SEQUENCE LISTING

<110> Eli Lilly and Company

<120> pan-ELR+ CXC Chemokine Antibodies

<130> X19897

<150> 61/792800
<151> 2013-03-15

<160> 27

<170> PatentIn version 3.5

<210> 1
<211> 452
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<400> 1

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

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

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

Lys Ser Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

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

Ala Arg Glu Gly Pro Tyr Ser Tyr Tyr Pro Ser Arg Glu Tyr Tyr Gly
            100                 105                 110

Ser Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
        115                 120                 125

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr
    130                 135                 140

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

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
                165                 170                 175
```

```
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
            180                 185                 190

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr
        195                 200                 205

Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val
    210                 215                 220

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
                325                 330                 335

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

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445
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Leu Ser Leu Gly
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<210> 2
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<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 2

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 Glu Phe Thr Ser Tyr
20 25 30

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

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

Lys Ser Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Glu Gly Pro Tyr Ser Tyr Tyr Pro Ser Arg Glu Tyr Tyr Gly
100 105 110

Ser Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 3
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 3

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asn Asn
20 25 30

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

```
Tyr Tyr Thr Ser Arg Ser Val Ser Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gly Gln Asn Asn Glu Trp Pro Glu
                85                  90                  95

Val Phe Gly Gly Gly Thr Lys Val 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
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<210> 4
<211> 107
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<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 4

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asn Asn
            20                  25                  30

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

Tyr Tyr Thr Ser Arg Ser Val Ser Gly Ile Pro Ala Arg Phe Ser Gly
```

50 55 60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gly Gln Asn Asn Glu Trp Pro Glu
85 90 95

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

<210> 5
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
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tcctgcaagg catctggcta cgagttcacc agctactgga ttcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaaat atttctccta atagtggtag tgctaactac 180

aatgagaagt tcaagagcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagagggc 300

ccttacagtt attatccgag tagggagtac tatggctctg acctctgggg gcaagggacc 360

ctagtcacag tctcctcagc ctccaccaag ggcccatcgg tcttcccgct agcgccctgc 420

tccaggagca cctccgagag cacagccgcc ctgggctgcc tggtcaagga ctacttcccc 480

gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 540

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 600

agcttgggca cgaagaccta cacctgcaac gtagatcaca agcccagcaa caccaaggtg 660

gacaagagag ttgagtccaa atatggtccc ccatgcccac cctgcccagc acctgagttc 720

ctgggggggac catcagtctt cctgttcccc ccaaaaccca aggacactct catgatctcc 780

cggacccctg aggtcacgtg cgtggtggtg gacgtgagcc aggaagaccc cgaggtccag 840

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cagttcaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 960

aacggcaagg agtacaagtg caaggtctcc aacaaaggcc tcccgtcctc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gagccacagg tgtacaccct gccccatcc 1080

caggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctacccc 1140

agcgacatcg ccgtggagtg ggaaagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaggctaac cgtggacaag 1260

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cactacacac agaagagcct ctccctgtct ctgggt 1356

<210> 6
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 6
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ggccaggctc ccaggctcct catctattat acttcccggt ccgtctctgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtggacag aataacgagt ggcctgaggt gttcggcgga 300

gggaccaagg tggagatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gc 642

<210> 7
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 7

Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu His
1 5 10

<210> 8
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 8

Tyr Thr Ser Arg Ser Val Ser
1 5

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

<220>
<223> synthetic construct

<400> 9

Gly Gln Asn Asn Glu Trp Pro Glu Val
1 5

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

<220>
<223> synthetic construct

<400> 10

Gly Tyr Glu Phe Thr Ser Tyr Trp Ile His
1 5 10

<210> 11
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 11

Asn Ile Ser Pro Asn Ser Gly Ser Ala Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ser

<210> 12
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 12

Glu Gly Pro Tyr Ser Tyr Tyr Pro Ser Arg Glu Tyr Tyr Gly Ser Asp
1 5 10 15

Leu

<210> 13
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 13

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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 Glu Phe Thr Ser Tyr
            20                  25                  30

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

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

Lys Ser Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

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

Ala Arg Glu Gly Pro Tyr Ser Tyr Tyr Pro Ser Arg Gln Tyr Tyr Gly
            100                 105                 110

Ser Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
        115                 120                 125

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr
    130                 135                 140

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

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
                165                 170                 175

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
            180                 185                 190

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr
        195                 200                 205

Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val
    210                 215                 220

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270
```

```
Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
                325                 330                 335

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

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Leu Gly
    450
```

<210> 14
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 14

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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 Glu Phe Thr Ser Tyr
            20                  25                  30

Trp Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
```

35 40 45

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

Lys Ser Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Glu Gly Pro Tyr Ser Tyr Tyr Pro Ser Arg Gln Tyr Tyr Gly
100 105 110

Ser Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 15
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 15

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asn Asn
20 25 30

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gly Gln Asn Asn Glu Trp Pro Glu
85 90 95

Val Phe Gly Gly Gly Thr Lys Val 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> 16
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 16

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asn Asn
20 25 30

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gly Gln Asn Asn Glu Trp Pro Glu
85 90 95

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

<210> 17
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 17

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tcctgcaagg catctggcta cgagttcacc agctactgga ttcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaaat atttctccta atagtggtag tgctaactac 180

aatgagaagt tcaagagcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagagggc 300

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aacggcaagg agtacaagtg caaggtctcc aacaaaggcc tcccgtcctc catcgagaaa 1020

accatctcca aagccaaagg gcagccccga gagccacagg tgtacaccct gcccccatcc 1080

caggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctacccc 1140

agcgacatcg ccgtggagtg ggaaagcaat gggcagccgg agaacaacta caagaccacg 1200

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaggctaac cgtggacaag 1260

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cactacacac agaagagcct ctccctgtct ctgggt 1356

<210> 18
<211> 642
<212> DNA
<213> Artificial Sequence

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<400> 18
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ctctcctgca gggccagtca aagtatcagc aataacctac actggtacca acagaaacct 120

ggccaggctc ccaggctcct catctattat acttcccggt ccgtctctgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtggacag aataacgagt ggcctgaggt gttcggcgga 300

gggaccaagg tggagatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gc 642

<210> 19
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 19

Glu Gly Pro Tyr Ser Tyr Tyr Pro Ser Arg Gln Tyr Tyr Gly Ser Asp
1 5 10 15

Leu

<210> 20
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa position 11 is Glu or Gln

<400> 20

Glu Gly Pro Tyr Ser Tyr Tyr Pro Ser Arg Xaa Tyr Tyr Gly Ser Asp
1 5 10 15

Leu

<210> 21
<211> 73
<212> PRT
<213> Homo sapiens

<400> 21

Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln
1 5 10 15

Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser Pro Gly
20 25 30

Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Arg
35 40 45

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

Lys Met Leu Asn Ser Asp Lys Ser Asn
65 70

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<400> 22

Ala Pro Leu Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln
1 5 10 15

Gly Ile His Leu Lys Asn Ile Gln Ser Val Lys Val Lys Ser Pro Gly
20 25 30

Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Gln
35 40 45

Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Lys Lys Ile Ile Glu
50 55 60

Lys Met Leu Lys Asn Gly Lys Ser Asn
65 70

<210> 23
<211> 73
<212> PRT
<213> Homo sapiens

<400> 23

Ala Ser Val Val Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln
1 5 10 15

Gly Ile His Leu Lys Asn Ile Gln Ser Val Asn Val Arg Ser Pro Gly
20 25 30

Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Lys
35 40 45

Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Gln Lys Ile Ile Glu
50 55 60

Lys Ile Leu Asn Lys Gly Ser Thr Asn
65 70

<210> 24
<211> 74

<212> PRT
<213> Homo sapiens

<400> 24

Ala Ala Val Leu Arg Glu Leu Arg Cys Val Cys Leu Gln Thr Thr Gln
1 5 10 15

Gly Val His Pro Lys Met Ile Ser Asn Leu Gln Val Phe Ala Ile Gly
20 25 30

Pro Gln Cys Ser Lys Val Glu Val Val Ala Ser Leu Lys Asn Gly Lys
35 40 45

Glu Ile Cys Leu Asp Pro Glu Ala Pro Phe Leu Lys Lys Val Ile Gln
50 55 60

Lys Ile Leu Asp Gly Gly Asn Lys Glu Asn
65 70

<210> 25
<211> 75
<212> PRT
<213> Homo sapiens

<400> 25

Val Ser Ala Val Leu Thr Glu Leu Arg Cys Thr Cys Leu Arg Val Thr
1 5 10 15

Leu Arg Val Asn Pro Lys Thr Ile Gly Lys Leu Gln Val Phe Pro Ala
20 25 30

Gly Pro Gln Cys Ser Lys Val Glu Val Val Ala Ser Leu Lys Asn Gly
35 40 45

Lys Gln Val Cys Leu Asp Pro Glu Ala Pro Phe Leu Lys Lys Val Ile
50 55 60

Gln Lys Ile Leu Asp Ser Gly Asn Lys Lys Asn
65 70 75

<210> 26
<211> 70
<212> PRT
<213> Homo sapiens

<400> 26

Ala Glu Leu Arg Cys Met Cys Ile Lys Thr Thr Ser Gly Ile His Pro
1 5 10 15

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

Gln Val Glu Val Ile Ala Thr Leu Lys Asp Gly Arg Lys Ile Cys Leu

35 40 45

Asp Pro Asp Ala Pro Arg Ile Lys Lys Ile Val Gln Lys Lys Leu Ala
50 55 60

Gly Asp Glu Ser Ala Asp
65 70

<210> 27
<211> 72
<212> PRT
<213> Homo sapiens

<400> 27

Ser Ala Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro
1 5 10 15

Phe His Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro
20 25 30

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

Leu Cys Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys
50 55 60

Phe Leu Lys Arg Ala Glu Asn Ser
65 70