
ggattcaccc ttaggagcta tttc 24

<210> 244
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 244
Gly Phe Thr Leu Arg Ser Tyr Phe
 1 5

<210> 245
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 245
attagtggca ttagtggtgg caca 24

<210> 246
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 246
Ile Ser Gly Ile Ser Gly Gly Thr
 1 5

<210> 247
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 247
gcgagaacgg tgtatagtag tagttactac gggggcttcc agcac 45

<210> 248
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 248
Ala Arg Thr Val Tyr Ser Ser Ser Tyr Tyr Gly Gly Phe Gln His
 1   5   10   15

<210> 249
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 249
gacatccaga tgacccagtc tccatcttcc gtgtctgtat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggtattagc agttggttag cctggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgtt gcatccagtt tacaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttacta ttgtcaacag actaacagtt tccctctcac tttcggcgga 300
gggaccaagg tggagatcaa a   321

<210> 250
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 250
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Val Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Ser Phe Pro Leu
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 251
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 251
cagggtatta gcagttgg 18

<210> 252
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 252
Gln Gly Ile Ser Ser Trp
1 5

<210> 253
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 253
gttgcatcc 9

<210> 254
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 254
Val Ala Ser
1

<210> 255
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 255
caacagacta acagtttccc tctcact 27

<210> 256

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

<220>
<223> Synthetic

<400> 256
Gln Gln Thr Asn Ser Phe Pro Leu Thr
 1   5

<210> 257
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 257
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt cacccttagg agttatgtca tgtactgggt ccgccagggt 120
ccagggaagg ggctggaggg ggtctcaggt attagtggca gtagtggtgg cacatactac 180
acagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgttt 240
ctgcaaatga acagcctgag agccgaggac acggccgtat atttctgtgc gagatcggtg 300
tatagtacca cctggtacgg gggcttccag cactggggcc agggcaccct ggtcaccgtc 360
tcctca   366

<210> 258
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 258
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Arg Ser Tyr
            20   25   30
Val Met Tyr Trp Val Arg Gln Gly Pro Gly Lys Gly Leu Glu Gly Val
        35   40   45
Ser Gly Ile Ser Gly Ser Ser Gly Gly Thr Tyr Tyr Thr Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85   90   95
Ala Arg Ser Val Tyr Ser Thr Thr Trp Tyr Gly Gly Phe Gln His Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 259
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 259
ggattcaccc ttaggagtta tgtc 24

<210> 260
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 260
Gly Phe Thr Leu Arg Ser Tyr Val
 1 5

<210> 261
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 261
attagtggca gtagtggtgg caca 24

<210> 262
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 262
Ile Ser Gly Ser Ser Gly Gly Thr
 1 5

<210> 263
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 263
gcgagatcgg tgtatagtac cacctggtac gggggcttcc agcac 45

<210> 264
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 264
Ala Arg Ser Val Tyr Ser Thr Thr Trp Tyr Gly Gly Phe Gln His
1 5 10 15

<210> 265
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 265
gacatccaga tgacccagtc tccatcttcc gtgtctgtat ctgtgggaga cagagtcacc 60
atcacttgtc gggcgagtca ggttattagc agttggttag cctggtatca gctgaaacca 120
gggaaagccc ctaaactcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcgg cctgcagcct 240
gaagattttg cagtttacta ttgtcaacag actaacagtt tccctctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 266
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 266
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Val Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Val Ile Ser Ser Trp
20 25 30
Leu Ala Trp Tyr Gln Leu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Thr Asn Ser Phe Pro Leu
85 90 95

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

<210> 267
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 267
caggttatta gcagttgg 18

<210> 268
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 268
Gln Val Ile Ser Ser Trp
1 5

<210> 269
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 269
gctgcatcc 9

<210> 270
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 270
Ala Ala Ser
1

<210> 271
<211> 27
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 271
caacagacta acagtttccc tctcact 27

<210> 272
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 272
Gln Gln Thr Asn Ser Phe Pro Leu Thr
 1 5

<210> 273
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 273
gaggtgcagc tggtggagtc tgggggaaac ttggaacagc ctgggggtc ccttagactc 60
tcctgtacag cctctggatt cacctttagc agatctgcca tgaactgggt ccgccgggct 120
ccagggaagg ggctggagtg ggtctcagga attagtggta gtggtggtcg aacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa tacgctatat 240
ctgcaaatga acagcctgag cgccgaggac acggccgcat attactgtgc gaaagattcg 300
tatactacca gttggtacgg aggtatggac gtctggggcc acgggaccac ggtcaccgtc 360
tcctca 366

<210> 274
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 274
Glu Val Gln Leu Val Glu Ser Gly Gly Asn Leu Glu Gln Pro Gly Gly
 1 5 10 15
Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Arg Ser
 20 25 30
Ala Met Asn Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
Ser Gly Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Ser Ala Glu Asp Thr Ala Ala Tyr Tyr Cys
                85                  90                  95
Ala Lys Asp Ser Tyr Thr Thr Ser Trp Tyr Gly Gly Met Asp Val Trp
            100                 105                 110
Gly His Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 275
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 275
ggattcacct ttagcagatc tgcc 24

<210> 276
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 276
```
Gly Phe Thr Phe Ser Arg Ser Ala
 1               5
```

<210> 277
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 277
attagtggta gtggtggtcg aaca 24

<210> 278
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 278
```
Ile Ser Gly Ser Gly Gly Arg Thr
```

1 5

<210> 279
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 279
gcgaaagatt cgtatactac cagttggtac ggaggtatgg acgtc 45

<210> 280
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 280
Ala Lys Asp Ser Tyr Thr Thr Ser Trp Tyr Gly Gly Met Asp Val
1 5 10 15

<210> 281
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 281
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggtattttc agctggttag cctggtatca gcagaaacca 120
ggaaaagccc ctaagctcct gatctatgct gcttccagtt tacaaagtgg ggtcccatca 180
agattcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaggattttg caatttacta ttgtcaacag gctaacagtg tcccgatcac cttcggccaa 300
gggacacgac tggagattaa a 321

<210> 282
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 282
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Phe Ser Trp

```
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Ala Asn Ser Val Pro Ile
                85                  90                  95
Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105
```

<210> 283
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 283
cagggtattt tcagctgg 18

<210> 284
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 284
Gln Gly Ile Phe Ser Trp
 1   5

<210> 285
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 285
gctgcttcc 9

<210> 286
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 286
Ala Ala Ser
 1

<210> 287
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 287
caacaggcta acagtgtccc gatcacc 27

<210> 288
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 288
Gln Gln Ala Asn Ser Val Pro Ile Thr
 1   5

<210> 289
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 289
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60
tcctgttcag cctctggatt cacctttagc agctatgcca tgaactgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtcaccgct attagtggca gtggtggtgg cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa ctcgctgttt 240
ctgcaattga acagcctgag agccgaggac acggccgtgt attactgtgc gaaacaaacg 300
tataccagca gctggtacgg tggctttgat atctggggcc aggggacaat ggtcaccgtc 360
tcttca 366

<210> 290
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 290
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Thr Ala Ile Ser Gly Ser Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Phe
65   70   75   80
Leu Gln Leu Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Gln Thr Tyr Thr Ser Ser Trp Tyr Gly Gly Phe Asp Ile Trp
            100   105   110
Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 291
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 291
ggattcacct ttagcagcta tgcc   24

<210> 292
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 292
Gly Phe Thr Phe Ser Ser Tyr Ala
 1   5

<210> 293
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 293
attagtggca gtggtggtgg caca   24

<210> 294

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

<220>
<223> Synthetic

<400> 294
Ile Ser Gly Ser Gly Gly Gly Thr
 1   5

<210> 295
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 295
gcgaaacaaa cgtataccag cagctggtac ggtggctttg atatc   45

<210> 296
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 296
Ala Lys Gln Thr Tyr Thr Ser Ser Trp Tyr Gly Gly Phe Asp Ile
 1   5   10   15

<210> 297
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 297
gacatccaga tgacccagtc gccatcttcc gtgtccgcgt ctgtaggaga cagagtcacc 60
atcacttgtc gggcgagtca gggttttagt tcctggttag cctggtatca gcagatacca 120
gggaaagccc ccaagctcct gatctatgct gcatcaaggt tgcaaagtgg ggtcccatcc 180
aggttccgcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaggattttg caacttacta ttgtcaacag gctaacagtt tcccgctcac tttcggcgga 300
gggaccaagg tggagatcaa a   321

<210> 298
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 298
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Phe Ser Ser Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Ile Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Leu
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 299
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 299
cagggtttta gttcctgg   18

<210> 300
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 300
Gln Gly Phe Ser Ser Trp
 1   5

<210> 301
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 301

gctgcatca 9

<210> 302
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 302
Ala Ala Ser
 1

<210> 303
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 303
caacaggcta acagtttccc gctcact 27

<210> 304
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 304
Gln Gln Ala Asn Ser Phe Pro Leu Thr
 1   5

<210> 305
<211> 167
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 305
Ser Ile Thr Gly Ile Ser Pro Ile Thr Glu Ser Leu Ala Ser Leu Ser
 1   5   10   15
Thr Tyr Asn Asp Gln Ser Ile Thr Phe Ala Leu Glu Asp Glu Ser Tyr
            20   25   30
Glu Ile Tyr Val Glu Asp Leu Lys Lys Asp Lys Lys Lys Asp Lys Val
        35   40   45
Leu Leu Ser Tyr Tyr Glu Ser Gln His Pro Ser Ser Glu Ser Gly Asp

```
    50                  55                  60
Gly Val Asp Gly Lys Met Leu Met Val Thr Leu Ser Pro Thr Lys Asp
65                  70                  75                  80
Phe Trp Leu Gln Ala Asn Asn Lys Glu His Ser Val Glu Leu His Lys
                85                  90                  95
Cys Glu Lys Pro Leu Pro Asp Gln Ala Phe Phe Val Leu His Asn Arg
            100                 105                 110
Ser Phe Asn Cys Val Ser Phe Glu Cys Lys Thr Asp Pro Gly Val Phe
        115                 120                 125
Ile Gly Val Lys Asp Asn His Leu Ala Leu Ile Lys Val Asp Tyr Ser
    130                 135                 140
Glu Asn Leu Gly Ser Glu Asn Ile Leu Phe Lys Leu Ser Glu Ile Leu
145                 150                 155                 160
Glu His His His His His His
                165


<210> 306
<211> 167
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 306
Ser Ile Thr Gly Ile Ser Pro Ile Thr Glu Ser Leu Ala Ser Leu Ser
 1               5                  10                  15
Thr Tyr Asn Asp Gln Ser Ile Thr Phe Ala Leu Glu Asp Glu Ser Tyr
            20                  25                  30
Glu Ile Tyr Val Glu Asp Leu Lys Lys Asp Lys Lys Lys Asp Lys Val
        35                  40                  45
Leu Leu Ser Tyr Tyr Glu Ser Gln His Pro Ser Ser Glu Ser Gly Asp
    50                  55                  60
Gly Val Asp Gly Lys Met Leu Met Val Thr Leu Ser Pro Thr Lys Asp
65                  70                  75                  80
Phe Trp Leu Gln Ala Asn Asn Lys Glu His Ser Val Glu Leu His Lys
                85                  90                  95
Cys Glu Lys Pro Leu Pro Asp Gln Ala Phe Phe Val Leu His Asn Arg
            100                 105                 110
Ser Phe Asn Cys Val Ser Phe Glu Cys Lys Thr Asp Pro Gly Val Phe
        115                 120                 125
Ile Gly Val Lys Asp Asn His Leu Ala Leu Ile Lys Val Asp Tyr Ser
    130                 135                 140
Glu Asn Leu Gly Ser Glu Asn Ile Leu Phe Lys Leu Ser Glu Ile Leu
145                 150                 155                 160
Glu His His His His His His
                165


<210> 307
<211> 354
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Synthetic

<400> 307
caggtcacct tgaaggagtc tggtcctgtg ctggtgaaac ccacagagag cctcacgctg 60
acctgctccg tctctggatt ctcactcagt aatgttagaa tgggtgtgag ctggatccgt 120
cagtccccag ggaaggccct ggagtggctt gcacacattt tttcgaatga cgaaaaatcc 180
tacaccacat ctctgaagac caggctcacc atctccaagg acacctccag aagccaggtg 240
gtccttacca tgaccgacat ggaccctggg gacacagcca catattactg tgcacggata 300
cggaatttgg cctttaatta ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 308
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 308
Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
 1   5   10   15
Ser Leu Thr Leu Thr Cys Ser Val Ser Gly Phe Ser Leu Ser Asn Val
            20   25   30
Arg Met Gly Val Ser Trp Ile Arg Gln Ser Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Thr Thr Ser
    50   55   60
Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg Ser Gln Val
65   70   75   80
Val Leu Thr Met Thr Asp Met Asp Pro Gly Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Ile Arg Asn Leu Ala Phe Asn Tyr Trp Gly Gln Gly Thr
            100   105   110
Leu Val Thr Val Ser Ser
        115

<210> 309
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 309
ggattctcac tcagtaatgt tagaatgggt 30

<210> 310
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 310
Gly Phe Ser Leu Ser Asn Val Arg Met Gly
 1   5   10

<210> 311
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 311
atttttcga atgacgaaaa a   21

<210> 312
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 312
Ile Phe Ser Asn Asp Glu Lys
 1   5

<210> 313
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 313
gcacggatac ggaatttggc ctttaattac   30

<210> 314
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 314
Ala Arg Ile Arg Asn Leu Ala Phe Asn Tyr
 1   5   10

<210> 315
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 315
gacttcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
atcaactgca agtccagcca gagtgtgtta cacaggtcca gcaataagaa ctacttagct 120
tggtatcagc agaagccagg acagcctcct aacctgctca tttactgggc atctacccgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatggtact 300
ctatttactt tcggccctgg gaccaaagtg gatatcaaa 339

<210> 316
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 316
Asp Phe Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu His Arg
            20   25   30
Ser Ser Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45
Pro Pro Asn Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85   90   95
Tyr Tyr Gly Thr Leu Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile
            100   105   110
Lys

<210> 317
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 317
cagagtgtgt tacacaggtc cagcaataag aactac 36

<210> 318

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

<220>
<223> Synthetic

<400> 318
Gln Ser Val Leu His Arg Ser Ser Asn Lys Asn Tyr
 1   5   10

<210> 319
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 319
tgggcatct   9

<210> 320
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 320
Trp Ala Ser
 1

<210> 321
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 321
cagcaatatt atggtactct atttact   27

<210> 322
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 322
Gln Gln Tyr Tyr Gly Thr Leu Phe Thr
 1   5

<210> 323
<211> 537
<212> PRT
<213> Artificial Sequence

<220>
<223> hST2-hFc

<400> 323
Lys Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu Ile Val
 1   5   10   15
Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp Tyr Tyr
            20   25   30
Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg Val Phe
        35   40   45
Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Ala Val Ala Asp Ser
    50   55   60
Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg Thr Gly
65   70   75   80
Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn Val Pro
                85   90   95
Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn Ser Lys
            100   105   110
Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro Leu Glu
        115   120   125
Trp Phe Lys Asn Cys Gln Ala Leu Gln Gly Ser Arg Tyr Arg Ala His
    130   135   140
Lys Ser Phe Leu Val Ile Asp Asn Val Met Thr Glu Asp Ala Gly Asp
145   150   155   160
Tyr Thr Cys Lys Phe Ile His Asn Glu Asn Gly Ala Asn Tyr Ser Val
                165   170   175
Thr Ala Thr Arg Ser Phe Thr Val Lys Asp Glu Gln Gly Phe Ser Leu
            180   185   190
Phe Pro Val Ile Gly Ala Pro Ala Gln Asn Glu Ile Lys Glu Val Glu
        195   200   205
Ile Gly Lys Asn Ala Asn Leu Thr Cys Ser Ala Cys Phe Gly Lys Gly
    210   215   220
Thr Gln Phe Leu Ala Ala Val Leu Trp Gln Leu Asn Gly Thr Lys Ile
225   230   235   240
Thr Asp Phe Gly Glu Pro Arg Ile Gln Gln Glu Glu Gly Gln Asn Gln
                245   250   255
Ser Phe Ser Asn Gly Leu Ala Cys Leu Asp Met Val Leu Arg Ile Ala
            260   265   270
Asp Val Lys Glu Glu Asp Leu Leu Leu Gln Tyr Asp Cys Leu Ala Leu
        275   280   285
Asn Leu His Gly Leu Arg Arg His Thr Val Arg Leu Ser Arg Lys Asn
    290   295   300
Pro Ile Asp His His Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
305   310   315   320
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

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


<210> 324
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> hST2-mFc

<400> 324
Lys Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu Ile Val
 1               5                  10                  15
Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp Tyr Tyr
            20                  25                  30
Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg Val Phe
        35                  40                  45
Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Ala Val Ala Asp Ser
    50                  55                  60
Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg Thr Gly
65                  70                  75                  80
Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn Val Pro
                85                  90                  95
Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn Ser Lys
            100                 105                 110
Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro Leu Glu
        115                 120                 125
Trp Phe Lys Asn Cys Gln Ala Leu Gln Gly Ser Arg Tyr Arg Ala His
```

```
    130                 135                 140
Lys Ser Phe Leu Val Ile Asp Asn Val Met Thr Glu Asp Ala Gly Asp
145                 150                 155                 160
Tyr Thr Cys Lys Phe Ile His Asn Glu Asn Gly Ala Asn Tyr Ser Val
                165                 170                 175
Thr Ala Thr Arg Ser Phe Thr Val Lys Asp Glu Gln Gly Phe Ser Leu
            180                 185                 190
Phe Pro Val Ile Gly Ala Pro Ala Gln Asn Glu Ile Lys Glu Val Glu
        195                 200                 205
Ile Gly Lys Asn Ala Asn Leu Thr Cys Ser Ala Cys Phe Gly Lys Gly
    210                 215                 220
Thr Gln Phe Leu Ala Ala Val Leu Trp Gln Leu Asn Gly Thr Lys Ile
225                 230                 235                 240
Thr Asp Phe Gly Glu Pro Arg Ile Gln Gln Glu Glu Gly Gln Asn Gln
                245                 250                 255
Ser Phe Ser Asn Gly Leu Ala Cys Leu Asp Met Val Leu Arg Ile Ala
            260                 265                 270
Asp Val Lys Glu Glu Asp Leu Leu Leu Gln Tyr Asp Cys Leu Ala Leu
        275                 280                 285
Asn Leu His Gly Leu Arg Arg His Thr Val Arg Leu Ser Arg Lys Asn
    290                 295                 300
Pro Ile Asp His His Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
305                 310                 315                 320
Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
                325                 330                 335
Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
            340                 345                 350
Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
        355                 360                 365
Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
    370                 375                 380
Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
385                 390                 395                 400
Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
                405                 410                 415
Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
            420                 425                 430
Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
        435                 440                 445
Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
    450                 455                 460
Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
465                 470                 475                 480
Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
                485                 490                 495
Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
            500                 505                 510
Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
        515                 520                 525
His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
    530                 535                 540
```

<210> 325
<211> 884

<212> PRT
<213> Artificial Sequence

<220>
<223> hST2-hIL1RAcP-mFc

<400> 325
Lys Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu Ile Val
 1   5   10   15
Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp Tyr Tyr
            20   25   30
Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg Val Phe
        35   40   45
Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Ala Val Ala Asp Ser
    50   55   60
Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg Thr Gly
65   70   75   80
Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn Val Pro
                85   90   95
Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn Ser Lys
            100   105   110
Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro Leu Glu
        115   120   125
Trp Phe Lys Asn Cys Gln Ala Leu Gln Gly Ser Arg Tyr Arg Ala His
    130   135   140
Lys Ser Phe Leu Val Ile Asp Asn Val Met Thr Glu Asp Ala Gly Asp
145   150   155   160
Tyr Thr Cys Lys Phe Ile His Asn Glu Asn Gly Ala Asn Tyr Ser Val
                165   170   175
Thr Ala Thr Arg Ser Phe Thr Val Lys Asp Glu Gln Gly Phe Ser Leu
            180   185   190
Phe Pro Val Ile Gly Ala Pro Ala Gln Asn Glu Ile Lys Glu Val Glu
        195   200   205
Ile Gly Lys Asn Ala Asn Leu Thr Cys Ser Ala Cys Phe Gly Lys Gly
    210   215   220
Thr Gln Phe Leu Ala Ala Val Leu Trp Gln Leu Asn Gly Thr Lys Ile
225   230   235   240
Thr Asp Phe Gly Glu Pro Arg Ile Gln Gln Glu Glu Gly Gln Asn Gln
                245   250   255
Ser Phe Ser Asn Gly Leu Ala Cys Leu Asp Met Val Leu Arg Ile Ala
            260   265   270
Asp Val Lys Glu Glu Asp Leu Leu Leu Gln Tyr Asp Cys Leu Ala Leu
        275   280   285
Asn Leu His Gly Leu Arg Arg His Thr Val Arg Leu Ser Arg Lys Asn
    290   295   300
Pro Ile Asp His His Ser Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp
305   310   315   320
Thr Met Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys
                325   330   335
Cys Pro Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His
            340   345   350
Ser Ala Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp
        355   360   365
Leu Glu Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys
    370   375   380

Glu Lys Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly
385 390 395 400
Asn Tyr Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala
405 410 415
Phe Pro Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met
420 425 430
Lys Leu Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile
435 440 445
Thr Cys Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr
450 455 460
Ile Thr Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val
465 470 475 480
Ile Pro Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn
485 490 495
Asn Gly Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr
500 505 510
Phe His Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys
515 520 525
Asn Ala Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr
530 535 540
Glu Lys Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe
545 550 555 560
Ser Phe Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly
565 570 575
Lys Lys Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile
580 585 590
Ser His Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile
595 600 605
Lys Lys Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala
610 615 620
Arg Ser Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys
625 630 635 640
Val Pro Ala Pro Arg Tyr Thr Val Glu Ser Gly Glu Pro Arg Gly Pro
645 650 655
Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu
660 665 670
Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu
675 680 685
Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser
690 695 700
Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu
705 710 715 720
Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr
725 730 735
Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser
740 745 750
Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro
755 760 765
Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln
770 775 780
Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val
785 790 795 800
Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val
805 810 815
Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu

```
            820                 825                 830
Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg
        835                 840                 845
Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val
    850                 855                 860
Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg
865                 870                 875                 880
Thr Pro Gly Lys
```

<210> 326
<211> 880
<212> PRT
<213> Artificial Sequence

<220>
<223> mST2-mIL1RAcP-mFc

<400> 326

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

```
        275                 280                 285
Gly Met Ile Arg His Thr Ile Arg Leu Arg Arg Lys Gln Pro Ile Asp
    290                 295                 300
His Arg Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met Arg Gln
305                 310                 315                 320
Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro Leu Phe
                325                 330                 335
Glu His Phe Leu Lys Tyr Asn Tyr Ser Thr Ala His Ser Ser Gly Leu
            340                 345                 350
Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu Glu Pro
        355                 360                 365
Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys Asp Val
    370                 375                 380
Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr Thr Cys
385                 390                 395                 400
Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro Leu Glu
                405                 410                 415
Val Val Gln Lys Asp Ser Cys Phe Asn Ser Ala Met Arg Phe Pro Val
            420                 425                 430
His Lys Met Tyr Ile Glu His Gly Ile His Lys Ile Thr Cys Pro Asn
        435                 440                 445
Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Ser Val Thr Trp Tyr
    450                 455                 460
Lys Gly Cys Thr Glu Ile Val Asp Phe His Asn Val Leu Pro Glu Gly
465                 470                 475                 480
Met Asn Leu Ser Phe Phe Ile Pro Leu Val Ser Asn Asn Gly Asn Tyr
                485                 490                 495
Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Leu Phe His Leu Thr
            500                 505                 510
Arg Thr Val Thr Val Lys Val Val Gly Ser Pro Lys Asp Ala Leu Pro
        515                 520                 525
Pro Gln Ile Tyr Ser Pro Asn Asp Arg Val Val Tyr Glu Lys Glu Pro
    530                 535                 540
Gly Glu Glu Leu Val Ile Pro Cys Lys Val Tyr Phe Ser Phe Ile Met
545                 550                 555                 560
Asp Ser His Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys Pro Asp
                565                 570                 575
Asp Val Thr Val Asp Ile Thr Ile Asn Glu Ser Val Ser Tyr Ser Ser
            580                 585                 590
Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys Val Thr
        595                 600                 605
Pro Glu Asp Leu Arg Arg Asn Tyr Val Cys His Ala Arg Asn Thr Lys
    610                 615                 620
Gly Glu Ala Glu Gln Ala Ala Lys Val Lys Gln Lys Val Ile Pro Pro
625                 630                 635                 640
Arg Tyr Thr Val Glu Ser Gly Glu Pro Arg Gly Pro Thr Ile Lys Pro
                645                 650                 655
Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser
            660                 665                 670
Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu
        675                 680                 685
Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro
    690                 695                 700
Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala
705                 710                 715                 720
```

```
Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val
                725                 730                 735
Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe
            740                 745                 750
Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr
        755                 760                 765
Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu
    770                 775                 780
Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys
785                 790                 795                 800
Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn
                805                 810                 815
Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp
            820                 825                 830
Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys
        835                 840                 845
Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly
    850                 855                 860
Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
865                 870                 875                 880


<210> 327
<211> 876
<212> PRT
<213> Artificial Sequence

<220>
<223> hST2-hL1RAcP-hFc

<400> 327
Lys Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu Ile Val
 1               5                  10                  15
Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp Tyr Tyr
            20                  25                  30
Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg Val Phe
        35                  40                  45
Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Ala Val Ala Asp Ser
    50                  55                  60
Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg Thr Gly
65                  70                  75                  80
Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn Val Pro
                85                  90                  95
Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn Ser Lys
            100                 105                 110
Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro Leu Glu
        115                 120                 125
Trp Phe Lys Asn Cys Gln Ala Leu Gln Gly Ser Arg Tyr Arg Ala His
    130                 135                 140
Lys Ser Phe Leu Val Ile Asp Asn Val Met Thr Glu Asp Ala Gly Asp
145                 150                 155                 160
Tyr Thr Cys Lys Phe Ile His Asn Glu Asn Gly Ala Asn Tyr Ser Val
                165                 170                 175
Thr Ala Thr Arg Ser Phe Thr Val Lys Asp Glu Gln Gly Phe Ser Leu
            180                 185                 190
```

```
Phe Pro Val Ile Gly Ala Pro Ala Gln Asn Glu Ile Lys Glu Val Glu
        195                 200                 205
Ile Gly Lys Asn Ala Asn Leu Thr Cys Ser Ala Cys Phe Gly Lys Gly
    210                 215                 220
Thr Gln Phe Leu Ala Ala Val Leu Trp Gln Leu Asn Gly Thr Lys Ile
225                 230                 235                 240
Thr Asp Phe Gly Glu Pro Arg Ile Gln Gln Glu Glu Gly Gln Asn Gln
                245                 250                 255
Ser Phe Ser Asn Gly Leu Ala Cys Leu Asp Met Val Leu Arg Ile Ala
            260                 265                 270
Asp Val Lys Glu Glu Asp Leu Leu Leu Gln Tyr Asp Cys Leu Ala Leu
        275                 280                 285
Asn Leu His Gly Leu Arg Arg His Thr Val Arg Leu Ser Arg Lys Asn
    290                 295                 300
Pro Ile Asp His His Ser Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp
305                 310                 315                 320
Thr Met Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys
                325                 330                 335
Cys Pro Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His
            340                 345                 350
Ser Ala Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp
        355                 360                 365
Leu Glu Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys
    370                 375                 380
Glu Lys Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly
385                 390                 395                 400
Asn Tyr Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala
                405                 410                 415
Phe Pro Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met
            420                 425                 430
Lys Leu Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile
        435                 440                 445
Thr Cys Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr
    450                 455                 460
Ile Thr Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val
465                 470                 475                 480
Ile Pro Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn
                485                 490                 495
Asn Gly Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr
            500                 505                 510
Phe His Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys
        515                 520                 525
Asn Ala Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr
    530                 535                 540
Glu Lys Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe
545                 550                 555                 560
Ser Phe Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly
                565                 570                 575
Lys Lys Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile
            580                 585                 590
Ser His Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile
        595                 600                 605
Lys Lys Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala
    610                 615                 620
Arg Ser Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys
```

625 630 635 640
Val Pro Ala Pro Arg Tyr Thr Val Glu Asp Lys Thr His Thr Cys Pro
645 650 655
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
660 665 670
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
675 680 685
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
690 695 700
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
705 710 715 720
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
725 730 735
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
740 745 750
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
755 760 765
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
770 775 780
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
785 790 795 800
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
805 810 815
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
820 825 830
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
835 840 845
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
850 855 860
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
865 870 875

<210> 328
<211> 310
<212> PRT
<213> Artificial Sequence

<220>
<223> human ST2 extracellular domain

<400> 328
Lys Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu Ile Val
1 5 10 15
Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp Tyr Tyr
20 25 30
Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg Val Phe
35 40 45
Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Ala Val Ala Asp Ser
50 55 60
Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg Thr Gly
65 70 75 80
Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn Val Pro
85 90 95
Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn Ser Lys

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


<210> 329
<211> 306
<212> PRT
<213> Artificial Sequence

<220>
<223> mouse ST2 extracellular domain

<400> 329
Ser Lys Ser Ser Trp Gly Leu Glu Asn Glu Ala Leu Ile Val Arg Cys
 1               5                  10                  15
Pro Gln Arg Gly Arg Ser Thr Tyr Pro Val Glu Trp Tyr Tyr Ser Asp
            20                  25                  30
Thr Asn Glu Ser Ile Pro Thr Gln Lys Arg Asn Arg Ile Phe Val Ser
        35                  40                  45
Arg Asp Arg Leu Lys Phe Leu Pro Ala Arg Val Glu Asp Ser Gly Ile
    50                  55                  60
Tyr Ala Cys Val Ile Arg Ser Pro Asn Leu Asn Lys Thr Gly Tyr Leu
65                  70                  75                  80
Asn Val Thr Ile His Lys Lys Pro Pro Ser Cys Asn Ile Pro Asp Tyr
                85                  90                  95
Leu Met Tyr Ser Thr Val Arg Gly Ser Asp Lys Asn Phe Lys Ile Thr
            100                 105                 110
Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe
        115                 120                 125
Lys Asn Cys Lys Ala Leu Gln Glu Pro Arg Phe Arg Ala His Arg Ser
```

```
    130                 135                 140
Tyr Leu Phe Ile Asp Asn Val Thr His Asp Asp Glu Gly Asp Tyr Thr
145                 150                 155                 160
Cys Gln Phe Thr His Ala Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala
                165                 170                 175
Thr Arg Ser Phe Thr Val Glu Glu Lys Gly Phe Ser Met Phe Pro Val
            180                 185                 190
Ile Thr Asn Pro Pro Tyr Asn His Thr Met Glu Val Glu Ile Gly Lys
        195                 200                 205
Pro Ala Ser Ile Ala Cys Ser Ala Cys Phe Gly Lys Gly Ser His Phe
    210                 215                 220
Leu Ala Asp Val Leu Trp Gln Ile Asn Lys Thr Val Val Gly Asn Phe
225                 230                 235                 240
Gly Glu Ala Arg Ile Gln Glu Glu Glu Gly Arg Asn Glu Ser Ser Ser
                245                 250                 255
Asn Asp Met Asp Cys Leu Thr Ser Val Leu Arg Ile Thr Gly Val Thr
            260                 265                 270
Glu Lys Asp Leu Ser Leu Glu Tyr Asp Cys Leu Ala Leu Asn Leu His
        275                 280                 285
Gly Met Ile Arg His Thr Ile Arg Leu Arg Arg Lys Gln Pro Ile Asp
    290                 295                 300
His Arg
305
```

<210> 330
<211> 339
<212> PRT
<213> Artificial Sequence

<220>
<223> human IL1RAcP extracellular domain

<400> 330

```
Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met Arg Gln Ile Gln
 1               5                  10                  15
Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro Leu Phe Glu His
            20                  25                  30
Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala Gly Leu Thr Leu
        35                  40                  45
Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu Glu Pro Ile Asn
    50                  55                  60
Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys Asp Val Leu Trp
65                  70                  75                  80
Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr Thr Cys Met Leu
                85                  90                  95
Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro Leu Glu Val Val
            100                 105                 110
Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu Pro Val His Lys
        115                 120                 125
Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys Pro Asn Val Asp
    130                 135                 140
Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr Trp Tyr Met Gly
145                 150                 155                 160
Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro Glu Gly Met Asn
```

```
                165                 170                 175
Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly Asn Tyr Thr Cys
            180                 185                 190
Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His Leu Thr Arg Thr
        195                 200                 205
Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala Val Pro Pro Val
    210                 215                 220
Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys Glu Pro Gly Glu
225                 230                 235                 240
Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe Leu Met Asp Ser
                245                 250                 255
Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys Pro Asp Asp Ile
            260                 265                 270
Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His Ser Arg Thr Glu
        275                 280                 285
Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys Val Thr Ser Glu
    290                 295                 300
Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser Ala Lys Gly Glu
305                 310                 315                 320
Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro Ala Pro Arg Tyr
                325                 330                 335
Thr Val Glu
```

<210> 331
<211> 339
<212> PRT
<213> Artificial Sequence

<220>
<223> mouse IL1RAcP extracellular domain

<400> 331

```
Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met Arg Gln Ile Gln
 1               5                  10                  15
Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro Leu Phe Glu His
            20                  25                  30
Phe Leu Lys Tyr Asn Tyr Ser Thr Ala His Ser Ser Gly Leu Thr Leu
        35                  40                  45
Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu Glu Pro Ile Asn
    50                  55                  60
Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys Asp Val Leu Trp
65                  70                  75                  80
Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr Thr Cys Met Leu
                85                  90                  95
Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro Leu Glu Val Val
            100                 105                 110
Gln Lys Asp Ser Cys Phe Asn Ser Ala Met Arg Phe Pro Val His Lys
        115                 120                 125
Met Tyr Ile Glu His Gly Ile His Lys Ile Thr Cys Pro Asn Val Asp
    130                 135                 140
Gly Tyr Phe Pro Ser Ser Val Lys Pro Ser Val Thr Trp Tyr Lys Gly
145                 150                 155                 160
Cys Thr Glu Ile Val Asp Phe His Asn Val Leu Pro Glu Gly Met Asn
```

```
                165                 170                 175
Leu Ser Phe Phe Ile Pro Leu Val Ser Asn Asn Gly Asn Tyr Thr Cys
            180                 185                 190
Val Val Thr Tyr Pro Glu Asn Gly Arg Leu Phe His Leu Thr Arg Thr
        195                 200                 205
Val Thr Val Lys Val Val Gly Ser Pro Lys Asp Ala Leu Pro Pro Gln
    210                 215                 220
Ile Tyr Ser Pro Asn Asp Arg Val Val Tyr Glu Lys Glu Pro Gly Glu
225                 230                 235                 240
Glu Leu Val Ile Pro Cys Lys Val Tyr Phe Ser Phe Ile Met Asp Ser
                245                 250                 255
His Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys Pro Asp Asp Val
            260                 265                 270
Thr Val Asp Ile Thr Ile Asn Glu Ser Val Ser Tyr Ser Ser Thr Glu
        275                 280                 285
Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys Val Thr Pro Glu
    290                 295                 300
Asp Leu Arg Arg Asn Tyr Val Cys His Ala Arg Asn Thr Lys Gly Glu
305                 310                 315                 320
Ala Glu Gln Ala Ala Lys Val Lys Gln Lys Val Ile Pro Pro Arg Tyr
                325                 330                 335
Thr Val Glu
```

<210> 332
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG1 Fc

<400> 332

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1               5                  10                  15
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
```

```
                165                 170                 175
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
Pro Gly Lys
225
```

<210> 333
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> mouse IgG2a Fc

<400> 333

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

<210> 334
<211> 167
<212> PRT

<213> Artificial Sequence

<220>
<223> M.fascicularis IL-33-6His

<400> 334
Ser Ile Thr Gly Ile Ser Pro Ile Thr Glu Ser Leu Ala Ser Leu Ser
 1   5   10   15
Thr Tyr Asn Asp Gln Ser Ile Thr Phe Ala Leu Glu Asp Glu Ser Tyr
            20   25   30
Glu Ile Tyr Val Glu Asp Leu Lys Lys Asp Lys Lys Lys Asp Lys Val
        35   40   45
Leu Leu Ser Tyr Tyr Glu Ser Gln His Pro Ser Ser Glu Ser Gly Asp
    50   55   60
Gly Val Asp Gly Lys Met Leu Met Val Thr Leu Ser Pro Thr Lys Asp
65   70   75   80
Phe Trp Leu Gln Ala Asn Asn Lys Glu His Ser Val Glu Leu His Lys
                85   90   95
Cys Glu Lys Pro Leu Pro Asp Gln Ala Phe Phe Val Leu His Asn Arg
            100   105   110
Ser Phe Asn Cys Val Ser Phe Glu Cys Lys Thr Asp Pro Gly Val Phe
        115   120   125
Ile Gly Val Lys Asp Asn His Leu Ala Leu Ile Lys Val Asp Tyr Ser
    130   135   140
Glu Asn Leu Gly Ser Glu Asn Ile Leu Phe Lys Leu Ser Glu Ile Leu
145   150   155   160
Glu His His His His His His
                165

<210> 335
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> HCVR-mouse surrogate IL-4R Ab

<400> 335
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1   5   10   15
Ser Val Arg Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30
Asn Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Tyr Pro Asn Asn Gly Asp Asn Gly Tyr Asn Gln Lys Phe
    50   55   60
Arg Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Arg Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Arg Leu Arg Tyr Phe Asp Val Trp Gly Thr Gly Thr Thr
            100   105   110
Val Thr Val Ser Ser
        115

<210> 336
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> LCVR-mouse surrogate IL-4R Ab

<400> 336
Asn Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Asn Tyr
            20   25   30
Gly His Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Leu Asp
65   70   75   80
Pro Val Glu Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn
                85   90   95
Glu Asp Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 337
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Dupilumab HCVR

<400> 337
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Glu Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Arg Asp Tyr
            20   25   30
Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Gly Ser Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Asp Arg Leu Ser Ile Thr Ile Arg Pro Arg Tyr Tyr Gly Leu
            100   105   110
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
        115   120

<210> 338

<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Dupilumab LCVR

<400> 338
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1   5   10   15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Tyr Ser
            20   25   30
Ile Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Ser Gly Gln Ser
        35   40   45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
    50   55   60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80
Ser Arg Val Glu Ala Glu Asp Val Gly Phe Tyr Tyr Cys Met Gln Ala
                85   90   95
Leu Gln Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 339
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Dupilumab HCDR1

<400> 339
Gly Phe Thr Phe Arg Asp Tyr Ala
 1   5

<210> 340
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Dupilumab HCDR2

<400> 340
Ile Ser Gly Ser Gly Gly Asn Thr
 1   5

<210> 341
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Dupilumab HCDR3

<400> 341
Ala Lys Asp Arg Leu Ser Ile Thr Ile Arg Pro Arg Tyr Tyr Gly Leu
 1   5   10   15
Asp Val

<210> 342
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Dupilumab LCDR1

<400> 342
Gln Ser Leu Leu Tyr Ser Ile Gly Tyr Asn Tyr
 1   5   10

<210> 343
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Dupilumab LCDR2

<400> 343
Leu Gly Ser
 1

<210> 344
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Dupilumab LCDR3

<400> 344
Met Gln Ala Leu Gln Thr Pro Tyr Thr
 1   5

<210> 345
<211> 451
<212> PRT
<213> Artificial Sequence

<220>

<223> Dupilumab heavy chain

<400> 345
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Glu Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Arg Asp Tyr
            20   25   30
Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Ser Ile Ser Gly Ser Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Lys Asp Arg Leu Ser Ile Thr Ile Arg Pro Arg Tyr Tyr Gly Leu
            100   105   110
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
        115   120   125
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
    130   135   140
Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145   150   155   160
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                165   170   175
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180   185   190
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys
        195   200   205
Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
    210   215   220
Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu
225   230   235   240
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245   250   255
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260   265   270
Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
        275   280   285
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
    290   295   300
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305   310   315   320
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser
                325   330   335
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            340   345   350
Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val
        355   360   365
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    370   375   380
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385   390   395   400
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr
                405   410   415

```
Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
            420                 425                 430
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        435                 440                 445
Ser Leu Gly
    450
```

<210> 346
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> Dupilumab light chain

<400> 346

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

<210> 347
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> human IL-4Ralpha

<400> 347
Met Lys Val Leu Gln Glu Pro Thr Cys Val Ser Asp Tyr Met Ser Ile
 1   5   10   15
Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys Ser Thr Glu
            20   25   30
Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu Ala His Thr
        35   40   45
Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys His Leu Leu
    50   55   60
Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp Leu Trp Ala
65   70   75   80
Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser Glu His Val
                85   90   95
Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn Val Ser Asp
            100   105   110
Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp Asn Tyr Leu
        115   120   125
Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu Asn Asp Pro
    130   135   140
Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro Ser Leu Arg
145   150   155   160
Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg Ala Arg Val
                165   170   175
Arg Ala Trp Ala Gln Cys Tyr Asn Thr Thr Trp Ser Glu Trp Ser Pro
            180   185   190
Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu Gln His
        195   200   205

<210> 348
<211> 270
<212> PRT
<213> Artificial Sequence

<220>
<223> hIL33_O95760 (prior to proteolytic processing)

<400> 348
Met Lys Pro Lys Met Lys Tyr Ser Thr Asn Lys Ile Ser Thr Ala Lys
 1   5   10   15
Trp Lys Asn Thr Ala Ser Lys Ala Leu Cys Phe Lys Leu Gly Lys Ser
            20   25   30
Gln Gln Lys Ala Lys Glu Val Cys Pro Met Tyr Phe Met Lys Leu Arg
        35   40   45
Ser Gly Leu Met Ile Lys Lys Glu Ala Cys Tyr Phe Arg Arg Glu Thr
    50   55   60
Thr Lys Arg Pro Ser Leu Lys Thr Gly Arg Lys His Lys Arg His Leu
65   70   75   80
Val Leu Ala Ala Cys Gln Gln Gln Ser Thr Val Glu Cys Phe Ala Phe
                85   90   95
Gly Ile Ser Gly Val Gln Lys Tyr Thr Arg Ala Leu His Asp Ser Ser
            100   105   110
Ile Thr Gly Ile Ser Pro Ile Thr Glu Tyr Leu Ala Ser Leu Ser Thr
        115   120   125
Tyr Asn Asp Gln Ser Ile Thr Phe Ala Leu Glu Asp Glu Ser Tyr Glu

```
    130                 135                 140
Ile Tyr Val Glu Asp Leu Lys Lys Asp Glu Lys Lys Asp Lys Val Leu
145                 150                 155                 160
Leu Ser Tyr Tyr Glu Ser Gln His Pro Ser Asn Glu Ser Gly Asp Gly
                165                 170                 175
Val Asp Gly Lys Met Leu Met Val Thr Leu Ser Pro Thr Lys Asp Phe
            180                 185                 190
Trp Leu His Ala Asn Asn Lys Glu His Ser Val Glu Leu His Lys Cys
        195                 200                 205
Glu Lys Pro Leu Pro Asp Gln Ala Phe Phe Val Leu His Asn Met His
    210                 215                 220
Ser Asn Cys Val Ser Phe Glu Cys Lys Thr Asp Pro Gly Val Phe Ile
225                 230                 235                 240
Gly Val Lys Asp Asn His Leu Ala Leu Ile Lys Val Asp Ser Ser Glu
                245                 250                 255
Asn Leu Cys Thr Glu Asn Ile Leu Phe Lys Leu Ser Glu Thr
            260                 265                 270


<210> 349
<211> 159
<212> PRT
<213> Artificial Sequence

<220>
<223> hIL33_mature_PEPTIDE (after proteolytic
      processing)

<400> 349
Ser Ile Thr Gly Ile Ser Pro Ile Thr Glu Tyr Leu Ala Ser Leu Ser
 1               5                  10                  15
Thr Tyr Asn Asp Gln Ser Ile Thr Phe Ala Leu Glu Asp Glu Ser Tyr
            20                  25                  30
Glu Ile Tyr Val Glu Asp Leu Lys Lys Asp Glu Lys Lys Asp Lys Val
        35                  40                  45
Leu Leu Ser Tyr Tyr Glu Ser Gln His Pro Ser Asn Glu Ser Gly Asp
    50                  55                  60
Gly Val Asp Gly Lys Met Leu Met Val Thr Leu Ser Pro Thr Lys Asp
65                  70                  75                  80
Phe Trp Leu His Ala Asn Asn Lys Glu His Ser Val Glu Leu His Lys
                85                  90                  95
Cys Glu Lys Pro Leu Pro Asp Gln Ala Phe Phe Val Leu His Asn Met
            100                 105                 110
His Ser Asn Cys Val Ser Phe Glu Cys Lys Thr Asp Pro Gly Val Phe
        115                 120                 125
Ile Gly Val Lys Asp Asn His Leu Ala Leu Ile Lys Val Asp Ser Ser
    130                 135                 140
Glu Asn Leu Cys Thr Glu Asn Ile Leu Phe Lys Leu Ser Glu Thr
145                 150                 155


<210> 350
<211> 12
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Amino Acid residues 1-12 of SEQ ID NO: 349; also
corresponds to residues 112-123 of SEQ ID NO: 348
(Uniprot O95760)

<400> 350
Ser Ile Thr Gly Ile Ser Pro Ile Thr Glu Tyr Leu
1 5 10

<210> 351
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid residues 50-94 of SEQ ID NO: 349; also
corresponds to residues 161-205 of SEQ ID NO: 348
(Uniprot O95760)

<400> 351
Ile Thr Glu Tyr Leu Ala Ser Leu Ser Thr Tyr Asn Asp Gln Ser Ile
1 5 10 15
Thr Phe Ala Leu Glu Asp Glu Ser Tyr Glu Ile Tyr Val Glu Asp Leu
20 25 30
Lys Lys Asp Glu Lys Lys Asp Lys Val Leu Leu Ser Tyr Tyr Glu Ser
35 40 45
Gln His Pro Ser Asn Glu Ser Gly Asp Gly Val Asp Gly Lys Met Leu
50 55 60
Met Val Thr Leu Ser Pro Thr Lys Asp Phe Trp Leu His Ala Asn Asn
65 70 75 80
Lys Glu His Ser Val Glu Leu
85

<210> 352
<211> 556
<212> PRT
<213> Artificial Sequence

<220>
<223> Human ST2 (See GenBank accession number NP_057316)

<400> 352
Met Gly Phe Trp Ile Leu Ala Ile Leu Thr Ile Leu Met Tyr Ser Thr
1 5 10 15
Ala Ala Lys Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu
20 25 30
Ile Val Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp
35 40 45
Tyr Tyr Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg
50 55 60
Val Phe Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Ala Val Ala
65 70 75 80

```
Asp Ser Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg
                85                  90                  95
Thr Gly Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn
            100                 105                 110
Val Pro Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn
        115                 120                 125
Ser Lys Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro
    130                 135                 140
Leu Glu Trp Phe Lys Asn Cys Gln Ala Leu Gln Gly Ser Arg Tyr Arg
145                 150                 155                 160
Ala His Lys Ser Phe Leu Val Ile Asp Asn Val Met Thr Glu Asp Ala
                165                 170                 175
Gly Asp Tyr Thr Cys Lys Phe Ile His Asn Glu Asn Gly Ala Asn Tyr
            180                 185                 190
Ser Val Thr Ala Thr Arg Ser Phe Thr Val Lys Asp Glu Gln Gly Phe
        195                 200                 205
Ser Leu Phe Pro Val Ile Gly Ala Pro Ala Gln Asn Glu Ile Lys Glu
    210                 215                 220
Val Glu Ile Gly Lys Asn Ala Asn Leu Thr Cys Ser Ala Cys Phe Gly
225                 230                 235                 240
Lys Gly Thr Gln Phe Leu Ala Ala Val Leu Trp Gln Leu Asn Gly Thr
                245                 250                 255
Lys Ile Thr Asp Phe Gly Glu Pro Arg Ile Gln Gln Glu Glu Gly Gln
            260                 265                 270
Asn Gln Ser Phe Ser Asn Gly Leu Ala Cys Leu Asp Met Val Leu Arg
        275                 280                 285
Ile Ala Asp Val Lys Glu Glu Asp Leu Leu Leu Gln Tyr Asp Cys Leu
    290                 295                 300
Ala Leu Asn Leu His Gly Leu Arg Arg His Thr Val Arg Leu Ser Arg
305                 310                 315                 320
Lys Asn Pro Ile Asp His His Ser Ile Tyr Cys Ile Ile Ala Val Cys
                325                 330                 335
Ser Val Phe Leu Met Leu Ile Asn Val Leu Val Ile Ile Leu Lys Met
            340                 345                 350
Phe Trp Ile Glu Ala Thr Leu Leu Trp Arg Asp Ile Ala Lys Pro Tyr
        355                 360                 365
Lys Thr Arg Asn Asp Gly Lys Leu Tyr Asp Ala Tyr Val Val Tyr Pro
    370                 375                 380
Arg Asn Tyr Lys Ser Ser Thr Asp Gly Ala Ser Arg Val Glu His Phe
385                 390                 395                 400
Val His Gln Ile Leu Pro Asp Val Leu Glu Asn Lys Cys Gly Tyr Thr
                405                 410                 415
Leu Cys Ile Tyr Gly Arg Asp Met Leu Pro Gly Glu Asp Val Val Thr
            420                 425                 430
Ala Val Glu Thr Asn Ile Arg Lys Ser Arg Arg His Ile Phe Ile Leu
        435                 440                 445
Thr Pro Gln Ile Thr His Asn Lys Glu Phe Ala Tyr Glu Gln Glu Val
    450                 455                 460
Ala Leu His Cys Ala Leu Ile Gln Asn Asp Ala Lys Val Ile Leu Ile
465                 470                 475                 480
Glu Met Glu Ala Leu Ser Glu Leu Asp Met Leu Gln Ala Glu Ala Leu
                485                 490                 495
Gln Asp Ser Leu Gln His Leu Met Lys Val Gln Gly Thr Ile Lys Trp
            500                 505                 510
Arg Glu Asp His Ile Ala Asn Lys Arg Ser Leu Asn Ser Lys Phe Trp
```

```
        515                 520                 525
Lys His Val Arg Tyr Gln Met Pro Val Pro Ser Lys Ile Pro Arg Lys
    530                 535                 540
Ala Ser Ser Leu Thr Pro Leu Ala Ala Gln Lys Gln
545                 550                 555


<210> 353
<211> 570
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IL-1RAcP (See GenBank accession number
      Q9NPH3)

<400> 353
Met Thr Leu Leu Trp Cys Val Val Ser Leu Tyr Phe Tyr Gly Ile Leu
 1               5                  10                  15
Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
            20                  25                  30
Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro
        35                  40                  45
Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala
    50                  55                  60
Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu
65                  70                  75                  80
Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
                85                  90                  95
Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
            100                 105                 110
Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
        115                 120                 125
Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu
    130                 135                 140
Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys
145                 150                 155                 160
Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr
                165                 170                 175
Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro
            180                 185                 190
Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly
        195                 200                 205
Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His
    210                 215                 220
Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala
225                 230                 235                 240
Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys
                245                 250                 255
Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe
            260                 265                 270
Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
        275                 280                 285
Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His
    290                 295                 300
```

Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
305 310 315 320
Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser
325 330 335
Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro
340 345 350
Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val
355 360 365
Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu
370 375 380
Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu
385 390 395 400
Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Ala Glu
405 410 415
Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu
420 425 430
Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly
435 440 445
Ile Val Thr Asp Glu Thr Leu Ser Phe Ile Gln Lys Ser Arg Arg Leu
450 455 460
Leu Val Val Leu Ser Pro Asn Tyr Val Leu Gln Gly Thr Gln Ala Leu
465 470 475 480
Leu Glu Leu Lys Ala Gly Leu Glu Asn Met Ala Ser Arg Gly Asn Ile
485 490 495
Asn Val Ile Leu Val Gln Tyr Lys Ala Val Lys Glu Thr Lys Val Lys
500 505 510
Glu Leu Lys Arg Ala Lys Thr Val Leu Thr Val Ile Lys Trp Lys Gly
515 520 525
Glu Lys Ser Lys Tyr Pro Gln Gly Arg Phe Trp Lys Gln Leu Gln Val
530 535 540
Ala Met Pro Val Lys Lys Ser Pro Arg Arg Ser Ser Ser Asp Glu Gln
545 550 555 560
Gly Leu Ser Tyr Ser Ser Leu Lys Asn Val
565 570

<210> 354
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> HC OF H4H9675P

<400> 354
Glu Val Gln Leu Val Glu Ser Gly Gly Asn Leu Glu Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Arg Ser
20 25 30
Ala Met Asn Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

```
Leu Gln Met Asn Ser Leu Ser Ala Glu Asp Thr Ala Ala Tyr Tyr Cys
                85                  90                  95
Ala Lys Asp Ser Tyr Thr Thr Ser Trp Tyr Gly Gly Met Asp Val Trp
            100                 105                 110
Gly His Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
    130                 135                 140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190
Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
        195                 200                 205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
    210                 215                 220
Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225                 230                 235                 240
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
            260                 265                 270
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
    290                 295                 300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
                325                 330                 335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350
Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
                405                 410                 415
Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
        435                 440                 445
Lys
```

<210> 355
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> LC OF H4H9675P

<400> 355
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Phe Ser Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Ala Asn Ser Val Pro Ile
                85   90   95
Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
            100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195   200   205
Phe Asn Arg Gly Glu Cys
    210

<210> 356
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> HUMAN IL-33 WITH HEXA-HIS TAG (AMINO ACIDS 112-270
      OF GENBANK ACCESSION NO. O95760)

<400> 356
Met Ser Ile Thr Gly Ile Ser Pro Ile Thr Glu Tyr Leu Ala Ser Leu
 1   5   10   15
Ser Thr Tyr Asn Asp Gln Ser Ile Thr Phe Ala Leu Glu Asp Glu Ser
            20   25   30
Tyr Glu Ile Tyr Val Glu Asp Leu Lys Lys Asp Glu Lys Lys Asp Lys
        35   40   45
Val Leu Leu Ser Tyr Tyr Glu Ser Gln His Pro Ser Asn Glu Ser Gly
    50   55   60
Asp Gly Val Asp Gly Lys Met Leu Met Val Thr Leu Ser Pro Thr Lys
65   70   75   80
Asp Phe Trp Leu His Ala Asn Asn Lys Glu His Ser Val Glu Leu His

```
                85                  90                  95
Lys Cys Glu Lys Pro Leu Pro Asp Gln Ala Phe Phe Val Leu His Asn
            100                 105                 110
Met His Ser Asn Cys Val Ser Phe Glu Cys Lys Thr Asp Pro Gly Val
        115                 120                 125
Phe Ile Gly Val Lys Asp Asn His Leu Ala Leu Ile Lys Val Asp Ser
    130                 135                 140
Ser Glu Asn Leu Cys Thr Glu Asn Ile Leu Phe Lys Leu Ser Glu Thr
145                 150                 155                 160
His His His His His His
                165
```