SEQUENCE LISTING

<110> Saiba GmbH

<120> VIRUS-LIKE PARTICLES OF CMV MODIFIED BY FUSION

<130> P5412PC00

<150> EP18214639.9
<151> 2018-12-20

<160> 145

<170> PatentIn version 3.5

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Met Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
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Arg Arg Arg Arg Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala
20 25 30

Asp Ala Asn Phe Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys
35 40 45

Thr Leu Ala Ala Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly
50 55 60

Ser Glu Arg Cys Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys
65 70 75 80

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Pro Pro Lys Ile Asp Arg Gly Ser Tyr Tyr Gly Lys Arg Leu Leu Leu
                85                  90                  95

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

Ile Arg Val Asn Pro Leu Pro Lys Phe Asp Ser Thr Val Trp Val Thr
        115                 120                 125

Val Arg Lys Val Pro Ala Ser Ser Asp Leu Ser Val Ala Ala Ile Ser
    130                 135                 140

Ala Met Phe Ala Asp Gly Ala Ser Pro Val Leu Val Tyr Gln Tyr Ala
145                 150                 155                 160

Ala Ser Gly Val Gln Ala Asn Asn Lys Leu Leu Tyr Asp Leu Ser Ala
                165                 170                 175

Met Arg Ala Asp Ile Gly Asp Met Arg Lys Tyr Ala Val Leu Val Tyr
            180                 185                 190

Ser Lys Asp Asp Ala Leu Glu Thr Asp Glu Leu Val Leu His Val Asp
        195                 200                 205

Val Glu His Gln Arg Ile Pro Thr Ser Gly Val Leu Pro Val
    210                 215                 220
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<400> 6

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Met Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
1               5                   10                  15
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Arg Arg Arg Arg Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala
            20                  25                  30

Asp Ala Asn Phe Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys
        35                  40                  45

Thr Leu Ala Ala Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly
    50                  55                  60

Ser Glu Arg Cys Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys
65                  70                  75                  80

Pro Pro Lys Ile Asp Arg Gly Ser Gly Gly Gly Ser Asp Ala Glu Phe
                85                  90                  95

Arg His Gly Gly Gly Ser Gly Ser Tyr Tyr Gly Lys Arg Leu Leu Leu
            100                 105                 110

Pro Asp Ser Val Thr Glu Tyr Asp Lys Lys Leu Val Ser Arg Ile Gln
        115                 120                 125

Ile Arg Val Asn Pro Leu Pro Lys Phe Asp Ser Thr Val Trp Val Thr
    130                 135                 140

Val Arg Lys Val Pro Ala Ser Ser Asp Leu Ser Val Ala Ala Ile Ser
145                 150                 155                 160

Ala Met Phe Ala Asp Gly Ala Ser Pro Val Leu Val Tyr Gln Tyr Ala
                165                 170                 175

Ala Ser Gly Val Gln Ala Asn Asn Lys Leu Leu Tyr Asp Leu Ser Ala
            180                 185                 190

Met Arg Ala Asp Ile Gly Asp Met Arg Lys Tyr Ala Val Leu Val Tyr
        195                 200                 205

Ser Lys Asp Asp Ala Leu Glu Thr Asp Glu Leu Val Leu His Val Asp
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210 215 220

Val Glu His Gln Arg Ile Pro Thr Ser Gly Val Leu Pro Val
225 230 235

<210> 7
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<400> 7

Met Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
1 5 10 15

Arg Arg Arg Arg Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala
20 25 30

Asp Ala Asn Phe Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys
35 40 45

Thr Leu Ala Ala Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly
50 55 60

Ser Glu Arg Cys Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys
65 70 75 80

Pro Pro Lys Ile Asp Arg Gly Ser Gly Gly Gly Ser Asp Ala Glu Phe
85 90 95

Arg His Asp Gly Gly Gly Ser Gly Ser Tyr Tyr Gly Lys Arg Leu Leu
100 105 110

Leu Pro Asp Ser Val Thr Glu Tyr Asp Lys Lys Leu Val Ser Arg Ile
115 120 125

Gln Ile Arg Val Asn Pro Leu Pro Lys Phe Asp Ser Thr Val Trp Val

130 135 140

Thr Val Arg Lys Val Pro Ala Ser Ser Asp Leu Ser Val Ala Ala Ile
145 150 155 160

Ser Ala Met Phe Ala Asp Gly Ala Ser Pro Val Leu Val Tyr Gln Tyr
165 170 175

Ala Ala Ser Gly Val Gln Ala Asn Asn Lys Leu Leu Tyr Asp Leu Ser
180 185 190

Ala Met Arg Ala Asp Ile Gly Asp Met Arg Lys Tyr Ala Val Leu Val
195 200 205

Tyr Ser Lys Asp Asp Ala Leu Glu Thr Asp Glu Leu Val Leu His Val
210 215 220

Asp Val Glu His Gln Arg Ile Pro Thr Ser Gly Val Leu Pro Val
225 230 235

<210> 8
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<223> CMV-Ntt830-Ab36

<400> 8

Cys Met Val Asn Thr Thr Ala Asx Met Gly Gln Tyr Ile Lys Ala Asn
1 5 10 15

Ser Lys Phe Ile Gly Ile Thr Glu Arg Arg Arg Arg Pro Arg Arg Gly
20 25 30

Ser Arg Ser Ala Pro Ser Ser Ala Asp Ala Asn Phe Arg Val Leu Ser
35 40 45

Gln Gln Leu Ser Arg Leu Asn Lys Thr Leu Ala Ala Gly Arg Pro Thr

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    50                  55                  60

Ile Asn His Pro Thr Phe Val Gly Ser Glu Arg Cys Lys Pro Gly Tyr
65                  70                  75                  80

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

Gly Gly Gly Ser Glu Phe Arg His Gly Gly Gly Ser Gly Ser Tyr Tyr
            100                 105                 110

Gly Lys Arg Leu Leu Leu Pro Asp Ser Val Thr Glu Tyr Asp Lys Lys
        115                 120                 125

Leu Val Ser Arg Ile Gln Ile Arg Val Asn Pro Leu Pro Lys Phe Asp
    130                 135                 140

Ser Thr Val Trp Val Thr Val Arg Lys Val Pro Ala Ser Ser Asp Leu
145                 150                 155                 160

Ser Val Ala Ala Ile Ser Ala Met Phe Ala Asp Gly Ala Ser Pro Val
                165                 170                 175

Leu Val Tyr Gln Tyr Ala Ala Ser Gly Val Gln Ala Asn Asn Lys Leu
            180                 185                 190

Leu Tyr Asp Leu Ser Ala Met Arg Ala Asp Ile Gly Asp Met Arg Lys
        195                 200                 205

Tyr Ala Val Leu Val Tyr Ser Lys Asp Asp Ala Leu Glu Thr Asp Glu
    210                 215                 220

Leu Val Leu His Val Asp Val Glu His Gln Arg Ile Pro Thr Ser Gly
225                 230                 235                 240

Val Leu Pro Val
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<210> 9
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<213> artificial sequence

<220>
<223> CMV-Ntt830-Ab15

<400> 9

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Met Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
1               5                  10                  15


Arg Arg Arg Arg Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala
            20                  25                  30


Asp Ala Asn Phe Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys
        35                  40                  45


Thr Leu Ala Ala Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly
    50                  55                  60


Ser Glu Arg Cys Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys
65                  70                  75                  80


Pro Pro Lys Ile Asp Arg Gly Ser Gly Gly Gly Ser Asp Ala Glu Phe
                85                  90                  95


Arg Gly Gly Gly Ser Gly Ser Tyr Tyr Gly Lys Arg Leu Leu Leu Pro
            100                 105                 110


Asp Ser Val Thr Glu Tyr Asp Lys Lys Leu Val Ser Arg Ile Gln Ile
        115                 120                 125


Arg Val Asn Pro Leu Pro Lys Phe Asp Ser Thr Val Trp Val Thr Val
    130                 135                 140


Arg Lys Val Pro Ala Ser Ser Asp Leu Ser Val Ala Ala Ile Ser Ala
145                 150                 155                 160
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Met Phe Ala Asp Gly Ala Ser Pro Val Leu Val Tyr Gln Tyr Ala Ala
165 170 175

Ser Gly Val Gln Ala Asn Asn Lys Leu Leu Tyr Asp Leu Ser Ala Met
180 185 190

Arg Ala Asp Ile Gly Asp Met Arg Lys Tyr Ala Val Leu Val Tyr Ser
195 200 205

Lys Asp Asp Ala Leu Glu Thr Asp Glu Leu Val Leu His Val Asp Val
210 215 220

Glu His Gln Arg Ile Pro Thr Ser Gly Val Leu Pro Val
225 230 235

<210> 10
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<220>
<223> GGGS-linker

<400> 10

Gly Gly Gly Ser
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<210> 11
<211> 6
<212> PRT
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<220>
<223> GGGSGS-linker

<400> 11

Gly Gly Gly Ser Gly Ser
1 5

<210> 12

<211> 726
<212> DNA
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<220>
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gtccgcgtcg tggttcccgc tccgccccct cctccgcgga tgctaacttt agagtcttgt 120

cgcagcagct ttcgcgactt aataagacgt tagcagctgg tcgtccaact attaaccacc 180

caacctttgt agggagtgaa cgctgtaaac ctgggtacac gttcacatct atcaccctaa 240

agccaccaaa aatagaccgt ggatccggtg gcggtagcga tgcggagttt cgccatgggg 300

gtggttcggg ttcctattat ggtaaaaggt tgttattacc tgattcagtc acggaatatg 360

ataagaaact tgtttcgcgc attcaaattc gagttaatcc tttgccgaaa tttgattcaa 420

ccgtgtgggt gacagtccgt aaagttcctg cctcttcgga cttatccgtt gccgccattt 480

ctgctatgtt tgcggacgga gcctcaccgg tactggttta tcagtacgct gcatctggag 540

tccaagctaa caacaaactg ttgtatgatc tttcggcgat gcgcgctgat ataggcgaca 600

tgagaaagta cgccgtcctc gtgtattcaa aagacgatgc actcgagaca gacgagttag 660

tacttcatgt tgacgtcgag caccaacgta ttcccacatc tggggtgctc ccagtttgat 720

aagctt 726

<210> 13
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<212> DNA
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<220>
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<400> 13
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gtccgcgtcg tggttcccgc tccgccccct cctccgcgga tgctaacttt agagtcttgt 120

cgcagcagct ttcgcgactt aataagacgt tagcagctgg tcgtccaact attaaccacc 180

caacctttgt agggagtgaa cgctgtaaac ctgggtacac gttcacatct atcaccctaa 240

agccaccaaa aatagaccgt ggatccggtg gcggtagcga tgcggagttt cgccatgatg 300

ggggtggttc gggttcctat tatggtaaaa ggttgttatt acctgattca gtcacggaat 360

atgataagaa acttgtttcg cgcattcaaa ttcgagttaa tcctttgccg aaatttgatt 420

caaccgtgtg ggtgacagtc cgtaaagttc ctgcctcttc ggacttatcc gttgccgcca 480

tttctgctat gtttgcggac ggagcctcac cggtactggt ttatcagtac gctgcatctg 540

gagtccaagc taacaacaaa ctgttgtatg atctttcggc gatgcgcgct gatataggcg 600

acatgagaaa gtacgccgtc ctcgtgtatt caaaagacga tgcactcgag acagacgagt 660

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gataagctt 729

<210> 14
<211> 720
<212> DNA
<213> artificial sequence

<220>
<223> CMV-Ntt830-Ab36

<400> 14
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gtccgcgtcg tggttcccgc tccgccccct cctccgcgga tgctaacttt agagtcttgt 120

cgcagcagct ttcgcgactt aataagacgt tagcagctgg tcgtccaact attaaccacc 180

caacctttgt agggagtgaa cgctgtaaac ctgggtacac gttcacatct atcaccctaa 240

agccaccaaa aatagaccgt ggatccggtg gcggtagcga gtttcgccat gggggtggtt 300

cgggttccta ttatggtaaa aggttgttat tacctgattc agtcacggaa tatgataaga 360

aacttgtttc gcgcattcaa attcgagtta atcctttgcc gaaatttgat tcaaccgtgt 420

gggtgacagt ccgtaaagtt cctgcctctt cggacttatc cgttgccgcc atttctgcta 480

tgtttgcgga cggagcctca ccggtactgg tttatcagta cgctgcatct ggagtccaag 540

ctaacaacaa actgttgtat gatctttcgg cgatgcgcgc tgatataggc gacatgagaa 600

agtacgccgt cctcgtgtat tcaaaagacg atgcactcga gacagacgag ttagtacttc 660

atgttgacgt cgagcaccaa cgtattccca catctggggt gctcccagtt tgataagctt 720

<210> 15
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<212> DNA
<213> artificial sequence

<220>
<223> CMV-Ntt830-Ab15

<400> 15
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gtccgcgtcg tggttcccgc tccgcccccc cctccgcgga tgctaacttt agagtcttgt 120

cgcagcagct ttcgcgactt aataagacgt tagcagctgg tcgtccaact attaaccacc 180

caacctttgt agggagtgaa cgctgtaaac ctgggtacac gttcacatct atcaccctaa 240

agccaccaaa aatagaccgt ggatccggtg gcggtagcga tgcggagttc cgcgggggtg 300

gttcgggatc ctattatggt aaaaggttgt tattacctga ttcagtcacg gaatatgata 360

agaaacttgt ttcgcgcatt caaattcgag ttaatccttt gccgaaattt gattcaaccg 420

tgtgggtgac agtccgtaaa gttcctgcct cttcggactt atccgttgcc gccatttctg 480

ctatgtttgc ggacggagcc tcaccggtac tggtttatca gtacgctgca tctggagtcc 540

aagctaacaa caaactgttg tatgatcttt cggcgatgcg cgctgatata ggcgacatga 600

gaaagtacgc cgtcctcgtg tattcaaaag acgatgcact cgagacagac gagttagtac 660

ttcatgttga cgtcgagcac caacgtattc ccacatctgg ggtgctccca gtttgataag 720

ctt 723

<210> 16
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> Forward - pET-90 primer

<400> 16

aggatcgaga tctcgatccc gcga 24

<210> 17
<211> 35
<212> DNA
<213> artificial sequence

<220>
<223> Reverse - RGSYrev

<400> 17
accataatag gatccacggt ctatttttgg tggct 35

<210> 18
<211> 40
<212> DNA
<213> artificial sequence

<220>
<223> Forward - RGSYdir

<400> 18
agaccgtgga tcctattatg gtaaaaggtt gttattacct 40

<210> 19
<211> 25
<212> DNA
<213> artificial sequence

<220>
<223> Reverse - CMV-AgeR

<400> 19
agtaccggtg aggctccgtc cgcaa 25

<210> 20
<211> 77
<212> DNA
<213> artificial sequence

<220>
<223> Forward - C-Ab15

<400> 20
tggatccggt ggcggtagcg atgcggagtt ccgcgggggt ggttcgggtt cctattatgg 60

taaaaggttg ttattac 77

<210> 21
<211> 37
<212> DNA
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<220>
<223> Reverse - CMcpR

<400> 21
caaagcttat caaactggga gcaccccaga tgtggga 37

<210> 22
<211> 82
<212> DNA
<213> artificial sequence

<220>
<223> Forward - C-Ab16

<400> 22
cgtggatccg gtggcggtag cgatgcggag tttcgccatg ggggtggttc gggttcctat 60

tatggtaaaa ggttgttatt ac 82

<210> 23
<211> 85
<212> DNA
<213> artificial sequence

<220>
<223> Forward - C-Ab17

<400> 23
cgtggatccg gtggcggtag cgatgcggag tttcgccatg atgggggtgg ttcgggttcc 60

tattatggta aaaggttgtt attac 85

<210> 24
<211> 76
<212> DNA
<213> artificial sequence

<220>
<223> Forward - C-Ab36

<400> 24
cgtggatccg gtggcggtag cgagtttcgc catgggggtg gttcgggttc ctattatggt 60

aaaaggttgt tattac 76

<210> 25
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> Forward - CM-830NdeF

<400> 25
acacatatgg gccagtatat taaggccaac tcca 34

<210> 26
<211> 37
<212> DNA
<213> artificial sequence

<220>
<223> Reverse - CM-cpR

<400> 26
caaagcttat caaactggga gcaccccaga tgtggga 37

<210> 27
<211> 151
<212> PRT
<213> artificial sequence

<220>
<223> Ara-h202

<400> 27

Arg Gln Gln Trp Glu Leu Gln Gly Asp Arg Arg Cys Gln Ser Gln Leu
1 5 10 15

Glu Arg Ala Asn Leu Arg Pro Cys Glu Gln His Leu Met Gln Lys Ile
20 25 30

Gln Arg Asp Glu Asp Ser Tyr Gly Arg Asp Pro Tyr Ser Pro Ser Gln

```
        35                  40                  45

Asp Pro Tyr Ser Pro Ser Gln Asp Pro Asp Arg Arg Asp Pro Tyr Ser
    50                  55                  60

Pro Ser Pro Tyr Asp Arg Arg Gly Ala Gly Ser Ser Gln His Gln Glu
65                  70                  75                  80

Arg Cys Cys Asn Glu Leu Asn Glu Phe Glu Asn Asn Gln Arg Cys Met
                85                  90                  95

Cys Glu Ala Leu Gln Gln Ile Met Glu Asn Gln Ser Asp Arg Leu Gln
            100                 105                 110

Gly Arg Gln Gln Glu Gln Gln Phe Lys Arg Glu Leu Arg Asn Leu Pro
        115                 120                 125

Gln Gln Cys Gly Leu Arg Ala Pro Gln Arg Cys Asp Leu Glu Val Glu
    130                 135                 140

Ser Gly Gly Arg Asp Arg Tyr
145                 150
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<210> 28
<211> 501
<212> DNA
<213> artificial sequence

<220>
<223> Ara-h202

<400> 28
atgggctgcc gccatcatca tcatcatcat ggcgcgcgcc agcgccagca gtgggaactg 60

cagggcgatc gtcgctgcca gagccagctg gaacgcgcga acctgcgtcc gtgcgaacag 120

catctgatgc agaaaattca gcgcgatgaa gatagctatg gccgcgatcc gtatagccca 180

agccaagatc cgtatagccc aagccaggat ccggatcgcc gtgatccgta tagcccaagc 240

ccgtatgatc gtcgcggcgc gggcagcagc cagcatcagg aacgctgctg caacgaactg 300

aacgaatttg aaaacaacca gcgctgcatg tgcgaagcgc tgcaacagat tatggaaaac 360

cagagcgatc gcctgcaagg ccgccagcaa gaacagcagt ttaaacgcga actgcgtaac 420

ctgccgcagc agtgcggcct gcgtgcgccg cagcgctgcg atctggaagt ggaaagcggc 480

ggccgtgatc gctattaata a 501

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<223> CMV-Ntt830-Arah202

<400> 29

Met Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
1 5 10 15

Arg Arg Arg Arg Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala
20 25 30

Asp Ala Asn Phe Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys
35 40 45

Thr Leu Ala Ala Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly
50 55 60

Ser Glu Arg Cys Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys
65 70 75 80

Pro Pro Lys Ile Asp Arg Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
85 90 95

Gly Ser Gly Gly Gly Gly Ser Arg Gln Gln Trp Glu Leu Gln Gly Asp
100 105 110

Arg Arg Cys Gln Ser Gln Leu Glu Arg Ala Asn Leu Arg Pro Cys Glu
115 120 125

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Gln His Leu Met Gln Lys Ile Gln Arg Asp Glu Asp Ser Tyr Gly Arg
    130                 135                 140

Asp Pro Tyr Ser Pro Ser Gln Asp Pro Tyr Ser Pro Ser Gln Asp Pro
145                 150                 155                 160

Asp Arg Arg Asp Pro Tyr Ser Pro Ser Pro Tyr Asp Arg Arg Gly Ala
                165                 170                 175

Gly Ser Ser Gln His Gln Glu Arg Cys Cys Asn Glu Leu Asn Glu Phe
            180                 185                 190

Glu Asn Asn Gln Arg Cys Met Cys Glu Ala Leu Gln Gln Ile Met Glu
        195                 200                 205

Asn Gln Ser Asp Arg Leu Gln Gly Arg Gln Gln Glu Gln Gln Phe Lys
    210                 215                 220

Arg Glu Leu Arg Asn Leu Pro Gln Gln Cys Gly Leu Arg Ala Pro Gln
225                 230                 235                 240

Arg Cys Asp Leu Glu Val Glu Ser Gly Gly Arg Asp Arg Tyr Gly Gly
                245                 250                 255

Gly Gly Ser Gly Gly Gly Gly Ser Tyr Tyr Gly Lys Arg Leu Leu Leu
            260                 265                 270

Pro Asp Ser Val Thr Glu Tyr Asp Lys Lys Leu Val Ser Arg Ile Gln
        275                 280                 285

Ile Arg Val Asn Pro Leu Pro Lys Phe Asp Ser Thr Val Trp Val Thr
    290                 295                 300

Val Arg Lys Val Pro Ala Ser Ser Asp Leu Ser Val Ala Ala Ile Ser
305                 310                 315                 320

Ala Met Phe Ala Asp Gly Ala Ser Pro Val Leu Val Tyr Gln Tyr Ala
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```
                325                 330                 335

Ala Ser Gly Val Gln Ala Asn Asn Lys Leu Leu Tyr Asp Leu Ser Ala
            340                 345                 350

Met Arg Ala Asp Ile Gly Asp Met Arg Lys Tyr Ala Val Leu Val Tyr
        355                 360                 365

Ser Lys Asp Asp Ala Leu Glu Thr Asp Glu Leu Val Leu His Val Asp
    370                 375                 380

Val Glu His Gln Arg Ile Pro Thr Ser Gly Val Leu Pro Val
385                 390                 395
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<210> 30
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> 15aa GS-linker

<400> 30

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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1               5                   10                  15
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<210> 31
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> 10aa GS-linker

<400> 31

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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1               5                   10
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<210> 32
<211> 1215
<212> DNA

<213> artificial sequence

<220>
<223> CMV-Ntt830-Arah202

<400> 32
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gtccgcgtcg tggttcccgc tccgcccccc cctccgcgga tgctaacttt agagtcttgt 120

cgcagcagct ttcgcgactt aataagacgt tagcagctgg tcgtccaact attaaccacc 180

caacctttgt agggagtgaa cgctgtaaac ctgggtacac gttcacatct atcaccctaa 240

agccaccaaa aatagaccgt ggatctggag gaggtggtag tggtggaggt ggatctggag 300

gaggtggatc cggtcgccag cagtgggaac tgcagggcga tcgtcgctgc cagagccagc 360

tggaacgcgc gaacctgcgt ccgtgcgaac agcatctgat gcagaaaatt cagcgcgatg 420

aagatagcta tggccgcgat ccgtatagcc caagccaaga tccgtatagc ccaagccagg 480

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cggaatatga taagaaactt gtttcgcgca ttcaaattcg agttaatcct ttgccgaaat 900

ttgattcaac cgtgtgggtg acagtccgta aagttcctgc ctcttcggac ttatccgttg 960

ccgccatttc tgctatgttt gcggacggag cctcaccggt actggtttat cagtacgctg 1020

catctggagt ccaagctaac aacaaactgt tgtatgatct ttcggcgatg cgcgctgata 1080

taggcgacat gagaaagtac gccgtcctcg tgtattcaaa agacgatgca ctcgagacag 1140

acgagttagt acttcatgtt gacgtcgagc accaacgtat tcccacatct ggggtgctcc 1200

cagtttgata agctt 1215

<210> 33

<211> 27
<212> DNA
<213> artificial sequence

<220>
<223> Forward - 830-NcoF

<400> 33
ataccatggg ccagtatatt aaggcca 27

<210> 34
<211> 78
<212> DNA
<213> artificial sequence

<220>
<223> Reverse - C-5xg4s-R

<400> 34
ggatccacct cctccagatc cacctccacc actaccacct cctccagatc cacggtctat 60

ttttggtggc tttagggt 78

<210> 35
<211> 65
<212> DNA
<213> artificial sequence

<220>
<223> Forward - C-5xg4s-F

<400> 35
ggatccggag gaggtggaag cggaggaggt ggatcttatt atggtaaaag gttgttatta 60

cctga 65

<210> 36
<211> 32
<212> DNA
<213> artificial sequence

<220>
<223> Forward - Ara-BamF2

<400> 36
acaggatccg gtcgccagca gtgggaactg ca 32

<210> 37
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> Reverse - Ara-BamR2

<400> 37
tgtggatcca tagcgatcac ggccgccgct 30

<210> 38
<211> 177
<212> PRT
<213> artificial sequence

<220>
<223> Feld12

<400> 38

Glu Ile Cys Pro Ala Val Lys Arg Asp Val Asp Leu Phe Leu Thr Gly
1 5 10 15

Thr Pro Asp Glu Tyr Val Glu Gln Val Ala Gln Tyr Lys Ala Leu Pro
20 25 30

Val Val Leu Glu Asn Ala Arg Ile Leu Lys Asn Cys Val Asp Ala Lys
35 40 45

Met Thr Glu Glu Asp Lys Glu Asn Ala Leu Ser Val Leu Asp Lys Ile
50 55 60

Tyr Thr Ser Pro Leu Cys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Ser Val Lys Met Ala Glu Thr Cys Pro Ile Phe Tyr
85 90 95

Asp Val Phe Phe Ala Val Ala Asn Gly Asn Glu Leu Leu Leu Asp Leu
100 105 110

Ser Leu Thr Lys Val Asn Ala Thr Glu Pro Glu Arg Thr Ala Met Lys
        115   120   125

Lys Ile Gln Asp Cys Tyr Val Glu Asn Gly Leu Ile Ser Arg Val Leu
    130   135   140

Asp Gly Leu Val Met Thr Thr Ile Ser Ser Ser Lys Asp Cys Met Gly
145   150   155   160

Glu Ala Val Gln Asn Thr Val Glu Asp Leu Lys Leu Asn Thr Leu Gly
                165   170   175

Arg

<210> 39
<211> 424
<212> PRT
<213> artificial sequence

<220>
<223> CMV-Ntt830-Feld12

<400> 39

Met Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
1   5   10   15

Arg Arg Arg Arg Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala
            20   25   30

Asp Ala Asn Phe Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys
        35   40   45

Thr Leu Ala Ala Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly
    50   55   60

Ser Glu Arg Cys Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys
65   70   75   80

```
Pro Pro Lys Ile Asp Arg Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
                85                  90                  95

Gly Ser Gly Gly Gly Gly Ser Glu Ile Cys Pro Ala Val Lys Arg Asp
            100                 105                 110

Val Asp Leu Phe Leu Thr Gly Thr Pro Asp Glu Tyr Val Glu Gln Val
        115                 120                 125

Ala Gln Tyr Lys Ala Leu Pro Val Val Leu Glu Asn Ala Arg Ile Leu
    130                 135                 140

Lys Asn Cys Val Asp Ala Lys Met Thr Glu Glu Asp Lys Glu Asn Ala
145                 150                 155                 160

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Val Lys Met Ala
            180                 185                 190

Glu Thr Cys Pro Ile Phe Tyr Asp Val Phe Phe Ala Val Ala Asn Gly
        195                 200                 205

Asn Glu Leu Leu Leu Asp Leu Ser Leu Thr Lys Val Asn Ala Thr Glu
    210                 215                 220

Pro Glu Arg Thr Ala Met Lys Lys Ile Gln Asp Cys Tyr Val Glu Asn
225                 230                 235                 240

Gly Leu Ile Ser Arg Val Leu Asp Gly Leu Val Met Thr Thr Ile Ser
                245                 250                 255

Ser Ser Lys Asp Cys Met Gly Glu Ala Val Gln Asn Thr Val Glu Asp
            260                 265                 270

Leu Lys Leu Asn Thr Leu Gly Arg Gly Gly Gly Gly Ser Gly Gly Gly
```

```
        275                 280                 285

Gly Ser Tyr Tyr Gly Lys Arg Leu Leu Leu Pro Asp Ser Val Thr Glu
    290                 295                 300

Tyr Asp Lys Lys Leu Val Ser Arg Ile Gln Ile Arg Val Asn Pro Leu
305                 310                 315                 320

Pro Lys Phe Asp Ser Thr Val Trp Val Thr Val Arg Lys Val Pro Ala
                325                 330                 335

Ser Ser Asp Leu Ser Val Ala Ala Ile Ser Ala Met Phe Ala Asp Gly
            340                 345                 350

Ala Ser Pro Val Leu Val Tyr Gln Tyr Ala Ala Ser Gly Val Gln Ala
        355                 360                 365

Asn Asn Lys Leu Leu Tyr Asp Leu Ser Ala Met Arg Ala Asp Ile Gly
    370                 375                 380

Asp Met Arg Lys Tyr Ala Val Leu Val Tyr Ser Lys Asp Asp Ala Leu
385                 390                 395                 400

Glu Thr Asp Glu Leu Val Leu His Val Asp Val Glu His Gln Arg Ile
                405                 410                 415

Pro Thr Ser Gly Val Leu Pro Val
            420
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<210> 40
<211> 1284
<212> DNA
<213> artificial sequence

<220>
<223> CMV-Ntt830-Feld12

<400> 40
ccatgggcca gtatattaag gccaactcca aatttatcgg gattaccgag cgtcgacgtc 60

gtccgcgtcg tggttcccgc tccgcccccc cctccgcgga tgctaacttt agagtcttgt 120

cgcagcagct ttcgcgactt aataagacgt tagcagctgg tcgtccaact attaaccacc 180

caacctttgt agggagtgaa cgctgtaaac ctgggtacac gttcacatct atcaccctaa 240

agccaccaaa aatagaccgt ggatccggag gaggtggtag tggtggaggt ggatctggag 300

gaggtggaag cgaaatttgt ccggcagtta aacgtgatgt tgacctgttt ctgaccggta 360

caccggatga atatgtggaa caggttgcac agtataaagc actgccggtt gttctggaaa 420

atgcacgtat tctgaaaaat tgcgtggatg ccaaaatgac cgaagaggat aaagaaaatg 480

ccctgagcgt tctggataaa atctatacca gtccgctgtg cggtggtggt ggtagtggtg 540

gcggtggttc aggcggtggc ggtagcgtta aaatggcaga aacctgtccg atcttttatg 600

atgttttttt tgccgtggcc aatggcaatg aactgctgct ggatctgagc ctgaccaaag 660

ttaatgcaac cgaaccggaa cgtaccgcaa tgaaaaaaat ccaggattgc tatgtggaaa 720

acggtctgat tagccgtgtt ctggatggtc tggttatgac caccattagc agcagcaaag 780

attgtatggg tgaagcagtg cagaataccg ttgaagatct gaaactgaat accctgggtc 840

gtggaggagg tggaagcgga ggaggtggat cctattatgg taaaaggttg ttattacctg 900

attcagtcac ggaatatgat aagaaacttg tttcgcgcat tcaaattcga gttaatcctt 960

tgccgaaatt tgattcaacc gtgtgggtga cagtccgtaa agttcctgcc tcttcggact 1020

tatccgttgc cgccatttct gctatgtttg cggacggagc ctcaccggta ctggtttatc 1080

agtacgctgc atctggagtc caagctaaca acaaactgtt gtatgatctt tcggcgatgc 1140

gcgctgatat aggcgacatg agaaagtacg ccgtcctcgt gtattcaaaa gacgatgcac 1200

tcgagacaga cgagttagta cttcatgttg acgtcgagca ccaacgtatt cccacatctg 1260

gggtgctccc agtttgataa gctt 1284

<210> 41
<211> 77
<212> DNA
<213> artificial sequence

<220>
<223> Forward - FG4S-BamF

<400> 41
caggatccgg aggaggtggt agtggtggag gtggatctgg aggaggtggt agcgaaattt 60

gtccggcagt taaacgt 77

<210> 42
<211> 56
<212> DNA
<213> artificial sequence

<220>
<223> Reverse - FG4S-BamR

<400> 42
ataggatcca cctcctccgc ttccacctcc tccacgaccc agggtattca gtttca 56

<210> 43
<211> 4
<212> PRT
<213> artificial sequence

<220>
<223> Plasmodium falciparum CS fragment

<400> 43

Asn Ala Asn Pro
1

<210> 44
<211> 76
<212> PRT
<213> artificial sequence

<220>
<223> Plasmodium falciparum CS protein fragment

<400> 44

Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro
1 5 10 15

Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro
20 25 30

Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro
35 40 45

Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro
50 55 60

Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro
65 70 75

<210> 45
<211> 754
<212> DNA
<213> artificial sequence

<220>
<223> Plasmodium falciparum CS protein fragment and CMVNtt830 3' terminal part

<400> 45
ccctaaagcc accaaaaata gaccgtggat ctggaggagg tggtagtggt ggaggtggat 60

ctggaggagg tggatccaac gcgaatccga acgcaaaccc gaacgcgaat ccgaacgcaa 120

acccaaacgc gaatccgaac gcaaacccga acgcgaaccc gaacgcgaac ccgaacgcga 180

acccgaacgc gaaccctaac gcgaacccga acgcgaaccc gaacgcgaac ccgaacgcga 240

acccgaacgc gaacccgaac gcgaacccga acgcgaaccc gaacgcgaac ccgaacgcga 300

acccgggatc tggaggaggt ggaagcggag gaggtggatc ttattatggt aaaaggttgt 360

tattacctga ttcagtcacg gaatatgata agaaacttgt ttcgcgcatt caaattcgag 420

ttaatccttt gccgaaattt gattcaaccg tgtgggtgac agtccgtaaa gttcctgcct 480

cttcggactt atccgttgcc gccatttctg ctatgtttgc ggacggagcc tcaccggtac 540

tggtttatca gtacgctgca tctggagtcc aagctaacaa caaactgttg tatgatcttt 600

cggcgatgcg cgctgatata ggcgacatga gaaagtacgc cgtcctcgtg tattcaaaag 660

acgatgcact cgagacagac gagttagtac ttcatgttga cgtcgagcac caacgtattc 720

ccacatctgg ggtgctccca gtttgataag cttt 754

<210> 46
<211> 325
<212> PRT
<213> artificial sequence

<220>
<223> CMV-Ntt830-19NANP

<400> 46

```
Met Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
1               5                  10                  15


Arg Arg Arg Arg Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala
            20                  25                  30


Asp Ala Asn Phe Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys
        35                  40                  45


Thr Leu Ala Ala Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly
    50                  55                  60


Ser Glu Arg Cys Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys
65                  70                  75                  80


Pro Pro Lys Ile Asp Arg Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
                85                  90                  95


Gly Ser Gly Gly Gly Gly Ser Asn Ala Asn Pro Asn Ala Asn Pro Asn
            100                 105                 110


Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
        115                 120                 125


Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
    130                 135                 140


Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
145                 150                 155                 160
```

```
Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
                165                 170                 175

Ala Asn Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Tyr
            180                 185                 190

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

Lys Leu Val Ser Arg Ile Gln Ile Arg Val Asn Pro Leu Pro Lys Phe
    210                 215                 220

Asp Ser Thr Val Trp Val Thr Val Arg Lys Val Pro Ala Ser Ser Asp
225                 230                 235                 240

Leu Ser Val Ala Ala Ile Ser Ala Met Phe Ala Asp Gly Ala Ser Pro
                245                 250                 255

Val Leu Val Tyr Gln Tyr Ala Ala Ser Gly Val Gln Ala Asn Asn Lys
            260                 265                 270

Leu Leu Tyr Asp Leu Ser Ala Met Arg Ala Asp Ile Gly Asp Met Arg
        275                 280                 285

Lys Tyr Ala Val Leu Val Tyr Ser Lys Asp Asp Ala Leu Glu Thr Asp
    290                 295                 300

Glu Leu Val Leu His Val Asp Val Glu His Gln Arg Ile Pro Thr Ser
305                 310                 315                 320

Gly Val Leu Pro Val
                325
```

<210> 47
<211> 12
<212> PRT
<213> artificial sequence

<220>

<223> 12aa GS-linker

<400> 47

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1   5   10

<210> 48
<211> 1215
<212> DNA
<213> artificial sequence

<220>
<223> CMV-Ntt830-19NANP

<400> 48
ccatgggcca gtatattaag gccaactcca aatttatcgg gattaccgag cgtcgacgtc   60

gtccgcgtcg tggttcccgc tccgccccct cctccgcgga tgctaacttt agagtcttgt   120

cgcagcagct ttcgcgactt aataagacgt tagcagctgg tcgtccaact attaaccacc   180

caacctttgt agggagtgaa cgctgtaaac ctgggtacac gttcacatct atcaccctaa   240

agccaccaaa aatagaccgt ggatctggag gaggtggtag tggtggaggt ggatctggag   300

gaggtggatc cggtcgccag cagtgggaac tgcagggcga tcgtcgctgc cagagccagc   360

tggaacgcgc gaacctgcgt ccgtgcgaac agcatctgat gcagaaaatt cagcgcgatg   420

aagatagcta tggccgcgat ccgtatagcc caagccaaga tccgtatagc ccaagccagg   480

atccggatcg ccgtgatccg tatagcccaa gcccgtatga tcgtcgcggc gcgggcagca   540

gccagcatca ggaacgctgc tgcaacgaac tgaacgaatt tgaaaacaac cagcgctgca   600

tgtgcgaagc gctgcaacag attatggaaa accagagcga tcgcctgcaa ggccgccagc   660

aagaacagca gtttaaacgc gaactgcgta acctgccgca gcagtgcggc ctgcgtgcgc   720

cgcagcgctg cgatctggaa gtggaaagcg gcggccgtga tcgctatgga tccggaggag   780

gtggaagcgg aggaggtgga tcttattatg gtaaaaggtt gttattacct gattcagtca   840

cggaatatga taagaaactt gtttcgcgca ttcaaattcg agttaatcct ttgccgaaat   900

ttgattcaac cgtgtgggtg acagtccgta aagttcctgc ctcttcggac ttatccgttg   960

ccgccatttc tgctatgttt gcggacggag cctcaccggt actggtttat cagtacgctg   1020

catctggagt ccaagctaac aacaaactgt tgtatgatct ttcggcgatg cgcgctgata 1080

taggcgacat gagaaagtac gccgtcctcg tgtattcaaa agacgatgca ctcgagacag 1140

acgagttagt acttcatgtt gacgtcgagc accaacgtat tcccacatct ggggtgctcc 1200

cagtttgata agctt 1215

<210> 49
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> alpha-synuclein peptide egy

<400> 49

Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala
1 5 10

<210> 50
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> alpha-synuclein petide kne

<400> 50

Lys Asn Glu Glu Gly Ala Pro Gln
1 5

<210> 51
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> alpha-synuclein petide mdv

<400> 51

Met Asp Val Phe Met Lys Gly Leu
1 5

<210> 52
<211> 242
<212> PRT
<213> artificial sequence

<220>
<223> CMV-Ntt830-egy

<400> 52

```
Met Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
1               5                   10                  15


Arg Arg Arg Arg Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala
            20                  25                  30


Asp Ala Asn Phe Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys
        35                  40                  45


Thr Leu Ala Ala Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly
    50                  55                  60


Ser Glu Arg Cys Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys
65                  70                  75                  80


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


Asp Tyr Glu Pro Glu Ala Gly Gly Gly Ser Gly Ser Tyr Tyr Gly Lys
            100                 105                 110


Arg Leu Leu Leu Pro Asp Ser Val Thr Glu Tyr Asp Lys Lys Leu Val
        115                 120                 125


Ser Arg Ile Gln Ile Arg Val Asn Pro Leu Pro Lys Phe Asp Ser Thr
    130                 135                 140


Val Trp Val Thr Val Arg Lys Val Pro Ala Ser Ser Asp Leu Ser Val
145                 150                 155                 160
```

```
Ala Ala Ile Ser Ala Met Phe Ala Asp Gly Ala Ser Pro Val Leu Val
                165                 170                 175


Tyr Gln Tyr Ala Ala Ser Gly Val Gln Ala Asn Asn Lys Leu Leu Tyr
            180                 185                 190


Asp Leu Ser Ala Met Arg Ala Asp Ile Gly Asp Met Arg Lys Tyr Ala
        195                 200                 205


Val Leu Val Tyr Ser Lys Asp Asp Ala Leu Glu Thr Asp Glu Leu Val
    210                 215                 220


Leu His Val Asp Val Glu His Gln Arg Ile Pro Thr Ser Gly Val Leu
225                 230                 235                 240


Pro Val
```

<210> 53
<211> 240
<212> PRT
<213> artificial sequence

<220>
<223> CMV-Ntt830-kne

<400> 53

```
Met Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
1               5                   10                  15


Arg Arg Arg Arg Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala
            20                  25                  30


Asp Ala Asn Phe Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys
        35                  40                  45


Thr Leu Ala Ala Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly
    50                  55                  60
```

```
Ser Glu Arg Cys Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys
65                  70                  75                  80

Pro Pro Lys Ile Asp Arg Gly Ser Gly Gly Gly Ser Lys Asn Glu Glu
                85                  90                  95

Gly Ala Pro Gln Gly Gly Gly Ser Gly Ser Tyr Tyr Gly Lys Arg Leu
            100                 105                 110

Leu Leu Pro Asp Ser Val Thr Glu Tyr Asp Lys Lys Leu Val Ser Arg
        115                 120                 125

Ile Gln Ile Arg Val Asn Pro Leu Pro Lys Phe Asp Ser Thr Val Trp
    130                 135                 140

Val Thr Val Arg Lys Val Pro Ala Ser Ser Asp Leu Ser Val Ala Ala
145                 150                 155                 160

Ile Ser Ala Met Phe Ala Asp Gly Ala Ser Pro Val Leu Val Tyr Gln
                165                 170                 175

Tyr Ala Ala Ser Gly Val Gln Ala Asn Asn Lys Leu Leu Tyr Asp Leu
            180                 185                 190

Ser Ala Met Arg Ala Asp Ile Gly Asp Met Arg Lys Tyr Ala Val Leu
        195                 200                 205

Val Tyr Ser Lys Asp Asp Ala Leu Glu Thr Asp Glu Leu Val Leu His
    210                 215                 220

Val Asp Val Glu His Gln Arg Ile Pro Thr Ser Gly Val Leu Pro Val
225                 230                 235                 240
```

<210> 54
<211> 240
<212> PRT
<213> artificial sequence

<220>
<223> CMV-Ntt830-mdv

<400> 54

```
Met Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
1               5                  10                  15


Arg Arg Arg Arg Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala
            20                  25                  30


Asp Ala Asn Phe Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys
        35                  40                  45


Thr Leu Ala Ala Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly
    50                  55                  60


Ser Glu Arg Cys Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys
65                  70                  75                  80


Pro Pro Lys Ile Asp Arg Gly Ser Gly Gly Gly Ser Met Asp Val Phe
                85                  90                  95


Met Lys Gly Leu Gly Gly Gly Ser Gly Ser Tyr Tyr Gly Lys Arg Leu
            100                 105                 110


Leu Leu Pro Asp Ser Val Thr Glu Tyr Asp Lys Lys Leu Val Ser Arg
        115                 120                 125


Ile Gln Ile Arg Val Asn Pro Leu Pro Lys Phe Asp Ser Thr Val Trp
    130                 135                 140


Val Thr Val Arg Lys Val Pro Ala Ser Ser Asp Leu Ser Val Ala Ala
145                 150                 155                 160


Ile Ser Ala Met Phe Ala Asp Gly Ala Ser Pro Val Leu Val Tyr Gln
                165                 170                 175
```

```
Tyr Ala Ala Ser Gly Val Gln Ala Asn Asn Lys Leu Leu Tyr Asp Leu
            180                 185                 190

Ser Ala Met Arg Ala Asp Ile Gly Asp Met Arg Lys Tyr Ala Val Leu
        195                 200                 205

Val Tyr Ser Lys Asp Asp Ala Leu Glu Thr Asp Glu Leu Val Leu His
    210                 215                 220

Val Asp Val Glu His Gln Arg Ile Pro Thr Ser Gly Val Leu Pro Val
225                 230                 235                 240
```

<210> 55
<211> 738
<212> DNA
<213> artificial sequence

<220>
<223> CMV-Ntt830-egy

<400> 55

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ccatgggcca gtatattaag gccaactcca aatttatcgg gattaccgag cgtcgacgtc       60

gtccgcgtcg tggttcccgc tccgccccct cctccgcgga tgctaacttt agagtcttgt      120

cgcagcagct ttcgcgactt aataagacgt tagcagctgg tcgtccaact attaaccacc      180

caacctttgt agggagtgaa cgctgtaaac ctgggtacac gttcacatct atcaccctaa      240

agccaccaaa aatagaccgt ggatccggtg gcggtagcga ggggtatcag gattatgagc      300

cggaggcggg gggtggttcg ggttcctatt atggtaaaag gttgttatta cctgattcag      360

tcacggaata tgataagaaa cttgtttcgc gcattcaaat tcgagttaat cctttgccga      420

aatttgattc aaccgtgtgg gtgacagtcc gtaaagttcc tgcctcttcg gacttatccg      480

ttgccgccat ttctgctatg tttgcggacg gagcctcacc ggtactggtt tatcagtacg      540

ctgcatctgg agtccaagct aacaacaaac tgttgtatga tctttcggcg atgcgcgctg      600

atataggcga catgagaaag tacgccgtcc tcgtgtattc aaaagacgat gcactcgaga      660

cagacgagtt agtacttcat gttgacgtcg agcaccaacg tattcccaca tctggggtgc      720

tcccagtttg ataagctt                                                    738
```

<210> 56
<211> 731
<212> DNA
<213> artificial sequence

<220>
<223> CMV-Ntt830-kne

<400> 56
ccatgggcca gtatattaag gccaactcca aatttatcgg gattaccgag cgtcgacgtc 60

gtccgcgtcg tggttcccgc tccgcccccc cctccgcgga tgctaacttt agagtcttgt 120

cgcagcagct ttcgcgactt aataagacgt tagcagctgg tcgtccaact attaaccacc 180

caacctttgt agggagtgaa cgctgtaaac ctgggtacac gttcacatct atcaccctaa 240

agccaccaaa aatagaccgt ggatccggtg gcggtagcaa gaatgaggag ggggcgccgc 300

agggggggtgg ttcgggttcc tattatggta aaaggttgtt attacctgat tcagtcacgg 360

aatatgataa gaaacttgtt tcgcgcattc aaattcgagt taatcctttg ccgaaatttg 420

attcaaccgt gtgggtgaca gtccgtaaag ttcctgcctc ttcggactta tccgttgccg 480

ccatttctgc tatgtttgcg gacggagcct caccggtact ggtttatcag tacgctgcat 540

ctggagtcca agctaacaac aaactgttgt atgatctttc ggcgatgcgc gctgatatag 600

gcgacatgag aaagtacgcc gtcctcgtgt attcaaaaga cgatgcactc gagacagacg 660

agttagtact tcatgttgac gtcgagcacc aacgtattcc cacatctggg gtgctcccag 720

tttgataagc t 731

<210> 57
<211> 732
<212> DNA
<213> artificial sequence

<220>
<223> CMV-Ntt830-mdv

<400> 57
ccatgggcca gtatattaag gccaactcca aatttatcgg gattaccgag cgtcgacgtc 60

gtccgcgtcg tggttcccgc tccgcccccc cctccgcgga tgctaacttt agagtcttgt 120

cgcagcagct ttcgcgactt aataagacgt tagcagctgg tcgtccaact attaaccacc 180

caacctttgt agggagtgaa cgctgtaaac ctgggtacac gttcacatct atcaccctaa 240

agccaccaaa aatagaccgt ggatccggtg gcggtagcat ggatgtgttt atgaaggggt 300

tgggggggtgg ttcgggttcc tattatggta aaaggttgtt attacctgat tcagtcacgg 360

aatatgataa gaaacttgtt tcgcgcattc aaattcgagt taatcctttg ccgaaatttg 420

attcaaccgt gtgggtgaca gtccgtaaag ttcctgcctc ttcggactta tccgttgccg 480

ccatttctgc tatgtttgcg gacggagcct caccggtact ggtttatcag tacgctgcat 540

ctggagtcca agctaacaac aaactgttgt atgatctttc ggcgatgcgc gctgatatag 600

gcgacatgag aaagtacgcc gtcctcgtgt attcaaaaga cgatgcactc gagacagacg 660

agttagtact tcatgttgac gtcgagcacc aacgtattcc cacatctggg gtgctcccag 720

tttgataagc tt 732

<210> 58
<211> 71
<212> DNA
<213> artificial sequence

<220>
<223> 1st PCR Forward: CM-egyF

<400> 58
gtggatccgg tggcggtagc gaggggtatc aggattatga gccggaggcg gggggtggtt 60

cgggttccta t 71

<210> 59
<211> 37
<212> DNA
<213> artificial sequence

<220>
<223> Reverse: CMcpR

<400> 59
caaagcttat caaactggga gcaccccaga tgtggga 37

<210> 60
<211> 65
<212> DNA
<213> artificial sequence

<220>
<223> 2nd PCR Forward: CM-kneF

<400> 60
gtggatccgg tggcggtagc aagaatgagg agggggcgcc gcaggggggt ggttcgggtt 60

cctat 65

<210> 61
<211> 65
<212> DNA
<213> artificial sequence

<220>
<223> 3rd PCR Forward: CM-mdvF

<400> 61
gtggatccgg tggcggtagc atggatgtgt ttatgaaggg gttggggggt ggttcgggtt 60

cctat 65

<210> 62
<211> 218
<212> PRT
<213> cucumber mosaic virus

<400> 62

Met Asp Lys Ser Glu Ser Thr Ser Ala Gly Arg Ser Arg Arg Arg Arg
1 5 10 15

Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala Asp Ala Asn Phe
20 25 30

Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys Thr Leu Ala Ala
35 40 45

Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly Ser Glu Arg Cys
50 55 60

```
Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys Pro Pro Lys Ile
65                  70                  75                  80


Asp Arg Gly Ser Tyr Tyr Gly Lys Arg Leu Leu Leu Pro Asp Ser Val
                85                  90                  95


Thr Glu Tyr Asp Lys Lys Leu Val Ser Arg Ile Gln Ile Arg Val Asn
            100                 105                 110


Pro Leu Pro Lys Phe Asp Ser Thr Val Trp Val Thr Val Arg Lys Val
        115                 120                 125


Pro Ala Ser Ser Asp Leu Ser Val Ala Ala Ile Ser Ala Met Phe Ala
    130                 135                 140


Asp Gly Ala Ser Pro Val Leu Val Tyr Gln Tyr Ala Ala Ser Gly Val
145                 150                 155                 160


Gln Ala Asn Asn Lys Leu Leu Tyr Asp Leu Ser Ala Met Arg Ala Asp
                165                 170                 175


Ile Gly Asp Met Arg Lys Tyr Ala Val Leu Val Tyr Ser Lys Asp Asp
            180                 185                 190


Ala Leu Glu Thr Asp Glu Leu Val Leu His Val Asp Val Glu His Gln
        195                 200                 205


Arg Ile Pro Thr Ser Gly Val Leu Pro Val
    210                 215


<210>  63
<211>  27
<212>  PRT
<213>  artificial sequence

<220>
<223>  aa 2-27 of SEQ ID NO:62

<400>  63
```

Asp Lys Ser Glu Ser Thr Ser Ala Gly Arg Ser Arg Arg Arg Arg Pro
1   5   10   15

Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala
            20   25

<210> 64
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> tetanus toxoid epitope tt830

<400> 64

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
1   5   10

<210> 65
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> PADRE

<400> 65

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
1   5   10

<210> 66
<211> 220
<212> PRT
<213> artificial sequence

<220>
<223> CMV-Npadr

<400> 66

Met Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala Arg Arg
1   5   10   15

```
Arg Arg Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala Asp Ala
            20                  25                  30

Asn Phe Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys Thr Leu
        35                  40                  45

Ala Ala Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly Ser Glu
    50                  55                  60

Arg Cys Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys Pro Pro
65                  70                  75                  80

Lys Ile Asp Arg Gly Ser Tyr Tyr Gly Lys Arg Leu Leu Leu Pro Asp
                85                  90                  95

Ser Val Thr Glu Tyr Asp Lys Lys Leu Val Ser Arg Ile Gln Ile Arg
            100                 105                 110

Val Asn Pro Leu Pro Lys Phe Asp Ser Thr Val Trp Val Thr Val Arg
        115                 120                 125

Lys Val Pro Ala Ser Ser Asp Leu Ser Val Ala Ala Ile Ser Ala Met
    130                 135                 140

Phe Ala Asp Gly Ala Ser Pro Val Leu Val Tyr Gln Tyr Ala Ala Ser
145                 150                 155                 160

Gly Val Gln Ala Asn Asn Lys Leu Leu Tyr Asp Leu Ser Ala Met Arg
                165                 170                 175

Ala Asp Ile Gly Asp Met Arg Lys Tyr Ala Val Leu Val Tyr Ser Lys
            180                 185                 190

Asp Asp Ala Leu Glu Thr Asp Glu Leu Val Leu His Val Asp Val Glu
        195                 200                 205

His Gln Arg Ile Pro Thr Ser Gly Val Leu Pro Val
```

210 215 220

<210> 67
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> HA 307-319

<400> 67

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

<210> 68
<211> 20
<212> PRT
<213> artificial sequence

<220>
<223> HBVnc 50-69

<400> 68

Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu
1 5 10 15

Met Thr Leu Ala
20

<210> 69
<211> 21
<212> PRT
<213> artificial sequence

<220>
<223> CS 378-398

<400> 69

Asp Ile Glu Lys Lys Ile Ala Lys Met Glu Lys Ala Ser Ser Val Phe
1 5 10 15

Asn Val Val Asn Ser

20

<210> 70
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> MT 17-31

<400> 70

Tyr Ser Gly Pro Leu Lys Ala Glu Ile Ala Gln Arg Leu Glu Asp Val
1 5 10 15

<210> 71
<211> 21
<212> PRT
<213> artificial sequence

<220>
<223> TT 947-967

<400> 71

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15

Ala Ser His Leu Glu
20

<210> 72
<211> 129
<212> PRT
<213> artificial sequence

<220>
<223> Ara h6

<400> 72

Ala His Ala Ser Ala Met Arg Arg Glu Arg Gly Arg Gln Gly Asp Ser
1 5 10 15

Ser Ser Cys Glu Arg Gln Val Asp Gly Val Asn Leu Lys Pro Cys Glu

20 25 30

Gln His Ile Met Gln Arg Ile Met Gly Glu Gln Glu Gln Tyr Asp Ser
35 40 45

Tyr Asn Phe Gly Ser Thr Arg Ser Ser Asp Gln Gln Gln Arg Cys Cys
50 55 60

Asp Glu Leu Asn Glu Met Glu Asn Thr Gln Arg Cys Met Cys Glu Ala
65 70 75 80

Leu Gln Gln Ile Met Glu Asn Gln Cys Asp Gly Leu Gln Asp Arg Gln
85 90 95

Met Val Gln His Phe Lys Arg Glu Leu Met Asn Leu Pro Gln Gln Cys
100 105 110

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

Cys

<210> 73
<211> 135
<212> PRT
<213> artificial sequence

<220>
<223> Ara h201

<400> 73

Arg Gln Gln Trp Glu Leu Gln Gly Asp Arg Arg Cys Gln Ser Gln Leu
1 5 10 15

Glu Arg Ala Asn Leu Arg Pro Cys Glu Gln His Leu Met Gln Lys Ile
20 25 30

Gln Arg Asp Glu Asp Ser Tyr Glu Arg Asp Pro Tyr Ser Pro Ser Gln

```
        35                  40                  45

Asp Pro Tyr Ser Pro Ser Pro Tyr Asp Arg Arg Gly Ala Gly Ser Ser
    50                  55                  60

Gln His Gln Glu Arg Cys Cys Asn Glu Leu Asn Glu Phe Glu Asn Asn
65                  70                  75                  80

Gln Arg Cys Met Cys Glu Ala Leu Gln Gln Ile Met Glu Asn Gln Ser
                85                  90                  95

Asp Arg Leu Gln Gly Arg Gln Gln Glu Gln Gln Phe Lys Arg Glu Leu
            100                 105                 110

Arg Asn Leu Pro Gln Gln Cys Gly Leu Arg Ala Pro Gln Arg Cys Asp
        115                 120                 125

Leu Asp Val Glu Ser Gly Gly
    130                 135


<210>  74
<211>  514
<212>  PRT
<213>  artificial sequence

<220>
<223>  Cry J2

<400>  74

Met Ala Met Lys Phe Ile Ala Pro Met Ala Phe Val Ala Met Gln Leu
1               5                   10                  15

Ile Ile Met Ala Ala Ala Glu Asp Gln Ser Ala Gln Ile Met Leu Asp
            20                  25                  30

Ser Asp Ile Glu Gln Tyr Leu Arg Ser Asn Arg Ser Leu Arg Lys Val
        35                  40                  45

Glu His Ser Arg His Asp Ala Ile Asn Ile Phe Asn Val Glu Lys Tyr
```

```
    50                  55                  60

Gly Ala Val Gly Asp Gly Lys His Asp Cys Thr Glu Ala Phe Ser Thr
65                  70                  75                  80

Ala Trp Gln Ala Ala Cys Lys Lys Pro Ser Ala Met Leu Leu Val Pro
                85                  90                  95

Gly Asn Lys Lys Phe Val Val Asn Asn Leu Phe Phe Asn Gly Pro Cys
            100                 105                 110

Gln Pro His Phe Thr Phe Lys Val Asp Gly Ile Ile Ala Ala Tyr Gln
        115                 120                 125

Asn Pro Ala Ser Trp Lys Asn Asn Arg Ile Trp Leu Gln Phe Ala Lys
    130                 135                 140

Leu Thr Gly Phe Thr Leu Met Gly Lys Gly Val Ile Asp Gly Gln Gly
145                 150                 155                 160

Lys Gln Trp Trp Ala Gly Gln Cys Lys Trp Val Asn Gly Arg Glu Ile
                165                 170                 175

Cys Asn Asp Arg Asp Arg Pro Thr Ala Ile Lys Phe Asp Phe Ser Thr
            180                 185                 190

Gly Leu Ile Ile Gln Gly Leu Lys Leu Met Asn Ser Pro Glu Phe His
        195                 200                 205

Leu Val Phe Gly Asn Cys Glu Gly Val Lys Ile Ile Gly Ile Ser Ile
    210                 215                 220

Thr Ala Pro Arg Asp Ser Pro Asn Thr Asp Gly Ile Asp Ile Phe Ala
225                 230                 235                 240

Ser Lys Asn Phe His Leu Gln Lys Asn Thr Ile Gly Thr Gly Asp Asp
                245                 250                 255
```

```
Cys Val Ala Ile Gly Thr Gly Ser Ser Asn Ile Val Ile Glu Asp Leu
            260                 265                 270

Ile Cys Gly Pro Gly His Gly Ile Ser Ile Gly Ser Leu Gly Arg Glu
        275                 280                 285

Asn Ser Arg Ala Glu Val Ser Tyr Val His Val Asn Gly Ala Lys Phe
    290                 295                 300

Ile Asp Thr Gln Asn Gly Leu Arg Ile Lys Thr Trp Gln Gly Gly Ser
305                 310                 315                 320

Gly Met Ala Ser His Ile Ile Tyr Glu Asn Val Glu Met Ile Asn Ser
                325                 330                 335

Glu Asn Pro Ile Leu Ile Asn Gln Phe Tyr Cys Thr Ser Ala Ser Ala
            340                 345                 350

Cys Gln Asn Gln Arg Ser Ala Val Gln Ile Gln Asp Val Thr Tyr Lys
        355                 360                 365

Asn Ile Arg Gly Thr Ser Ala Thr Ala Ala Ala Ile Gln Leu Lys Cys
    370                 375                 380

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

Lys Leu Thr Ser Gly Lys Ile Ala Ser Cys Leu Asn Asp Asn Ala Asn
                405                 410                 415

Gly Tyr Phe Ser Gly His Val Ile Pro Ala Cys Lys Asn Leu Ser Pro
            420                 425                 430

Ser Ala Lys Arg Lys Glu Ser Lys Ser His Lys His Pro Lys Thr Val
        435                 440                 445

Met Val Glu Asn Met Gly Ala Tyr Asp Lys Gly Asn Arg Thr Arg Ile
```

```
    450                 455                 460

Leu Leu Gly Ser Arg Pro Pro Asn Cys Thr Asn Lys Cys His Gly Cys
465                 470                 475                 480

Ser Pro Cys Lys Ala Lys Leu Val Ile Val His Arg Ile Met Pro Gln
                485                 490                 495

Glu Tyr Tyr Pro Gln Arg Trp Met Cys Ser Cys His Gly Lys Ile Tyr
            500                 505                 510

His Pro
```

<210> 75
<211> 371
<212> PRT
<213> artificial sequence

<220>
<223> Amb a1

<400> 75

```
Ala Glu Asp Leu Gln Glu Ile Leu Pro Val Asn Glu Thr Arg Arg Leu
1               5                   10                  15

Thr Thr Ser Gly Ala Tyr Asn Ile Ile Asp Gly Cys Trp Arg Gly Lys
            20                  25                  30

Ala Asp Trp Ala Glu Asn Arg Lys Ala Leu Ala Asp Cys Ala Gln Gly
        35                  40                  45

Phe Gly Lys Gly Thr Val Gly Gly Lys Asp Gly Asp Ile Tyr Thr Val
    50                  55                  60

Thr Ser Asp Leu Asp Asp Asp Val Ala Asn Pro Lys Glu Gly Thr Leu
65                  70                  75                  80

Arg Phe Gly Ala Ala Gln Asn Arg Pro Leu Trp Ile Ile Phe Glu Arg
```

```
                85                  90                  95

Asp Met Val Ile Arg Leu Asp Lys Glu Met Val Val Asn Ser Asp Lys
            100                 105                 110

Thr Ile Asp Gly Arg Gly Ala Lys Val Glu Ile Ile Asn Ala Gly Phe
        115                 120                 125

Thr Leu Asn Gly Val Lys Asn Val Ile Ile His Asn Ile Asn Met His
    130                 135                 140

Asp Val Lys Val Asn Pro Gly Gly Leu Ile Lys Ser Asn Asp Gly Pro
145                 150                 155                 160

Ala Ala Pro Arg Ala Gly Ser Asp Gly Asp Ala Ile Ser Ile Ser Gly
                165                 170                 175

Ser Ser Gln Ile Trp Ile Asp His Cys Ser Leu Ser Lys Ser Val Asp
            180                 185                 190

Gly Leu Val Asp Ala Lys Leu Gly Thr Thr Arg Leu Thr Val Ser Asn
        195                 200                 205

Ser Leu Phe Thr Gln His Gln Phe Val Leu Leu Phe Gly Ala Gly Asp
    210                 215                 220

Glu Asn Ile Glu Asp Arg Gly Met Leu Ala Thr Val Ala Phe Asn Thr
225                 230                 235                 240

Phe Thr Asp Asn Val Asp Gln Arg Met Pro Arg Cys Arg His Gly Phe
                245                 250                 255

Phe Gln Val Val Asn Asn Asn Tyr Asp Lys Trp Gly Ser Tyr Ala Ile
            260                 265                 270

Gly Gly Ser Ala Ser Pro Thr Ile Leu Ser Gln Gly Asn Arg Phe Cys
        275                 280                 285
```

```
Ala Pro Asp Glu Arg Ser Lys Lys Asn Val Leu Gly Arg His Gly Glu
    290                 295                 300

Ala Ala Ala Glu Ser Met Lys Trp Asn Trp Arg Thr Asn Lys Asp Val
305                 310                 315                 320

Leu Glu Asn Gly Ala Ile Phe Val Ala Ser Gly Val Asp Pro Val Leu
                325                 330                 335

Thr Pro Glu Gln Ser Ala Gly Met Ile Pro Ala Glu Pro Gly Glu Ser
            340                 345                 350

Ala Leu Ser Leu Thr Ser Ser Ala Gly Val Leu Ser Cys Gln Pro Gly
        355                 360                 365

Ala Pro Cys
    370
```

<210> 76
<211> 70
<212> PRT
<213> Felis domesticus

<400> 76

```
Glu Ile Cys Pro Ala Val Lys Arg Asp Val Asp Leu Phe Leu Thr Gly
1               5                   10                  15

Thr Pro Asp Glu Tyr Val Glu Gln Val Ala Gln Tyr Lys Ala Leu Pro
            20                  25                  30

Val Val Leu Glu Asn Ala Arg Ile Leu Lys Asn Cys Val Asp Ala Lys
        35                  40                  45

Met Thr Glu Glu Asp Lys Glu Asn Ala Leu Ser Leu Leu Asp Lys Ile
    50                  55                  60

Tyr Thr Ser Pro Leu Cys
65                  70
```

<210> 77
<211> 92
<212> PRT
<213> Felis domesticus

<400> 77

Val Lys Met Ala Glu Thr Cys Pro Ile Phe Tyr Asp Val Phe Phe Ala
1 5 10 15

Val Ala Asn Gly Asn Glu Leu Leu Leu Asp Leu Ser Leu Thr Lys Val
20 25 30

Asn Ala Thr Glu Pro Glu Arg Thr Ala Met Lys Lys Ile Gln Asp Cys
35 40 45

Tyr Val Glu Asn Gly Leu Ile Ser Arg Val Leu Asp Gly Leu Val Met
50 55 60

Thr Thr Ile Ser Ser Ser Lys Asp Cys Met Gly Glu Ala Val Gln Asn
65 70 75 80

Thr Val Glu Asp Leu Lys Leu Asn Thr Leu Gly Arg
85 90

<210> 78
<211> 90
<212> PRT
<213> Felis domesticus

<400> 78

Val Lys Met Ala Glu Thr Cys Pro Ile Phe Tyr Asp Val Phe Phe Ala
1 5 10 15

Val Ala Asn Gly Asn Glu Leu Leu Leu Asp Leu Ser Leu Thr Lys Val
20 25 30

Asn Ala Thr Glu Pro Glu Arg Thr Ala Met Lys Lys Ile Gln Asp Cys
35 40 45

```
Tyr Val Glu Asn Gly Leu Ile Ser Arg Val Leu Asp Gly Leu Val Met
    50                  55                  60


Ile Ala Ile Asn Glu Tyr Cys Met Gly Glu Ala Val Gln Asn Thr Val
65                  70                  75                  80


Glu Asp Leu Lys Leu Asn Thr Leu Gly Arg
                85                  90


<210>  79
<211>  78
<212>  PRT
<213>  Felis domesticus

<400>  79

Val Lys Met Ala Glu Thr Cys Pro Ile Phe Tyr Asp Val Phe Phe Ala
1               5                   10                  15


Val Ala Asn Gly Asn Glu Leu Leu Leu Asp Leu Ser Leu Thr Lys Val
            20                  25                  30


Asn Ala Thr Glu Pro Glu Arg Thr Ala Met Lys Lys Ile Gln Asp Cys
        35                  40                  45


Tyr Val Glu Asn Gly Leu Ile Ser Arg Val Leu Asp Gly Leu Val Met
    50                  55                  60


Pro Ser Thr Asn Ile Ala Trp Val Lys Gln Phe Arg Thr Pro
65                  70                  75


<210>  80
<211>  176
<212>  PRT
<213>  artificial sequence

<220>
<223>  rFel-2-G3-1

<400>  80
```

```
Val Lys Met Ala Glu Thr Cys Pro Ile Phe Tyr Asp Val Phe Phe Ala
1               5                  10                  15

Val Ala Asn Gly Asn Glu Leu Leu Leu Asp Leu Ser Leu Thr Lys Val
            20                  25                  30

Asn Ala Thr Glu Pro Glu Arg Thr Ala Met Lys Lys Ile Gln Asp Cys
        35                  40                  45

Tyr Val Glu Asn Gly Leu Ile Ser Arg Val Leu Asp Gly Leu Val Met
    50                  55                  60

Thr Thr Ile Ser Ser Ser Lys Asp Cys Met Gly Glu Ala Val Gln Asn
65                  70                  75                  80

Thr Val Glu Asp Leu Lys Leu Asn Thr Leu Gly Arg Gly Gly Gly Gly
                85                  90                  95

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Cys Glu Ile Cys Pro
            100                 105                 110

Ala Val Lys Arg Asp Val Asp Leu Phe Leu Thr Gly Thr Pro Asp Glu
        115                 120                 125

Tyr Val Glu Gln Val Ala Gln Tyr Lys Ala Leu Pro Val Val Leu Glu
    130                 135                 140

Asn Ala Arg Ile Leu Lys Asn Cys Val Asp Ala Lys Met Thr Glu Glu
145                 150                 155                 160

Asp Lys Glu Asn Ala Leu Ser Val Leu Asp Lys Ile Tyr Thr Ser Pro
                165                 170                 175
```

<210> 81
<211> 176
<212> PRT
<213> artificial sequence

<220>
<223> rFel-1-G3-2

<400> 81

```
Cys Glu Ile Cys Pro Ala Val Lys Arg Asp Val Asp Leu Phe Leu Thr
1               5                   10                  15


Gly Thr Pro Asp Glu Tyr Val Glu Gln Val Ala Gln Tyr Lys Ala Leu
            20                  25                  30


Pro Val Val Leu Glu Asn Ala Arg Ile Leu Lys Asn Cys Val Asp Ala
        35                  40                  45


Lys Met Thr Glu Glu Asp Lys Glu Asn Ala Leu Ser Val Leu Asp Lys
    50                  55                  60


Ile Tyr Thr Ser Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
65                  70                  75                  80


Gly Gly Gly Ser Val Lys Met Ala Glu Thr Cys Pro Ile Phe Tyr Asp
                85                  90                  95


Val Phe Phe Ala Val Ala Asn Gly Asn Glu Leu Leu Leu Asp Leu Ser
            100                 105                 110


Leu Thr Lys Val Asn Ala Thr Glu Pro Glu Arg Thr Ala Met Lys Lys
        115                 120                 125


Ile Gln Asp Cys Tyr Val Glu Asn Gly Leu Ile Ser Arg Val Leu Asp
    130                 135                 140


Gly Leu Val Met Thr Thr Ile Ser Ser Ser Lys Asp Cys Met Gly Glu
145                 150                 155                 160


Ala Val Gln Asn Thr Val Glu Asp Leu Lys Leu Asn Thr Leu Gly Arg
                165                 170                 175
```

<210> 82

<211> 132
<212> PRT
<213> Homo sapiens

<400> 82

Gly Ile Thr Ile Pro Arg Asn Pro Gly Cys Pro Asn Ser Glu Asp Lys
1 5 10 15

Asn Phe Pro Arg Thr Val Met Val Asn Leu Asn Ile His Asn Arg Asn
20 25 30

Thr Asn Thr Asn Pro Lys Arg Ser Ser Asp Tyr Tyr Asn Arg Ser Thr
35 40 45

Ser Pro Trp Asn Leu His Arg Asn Glu Asp Pro Glu Arg Tyr Pro Ser
50 55 60

Val Ile Trp Glu Ala Lys Cys Arg His Leu Gly Cys Ile Asn Ala Asp
65 70 75 80

Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln Gln Glu Ile
85 90 95

Leu Val Leu Arg Arg Glu Pro Pro His Cys Pro Asn Ser Phe Arg Leu
100 105 110

Glu Lys Ile Leu Val Ser Val Gly Cys Thr Cys Val Thr Pro Ile Val
115 120 125

His His Val Ala
130

<210> 83
<211> 115
<212> PRT
<213> Homo sapiens

<400> 83

Ile Pro Thr Glu Ile Pro Thr Ser Ala Leu Val Lys Glu Thr Leu Ala

1 5 10 15

Leu Leu Ser Thr His Arg Thr Leu Leu Ile Ala Asn Glu Thr Leu Arg
20 25 30

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

Phe Gln Gly Ile Gly Thr Leu Glu Ser Gln Thr Val Gln Gly Gly Thr
50 55 60

Val Glu Arg Leu Phe Lys Asn Leu Ser Leu Ile Lys Lys Tyr Ile Asp
65 70 75 80

Gly Gln Lys Lys Lys Cys Gly Glu Glu Arg Arg Arg Val Asn Gln Phe
85 90 95

Leu Asp Tyr Leu Gln Glu Phe Leu Gly Val Met Asn Thr Glu Trp Ile
100 105 110

Ile Glu Ser
115

<210> 84
<211> 114
<212> PRT
<213> artificial sequence

<220>
<223> canine IL-5

<400> 84

Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu Thr Leu Thr Leu
1 5 10 15

Leu Ser Thr His Arg Thr Trp Leu Ile Gly Asp Gly Asn Leu Met Ile
20 25 30

Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile Lys Glu Val Phe

```
        35                  40                  45

Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His Gly Glu Ala Val
    50                  55                  60

Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu His Ile Glu Arg
65                  70                  75                  80

Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val Thr Lys Phe Leu
                85                  90                  95

Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr Pro
            100                 105                 110

Glu Ser
```

<210> 85
<211> 114
<212> PRT
<213> artificial sequence

<220>
<223> feline IL-5

<400> 85

```
Ala Val Gln Ser Pro Met Asn Arg Leu Val Ala Glu Thr Leu Ala Leu
1               5                   10                  15

Leu Ser Thr His Arg Thr Leu Leu Ile Gly Asp Gly Asn Leu Met Ile
            20                  25                  30

Pro Thr Pro Glu His Asn Asn His Gln Leu Cys Ile Glu Glu Val Phe
        35                  40                  45

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

Glu Lys Leu Phe Arg Asn Leu Ser Leu Ile Lys Glu His Ile Asp Arg
```

65 70 75 80

Gln Lys Lys Lys Cys Gly Gly Glu Arg Trp Arg Val Lys Lys Phe Leu
85 90 95

Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr Met
100 105 110

Glu Ser

<210> 86
<211> 129
<212> PRT
<213> Homo sapiens

<400> 86

His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile Lys Thr Leu Asn Ser
1 5 10 15

Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu Thr Val Thr Asp Ile
20 25 30

Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg Ala
35 40 45

Ala Thr Val Leu Arg Gln Phe Tyr Ser His His Glu Lys Asp Thr Arg
50 55 60

Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu Ile
65 70 75 80

Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly Leu
85 90 95

Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn Phe
100 105 110

Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys Tyr Ser Lys Cys Ser
115 120 125

Ser

<210> 87
<211> 109
<212> PRT
<213> artificial sequence

<220>
<223> canine IL-4

<400> 87

Gly His Asn Phe Asn Ile Thr Ile Lys Glu Ile Ile Lys Met Leu Asn
1 5 10 15

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

Val Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile Phe Cys Arg
35 40 45

Ala Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys Ser Asn Arg
50 55 60

Tyr Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala Asn Lys Thr
65 70 75 80

Cys Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp Phe Leu Glu
85 90 95

Arg Leu Lys Val Ile Met Gln Lys Lys Tyr Tyr Arg His
100 105

<210> 88
<211> 109
<212> PRT
<213> artificial sequence

<220>
<223> feline IL-4

<400> 88

Gln Asn Phe Asn Asn Thr Leu Lys Glu Ile Ile Lys Thr Leu Asn Ile
1   5   10   15

Leu Thr Ala Arg Asn Asp Ser Cys Met Glu Leu Thr Val Met Asp Val
            20   25   30

Leu Ala Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile Phe Cys Arg Ala
        35   40   45

Thr Thr Val Leu Arg Gln Ile Tyr Thr His His Asn Cys Ser Thr Lys
    50   55   60

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

Cys Ser Val Asn Glu Val Lys Lys Cys Thr Leu Lys Asp Phe Leu Glu
                85   90   95

Arg Leu Lys Ala Ile Met Gln Lys Lys Tyr Ser Lys His
            100   105

<210> 89
<211> 122
<212> PRT
<213> Homo sapiens

<400> 89

Leu Thr Cys Leu Gly Gly Phe Ala Ser Pro Gly Pro Val Pro Pro Ser
1   5   10   15

Thr Ala Leu Arg Glu Leu Ile Glu Glu Leu Val Asn Ile Thr Gln Asn
            20   25   30

Gln Lys Ala Pro Leu Cys Asn Gly Ser Met Val Trp Ser Ile Asn Leu

```
        35                  40                  45

Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser Leu Ile Asn Val Ser
    50                  55                  60

Gly Cys Ser Ala Ile Glu Lys Thr Gln Arg Met Leu Ser Gly Phe Cys
65                  70                  75                  80

Pro His Lys Val Ser Ala Gly Gln Phe Ser Ser Leu His Val Arg Asp
                85                  90                  95

Thr Lys Ile Glu Val Ala Gln Phe Val Lys Asp Leu Leu Leu His Leu
            100                 105                 110

Lys Lys Leu Phe Arg Glu Gly Arg Phe Asn
        115                 120


<210>  90
<211>  113
<212>  PRT
<213>  artificial sequence

<220>
<223>  cIL13 - mature protein

<400>  90

Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu
1               5                   10                  15

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

Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu
        35                  40                  45

Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln
    50                  55                  60

Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile
```

65 70 75 80

Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val
85 90 95

Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe
100 105 110

Arg

<210> 91
<211> 113
<212> PRT
<213> artificial sequence

<220>
<223> feline IL13 - mature protein

<400> 91

Ser Pro Gly Pro His Ser Arg Arg Glu Leu Lys Glu Leu Ile Glu Glu
1 5 10 15

Leu Val Asn Ile Thr Gln Asn Gln Val Ser Leu Cys Asn Gly Ser Met
20 25 30

Val Trp Ser Val Asn Leu Thr Thr Gly Met Gln Tyr Cys Ala Ala Leu
35 40 45

Glu Ser Leu Ile Asn Val Ser Asp Cys Thr Ala Ile Gln Arg Thr Gln
50 55 60

Arg Met Leu Lys Ala Leu Cys Thr Gln Lys Pro Ser Ala Gly Gln Thr
65 70 75 80

Ala Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val
85 90 95

Lys Asn Leu Leu Asn His Leu Arg Arg Asn Phe Arg His Gly Asn Phe

100 105 110

Lys

<210> 92
<211> 121
<212> PRT
<213> artificial sequence

<220>
<223> equine IL13 - mature protein

<400> 92

Cys Leu Gly Gly Leu Ala Ser Pro Ala Pro Leu Pro Ser Ser Met Ala
1 5 10 15

Leu Lys Glu Leu Ile Lys Glu Leu Val Asn Ile Thr Gln Asn Gln Ala
20 25 30

Pro Leu Cys Asn Gly Ser Met Val Trp Ser Val Asn Leu Thr Ala Asp
35 40 45

Thr Tyr Cys Arg Ala Leu Glu Ser Leu Ser Asn Val Ser Thr Cys Ser
50 55 60

Ala Ile Gln Asn Thr Arg Lys Met Leu Thr Lys Leu Cys Pro His Gln
65 70 75 80

Leu Ser Ala Gly Gln Val Ser Ser Glu Arg Ala Arg Asp Thr Lys Ile
85 90 95

Glu Val Ile Val Leu Val Lys Asp Leu Leu Lys Asn Leu Arg Lys Ile
100 105 110

Phe His Gly Gly Lys His Val Asp Ala
115 120

<210> 93

<211> 159
<212> PRT
<213> Homo sapiens

<400> 93

Ser Ala Pro Phe Ser Phe Leu Ser Asn Val Lys Tyr Asn Phe Met Arg
1 5 10 15

Ile Ile Lys Tyr Glu Phe Ile Leu Asn Asp Ala Leu Asn Gln Ser Ile
20 25 30

Ile Arg Ala Asn Asp Gln Tyr Leu Thr Ala Ala Ala Leu His Asn Leu
35 40 45

Asp Glu Ala Val Lys Phe Asp Met Gly Ala Tyr Lys Ser Ser Lys Asp
50 55 60

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

Val Thr Ala Gln Asp Glu Asp Gln Pro Val Leu Leu Lys Glu Met Pro
85 90 95

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

Trp Glu Thr His Gly Thr Lys Asn Tyr Phe Thr Ser Val Ala His Pro
115 120 125

Asn Leu Phe Ile Ala Thr Lys Gln Asp Tyr Trp Val Cys Leu Ala Gly
130 135 140

Gly Pro Pro Ser Ile Thr Asp Phe Gln Ile Leu Glu Asn Gln Ala
145 150 155

<210> 94
<211> 157
<212> PRT
<213> artificial sequence

<220>
<223> canine IL-1alpha

<400> 94

Ser Val Ala Tyr Asn Phe His Asn Asn Glu Lys Tyr Asn Tyr Ile Arg
1   5   10   15

Ile Ile Lys Ser Gln Phe Ile Leu Asn Asp Asn Leu Asn Gln Ser Ile
            20   25   30

Val Arg Gln Thr Gly Gly Asn Tyr Leu Met Thr Ala Ala Leu Gln Asn
        35   40   45

Leu Asp Asp Ala Val Lys Phe Asp Met Gly Ala Tyr Thr Ser Glu Asp
    50   55   60

Ser Lys Leu Pro Val Thr Leu Arg Ile Ser Lys Thr Arg Leu Phe Val
65   70   75   80

Ser Ala Gln Asn Glu Asp Glu Pro Val Leu Leu Lys Glu Met Pro Glu
                85   90   95

Thr Pro Lys Thr Ile Arg Asp Glu Thr Asn Leu Leu Phe Phe Trp Glu
            100   105   110

Arg His Gly Ser Lys His Tyr Phe Lys Ser Val Ala Gln Pro Lys Leu
        115   120   125

Phe Ile Ala Thr Gln Glu Arg Lys Leu Val His Met Ala Arg Gly Gln
    130   135   140

Pro Ser Ile Thr Asp Phe Arg Leu Leu Glu Thr Gln Pro
145   150   155

<210> 95
<211> 158
<212> PRT
<213> artificial sequence

<220>
<223> feline IL-1alpha

<400> 95

Ser Val Ala Pro Asn Phe Tyr Ser Ser Glu Lys Tyr Asn Tyr Gln Lys
1   5   10   15

Ile Ile Lys Ser Gln Phe Ile Leu Asn Asp Asn Leu Ser Gln Ser Val
            20   25   30

Ile Arg Lys Ala Gly Gly Lys Tyr Leu Ala Ala Ala Ala Leu Gln Asn
        35   40   45

Leu Asp Asp Ala Val Lys Phe Asp Met Gly Ala Tyr Thr Ser Lys Glu
    50   55   60

Asp Ser Lys Leu Pro Val Thr Leu Arg Ile Ser Lys Thr Arg Leu Phe
65   70   75   80

Val Ser Ala Gln Asn Glu Asp Glu Pro Val Leu Leu Lys Glu Met Pro
                85   90   95

Glu Thr Pro Lys Thr Ile Arg Asp Glu Thr Asn Leu Leu Phe Phe Trp
            100   105   110

Glu Arg His Gly Ser Lys Asn Tyr Phe Lys Ser Val Ala His Pro Lys
        115   120   125

Leu Phe Ile Ala Thr Gln Glu Glu Gln Leu Val His Met Ala Arg Gly
    130   135   140

Leu Pro Ser Val Thr Asp Phe Gln Ile Leu Glu Thr Gln Ser
145   150   155

<210> 96
<211> 158
<212> PRT
<213> artificial sequence

<220>
<223> equine IL-1alpha

<400> 96

Ser Val His Tyr Asn Phe Gln Ser Asn Thr Lys Tyr Asn Phe Met Arg
1   5   10   15

Ile Val Asn His Gln Cys Thr Leu Asn Asp Ala Leu Asn Gln Ser Val
            20   25   30

Ile Arg Asp Thr Ser Gly Gln Tyr Leu Ala Thr Ala Ala Leu Asn Asn
        35   40   45

Leu Asp Asp Ala Val Lys Phe Asp Met Gly Ala Tyr Thr Ser Glu Glu
    50   55   60

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

Val Ser Ala Gln Asn Glu Asp Glu Pro Val Leu Leu Lys Glu Met Pro
                85   90   95

Asp Thr Pro Lys Thr Ile Lys Asp Glu Thr Asn Leu Leu Phe Phe Trp
            100   105   110

Glu Arg His Gly Ser Lys Asn Tyr Phe Lys Ser Val Ala His Pro Lys
        115   120   125

Leu Phe Ile Ala Thr Lys Gln Gly Lys Leu Val His Met Ala Arg Gly
    130   135   140

Gln Pro Ser Ile Thr Asp Phe Gln Ile Leu Asp Asn Gln Phe
145   150   155

<210> 97
<211> 175
<212> PRT
<213> Homo sapiens

<400> 97

```
Phe Gly Ile Ser Gly Val Gln Lys Tyr Thr Arg Ala Leu His Asp Ser
1               5                   10                  15


Ser Ile Thr Gly Ile Ser Pro Ile Thr Glu Tyr Leu Ala Ser Leu Ser
            20                  25                  30


Thr Tyr Asn Asp Gln Ser Ile Thr Phe Ala Leu Glu Asp Glu Ser Tyr
        35                  40                  45


Glu Ile Tyr Val Glu Asp Leu Lys Lys Asp Glu Lys Lys Asp Lys Val
    50                  55                  60


Leu Leu Ser Tyr Tyr Glu Ser Gln His Pro Ser Asn Glu Ser Gly Asp
65                  70                  75                  80


Gly Val Asp Gly Lys Met Leu Met Val Thr Leu Ser Pro Thr Lys Asp
                85                  90                  95


Phe Trp Leu His Ala Asn Asn Lys Glu His Ser Val Glu Leu His Lys
            100                 105                 110


Cys Glu Lys Pro Leu Pro Asp Gln Ala Phe Phe Val Leu His Asn Met
        115                 120                 125


His Ser Asn Cys Val Ser Phe Glu Cys Lys Thr Asp Pro Gly Val Phe
    130                 135                 140


Ile Gly Val Lys Asp Asn His Leu Ala Leu Ile Lys Val Asp Ser Ser
145                 150                 155                 160


Glu Asn Leu Cys Thr Glu Asn Ile Leu Phe Lys Leu Ser Glu Thr
                165                 170                 175
```

<210> 98
<211> 169
<212> PRT

<213> artificial sequence

<220>
<223> canine IL-33

<400> 98

Phe Met Gly Thr Ser Leu Phe Glu Phe Leu Met Thr Ser Phe Ser Leu
1 5 10 15

Val Thr Glu Tyr Ser Ala Ser Leu Ser Thr Tyr Asn Asp Gln Ser Ile
20 25 30

Thr Phe Val Phe Glu Asp Gly Ser Tyr Glu Ile Tyr Val Glu Asp Leu
35 40 45

Arg Lys Gly Gln Glu Lys Asp Lys Val Leu Phe Arg Tyr Tyr Asp Ser
50 55 60

Gln Ser Pro Ser His Glu Thr Gly Asp Asp Val Asp Gly Gln Thr Leu
65 70 75 80

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

Asn Asn Glu Glu His Ser Val Glu Leu Gln Lys Cys Glu Asn Gln Leu
100 105 110

Pro Asp Gln Ala Phe Phe Leu Leu His Arg Lys Ser Ser Glu Cys Val
115 120 125

Ser Phe Glu Cys Lys Asn Asn Pro Gly Val Phe Ile Gly Val Lys Asp
130 135 140

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

Ile Glu Lys Thr Ile Phe Lys Leu Ser
165

<210> 99
<211> 170
<212> PRT
<213> artificial sequence

<220>
<223> feline IL-33

<400> 99

```
Phe Gly Val Pro Met Val Gln Lys Cys Phe Gly Thr Thr Asp Val Pro
1               5                   10                  15


Ser Ile Gln Glu Tyr Ser Ala Ser Leu Ser Thr Tyr Asn Asp Gln Ser
            20                  25                  30


Ile Thr Phe Val Phe Glu Asp Gly Ser Tyr Glu Ile Tyr Val Glu Asp
        35                  40                  45


Leu Gly Lys Asp Gln Glu Lys Asp Lys Val Leu Phe Arg Tyr Tyr Asp
    50                  55                  60


Phe Gln Ser Pro Ser Arg Glu Thr Gly Asp Ala Asp Asp Gly His Thr
65                  70                  75                  80


Leu Leu Val Asn Leu Ser Pro Thr Lys Asp Lys Asp Phe Leu Leu His
                85                  90                  95


Ala Asn Asn Lys Glu His Ser Val Glu Leu Gln Lys Cys Lys Lys Pro
            100                 105                 110


Leu Pro Asp Gln Ala Phe Phe Arg Leu His Arg Lys Ser Ser Lys Cys
        115                 120                 125


Val Ser Phe Glu Cys Lys Asn Asp Pro Gly Val Phe Ile Gly Val Lys
    130                 135                 140


Asp Asn His Leu Ala Leu Ile Lys Val Glu Asp Gln Thr Glu Tyr Phe
145                 150                 155                 160
```

Ser Thr Glu Asn Ile Ile Phe Lys Leu Ser
165 170

<210> 100
<211> 170
<212> PRT
<213> artificial sequence

<220>
<223> equine IL-33

<400> 100

Phe Asp Val Pro Met Ile Gln Arg Cys Ala Arg Ser Thr Ala Gly Pro
1 5 10 15

Ile Phe Glu Glu Asp Phe Ala Ser Leu Ser Thr Tyr Asn Asp Gln Ser
20 25 30

Ile Ser Phe Val Ile Glu Asp Gly Ser Tyr Glu Ile Tyr Ile Glu Asp
35 40 45

Leu Ser Gly Gln Gln Glu Lys Asp Pro Val Leu Phe Arg Cys Tyr Pro
50 55 60

Ser Gln Cys Ser Ser Ser Glu Thr Ala Gly Gly Ala Asp Gly Gln Lys
65 70 75 80

Leu Met Val Asn Leu Ser Pro Lys Lys Tyr Lys Asp Phe Leu Leu His
85 90 95

Ala Asn Asn Lys Glu His Ser Val Glu Leu Gln Lys Cys Glu Asn Pro
100 105 110

Phe Pro Asp Gln Ala Phe Phe Leu Met His Lys Thr Ser Ser Arg Cys
115 120 125

Val Ser Phe Glu Cys Lys Asn Asn Pro Gly Val Phe Ile Gly Val Lys
130 135 140

```
Asp Lys His Leu Ala Leu Ile Lys Val Gly Glu Gln Thr Glu Pro Ser
145                 150                 155                 160


Ser Arg Gln Asn Ile Ile Phe Lys Leu Ser
                165                 170


<210>  101
<211>  145
<212>  PRT
<213>  Homo sapiens

<400>  101

Tyr Ser His Trp Pro Ser Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser
1               5                   10                  15


Glu Glu Leu Leu Arg Trp Ser Thr Val Pro Val Pro Pro Leu Glu Pro
            20                  25                  30


Ala Arg Pro Asn Arg His Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly
        35                  40                  45


Pro Leu Asn Ser Arg Ala Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg
    50                  55                  60


Asp Leu Asn Arg Leu Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys
65                  70                  75                  80


Pro His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Arg Gly
                85                  90                  95


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


Cys His Gly Glu Lys Gly Thr His Lys Gly Tyr Cys Leu Glu Arg Arg
        115                 120                 125


Leu Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg Val Met
    130                 135                 140
```

Gly
145

<210> 102
<211> 147
<212> PRT
<213> artificial sequence

<220>
<223> canine IL-25

<400> 102

Lys Asp Cys Thr His Trp Pro Asn Cys Cys Pro Ser Lys Arg Gln Asp
1   5   10   15

Pro Thr His Glu Trp Leu Lys Arg Asp Thr Val Leu Lys Phe Pro Gly
            20   25   30

Glu Thr Thr Ser Leu Thr His His Pro Glu Ser Cys Lys Ala Ser Glu
        35   40   45

Asp Gly Pro Leu Asn Ser Arg Ser Ile Ser Pro Trp Lys Tyr Glu Leu
    50   55   60

Asp Arg Asp Leu Asn Arg Leu Pro Gln Asp Leu Tyr His Ala Arg Cys
65   70   75   80

Leu Cys Gln His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro
                85   90   95

Leu Gly Asn Ser Glu Leu Leu Tyr His Asn Gln Thr Val Phe Tyr Arg
            100   105   110

Arg Pro Cys Pro Gly Glu Gln Gly Ala Pro Asp Gly Tyr Cys Leu Glu
        115   120   125

Gln Arg Leu Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg
    130   135   140

Val Met Ala
145

<210> 103
<211> 147
<212> PRT
<213> artificial sequence

<220>
<223> feline IL-25

<400> 103

Lys Asp Cys Ile His Trp Ser Ser Cys Cys Pro Ser Lys Gly Gln Asn
1 5 10 15

Pro Thr His Glu Trp Leu Thr Glu Asn Thr Val Leu Met Thr Pro Pro
20 25 30

Glu Ser Ala Ser Leu Ile His Ser Leu Glu Ser Cys Arg Ala Ser Glu
35 40 45

Asp Gly Pro Leu Asn Ser Arg Ser Ile Ser Pro Trp Arg Tyr Glu Leu
50 55 60

Asp Arg Asp Leu Asn Arg Leu Pro Gln Asp Leu Tyr His Ala Arg Cys
65 70 75 80

Leu Cys Pro His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro
85 90 95

Leu Gly Asn Ser Glu Leu Leu Tyr His Asn Gln Thr Val Phe Tyr Arg
100 105 110

Arg Pro Cys Pro Gly Glu Gln Gly Thr Arg Asp Gly Tyr Cys Leu Glu
115 120 125

Gln Arg Leu Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg
130 135 140

Val Met Ala
145

<210> 104
<211> 147
<212> PRT
<213> artificial sequence

<220>
<223> equine IL-25

<400> 104

Lys Glu Cys Thr His Trp Pro Ser Cys Cys Pro Lys Lys Gly Gln Asp
1 5 10 15

Pro Ile Glu Glu Trp Leu Lys Trp Ser Thr Ala His Val Pro Pro Pro
20 25 30

Glu Thr Ala Asn Leu Ala His His Pro Glu Ser Cys Arg Ala Ser Glu
35 40 45

Asp Gly Pro Leu Asn Ser Arg Ser Ile Ser Pro Trp Arg Tyr Glu Leu
50 55 60

Asp Arg Asp Leu Asn Arg Leu Pro Gln Asp Leu Tyr His Ala Arg Cys
65 70 75 80

Leu Cys Pro His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro
85 90 95

Leu Gly Asn Ser Glu Leu Leu Tyr His Asn Gln Thr Val Phe Tyr Arg
100 105 110

Arg Pro Cys Pro Gly Lys Arg Gly Ala His Asp Gly Tyr Cys Leu Glu
115 120 125

Arg Arg Leu Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg
130 135 140

Val Met Ala
145

<210> 105
<211> 153
<212> PRT
<213> Homo sapiens

<400> 105

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

Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala Leu His Leu Gln
            20   25   30

Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met Ser Phe Val Gln
        35   40   45

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

Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp Lys Pro Thr Leu
65   70   75   80

Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys Lys Lys Met Glu
                85   90   95

Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn Lys Leu Glu Phe
            100   105   110

Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr Ser Gln Ala Glu
        115   120   125

Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly Gln Asp Ile Thr
    130   135   140

Asp Phe Thr Met Gln Phe Val Ser Ser

145 150

<210> 106
<211> 141
<212> PRT
<213> Homo sapiens

<400> 106

Ser His Thr Leu Pro Val Arg Leu Leu Arg Pro Ser Asp Asp Val Gln
1 5 10 15

Lys Ile Val Glu Glu Leu Gln Ser Leu Ser Lys Met Leu Leu Lys Asp
20 25 30

Val Glu Glu Glu Lys Gly Val Leu Val Ser Gln Asn Tyr Thr Leu Pro
35 40 45

Cys Leu Ser Pro Asp Ala Gln Pro Pro Asn Asn Ile His Ser Pro Ala
50 55 60

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

Ile Asp Glu Ile Ile Glu His Leu Asp Lys Leu Ile Phe Gln Asp Ala
85 90 95

Pro Glu Thr Asn Ile Ser Val Pro Thr Asp Thr His Glu Cys Lys Arg
100 105 110

Phe Ile Leu Thr Ile Ser Gln Gln Phe Ser Glu Cys Met Asp Leu Ala
115 120 125

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

<210> 107
<211> 136
<212> PRT
<213> artificial sequence

<220>
<223> canine IL-31

<400> 107

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

Ile Ile Leu Glu Leu Gln Pro Leu Ser Arg Gly Leu Leu Glu Asp Tyr
            20   25   30

Gln Lys Lys Glu Thr Gly Val Pro Glu Ser Asn Arg Thr Leu Leu Leu
        35   40   45

Cys Leu Thr Ser Asp Ser Gln Pro Pro Arg Leu Asn Ser Ser Ala Ile
    50   55   60

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

Asp Lys Ile Ile Glu Gln Leu Asp Lys Leu Lys Phe Gln His Glu Pro
                85   90   95

Glu Thr Glu Ile Ser Val Pro Ala Asp Thr Phe Glu Cys Lys Ser Phe
            100   105   110

Ile Leu Thr Ile Leu Gln Gln Phe Ser Ala Cys Leu Glu Ser Val Phe
        115   120   125

Lys Ser Leu Asn Ser Gly Pro Gln
    130   135

<210> 108
<211> 136
<212> PRT
<213> artificial sequence

<220>
<223> feline IL-31

<400> 108

Ser His Met Ala Pro Ala His Arg Leu Gln Pro Ser Asp Val Arg Lys
1 5 10 15

Ile Ile Leu Glu Leu Arg Pro Met Ser Lys Gly Leu Leu Gln Asp Tyr
20 25 30

Leu Lys Lys Glu Ile Gly Leu Pro Glu Ser Asn His Ser Ser Leu Pro
35 40 45

Cys Leu Ser Ser Asp Ser Gln Leu Pro His Ile Asn Gly Ser Ala Ile
50 55 60

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

Asp Lys Ile Ile Glu Gln Leu Asp Lys Leu Lys Phe Gln Arg Glu Pro
85 90 95

Glu Ala Lys Val Ser Met Pro Ala Asp Asn Phe Glu Arg Lys Asn Phe
100 105 110

Ile Leu Ala Val Leu Gln Gln Phe Ser Ala Cys Leu Glu His Val Leu
115 120 125

Gln Ser Leu Asn Ser Gly Pro Gln
130 135

<210> 109
<211> 130
<212> PRT
<213> artificial sequence

<220>
<223> equine IL-31

<400> 109

Ser His Thr Gly Pro Ile Tyr Gln Leu Gln Pro Lys Glu Ile Gln Ala
1 5 10 15

```
Ile Ile Val Glu Leu Gln Asn Leu Ser Lys Lys Leu Leu Asp Asp Tyr
            20                  25                  30

Leu Asn Lys Glu Lys Gly Val Gln Lys Phe Asp Ser Asp Leu Pro Ser
        35                  40                  45

Cys Phe Thr Ser Asp Ser Gln Ala Pro Gly Asn Ile Asn Ser Ser Ala
    50                  55                  60

Ile Leu Pro Tyr Phe Lys Ala Ile Ser Pro Ser Leu Asn Asn Asp Lys
65                  70                  75                  80

Ser Leu Tyr Ile Ile Glu Gln Leu Asp Lys Leu Asn Phe Gln Asn Ala
                85                  90                  95

Pro Glu Thr Glu Val Ser Met Pro Thr Asp Asn Phe Glu Arg Lys Arg
            100                 105                 110

Phe Ile Leu Thr Ile Leu Arg Trp Phe Ser Asn Cys Leu Glu His Arg
        115                 120                 125

Ala Gln
    130
```

<210> 110
<211> 131
<212> PRT
<213> Homo sapiens

<400> 110

```
Tyr Asp Phe Thr Asn Cys Asp Phe Glu Lys Ile Lys Ala Ala Tyr Leu
1               5                   10                  15

Ser Thr Ile Ser Lys Asp Leu Ile Thr Tyr Met Ser Gly Thr Lys Ser
            20                  25                  30

Thr Glu Phe Asn Asn Thr Val Ser Cys Ser Asn Arg Pro His Cys Leu
```

```
        35                  40                  45

Thr Glu Ile Gln Ser Leu Thr Phe Asn Pro Thr Ala Gly Cys Ala Ser
    50                  55                  60

Leu Ala Lys Glu Met Phe Ala Met Lys Thr Lys Ala Ala Leu Ala Ile
65                  70                  75                  80

Trp Cys Pro Gly Tyr Ser Glu Thr Gln Ile Asn Ala Thr Gln Ala Met
                85                  90                  95

Lys Lys Arg Arg Lys Arg Lys Val Thr Thr Asn Lys Cys Leu Glu Gln
            100                 105                 110

Val Ser Gln Leu Gln Gly Leu Trp Arg Arg Phe Asn Arg Pro Leu Leu
        115                 120                 125

Lys Gln Gln
    130
```

<210> 111
<211> 127
<212> PRT
<213> artificial sequence

<220>
<223> canine TLSP

<400> 111

```
Tyr Asn Phe Ile Asp Cys Asp Phe Glu Lys Ile Arg Trp Lys Tyr Gln
1               5                   10                  15

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

Thr Glu Phe Ser His Pro Val Tyr Cys Ala Asp Pro Pro Asp Cys Leu
        35                  40                  45

Ala Arg Ile Glu Arg Leu Thr Leu His Arg Ile Arg Gly Cys Ala Ser
```

50 55 60

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

Glu Cys Pro Gly Tyr Ala Ala Ala Pro Ile Asn Asn Thr Gln Ala Lys
85 90 95

Lys Lys Arg Lys Lys Arg Gly Val Thr Thr Asn Lys Cys Arg Glu Gln
100 105 110

Val Ala His Leu Ile Gly Leu Trp Arg Arg Phe Ser Arg Ile Ser
115 120 125

<210> 112
<211> 127
<212> PRT
<213> artificial sequence

<220>
<223> feline TLSP

<400> 112

Tyr Asn Phe Thr Asp Cys Asp Phe Gly Lys Ile Arg Lys Lys Tyr Gln
1 5 10 15

Glu Val Ile Tyr Gln Ala Leu Asn Lys Tyr Met Asn Gly Val Lys Ser
20 25 30

Thr Glu Phe Asn Asn Tyr Ile Tyr Cys Glu Asp Pro Pro Asp Cys Leu
35 40 45

Ala Lys Ile Asp Leu Ile Thr Phe Tyr Pro Thr His Gly Cys Thr Thr
50 55 60

Leu Ala Lys Glu Ile Phe Ala Ile Arg Thr Asn Ala Thr Leu Thr Leu
65 70 75 80

Gln Cys Pro Gly Tyr Ser Gly Thr Gln Ile Asn Asn Thr Gln Ala Lys

```
                85                  90                  95

Lys Lys Arg Lys Lys Arg Gln Val Thr Thr Asn Lys Cys Arg Glu Gln
            100                 105                 110

Val Ser His Leu Met Glu Leu Trp Arg Arg Phe Ser Arg Ile Ser
        115                 120                 125
```

<210> 113
<211> 125
<212> PRT
<213> artificial sequence

<220>
<223> equine TLSP

<400> 113

```
Tyr Asp Phe Thr Asp Cys Asn Phe Ala Lys Ile Glu Glu Glu Tyr Gln
1               5                   10                  15

Asn Val Ile Phe Leu Ala Leu Lys Glu Tyr Met Asn Gly Ile Lys Ser
            20                  25                  30

Thr Gln Phe Asn His Thr Val Tyr Cys Gly Asp Arg Pro Ser Cys Leu
        35                  40                  45

Thr Glu Ile Glu Arg Leu Thr Phe Lys Ser Ser Gln Cys Leu Ser Leu
    50                  55                  60

Ala Lys Lys Ile Val Thr Ala Thr Asn Ala Thr Leu Asn Ser His Cys
65                  70                  75                  80

Pro Gly His Ser Gly Ile Gln Ile Asn Asn Thr Gln Ala Met Lys Lys
                85                  90                  95

Arg Lys Lys Arg Glu Val Thr Thr Asn Lys Cys Leu Lys Gln Val Ser
            100                 105                 110

Asn Leu Ile Glu Leu Trp Arg Tyr Phe Ser Arg Ser Gln
```

115 120 125

<210> 114
<211> 42
<212> PRT
<213> Homo sapiens

<400> 114

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

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala
35 40

<210> 115
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> Abeta 2-6

<400> 115

Ala Glu Phe Arg His
1 5

<210> 116
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> Abeta 3-7

<400> 116

Glu Phe Arg His Asp
1 5

<210> 117
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> alpha-syn kne*

<400> 117

Lys Asn Glu Glu Gly Ala Pro
1   5

<210> 118
<211> 95
<212> PRT
<213> artificial sequence

<220>
<223> cow myostatin

<400> 118

Cys Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu Ala Phe Gly Trp Asp
1   5   10   15

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

Cys Glu Phe Val Phe Leu Gln Lys Tyr Pro His Thr His Leu Val His
        35   40   45

Gln Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys Cys Thr Pro Thr Lys
    50   55   60

Met Ser Pro Ile Asn Met Leu Tyr Phe Asn Gly Glu Gly Gln Ile Ile
65   70   75   80

Tyr Gly Lys Ile Pro Ala Met Val Val Asp Arg Cys Gly Cys Ser
                85   90   95

<210> 119
<211> 165

<212> PRT
<213> artificial sequence

<220>
<223> plasmodium vivax

<400> 119

```
Asp Arg Ala Asp Gly Gln Pro Ala Gly Asp Arg Ala Asp Gly Gln Pro
1               5                   10                  15


Ala Gly Asp Arg Ala Ala Gly Gln Pro Ala Gly Asp Arg Ala Ala Gly
            20                  25                  30


Gln Pro Ala Gly Asp Arg Ala Asp Gly Gln Pro Ala Gly Asp Arg Ala
        35                  40                  45


Asp Gly Gln Pro Ala Gly Ala Pro Gly Ala Asn Gln Glu Gly Gly Ala
    50                  55                  60


Ala Ala Pro Gly Ala Asn Gln Glu Gly Gly Ala Ala Ala Pro Gly Ala
65                  70                  75                  80


Asn Gln Glu Gly Gly Ala Ala Ala Pro Gly Ala Asn Gln Glu Gly Gly
                85                  90                  95


Ala Ala Ala Pro Gly Ala Asn Gln Glu Gly Gly Ala Ala Ala Pro Gly
            100                 105                 110


Ala Asn Gln Glu Gly Gly Ala Ala Ala Asn Gly Ala Gly Asn Gln Pro
        115                 120                 125


Gly Ala Asn Gly Ala Gly Asn Gln Pro Gly Ala Asn Gly Ala Gly Asn
    130                 135                 140


Gln Pro Gly Ala Asn Gly Ala Gly Asn Gln Pro Gly Ala Asn Gly Ala
145                 150                 155                 160


Gly Asn Gln Pro Gly
                165
```

<210> 120
<211> 24
<212> PRT
<213> artificial sequence

<220>
<223> Influenza M2 peptide

<400> 120

Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu Trp Gly Cys
1 5 10 15

Arg Cys Asn Asp Ser Ser Asp Gly
20

<210> 121
<211> 42
<212> DNA
<213> artificial sequence

<220>
<223> Reverse Cmded-BamR

<400> 121
ggatccatcc tcgtcacctc ctccagatcc acctccacca ct 42

<210> 122
<211> 42
<212> DNA
<213> artificial sequence

<220>
<223> Forward CMded-BamF

<400> 122
ggatcccaga ctagtgacga ggatggagga ggtggaagcg ga 42

<210> 123
<211> 31
<212> DNA
<213> artificial sequence

<220>

<223> Forward I5-BamF

<400> 123
ggatccattg cagttcagag cccgatgaat c 31

<210> 124
<211> 27
<212> DNA
<213> artificial sequence

<220>
<223> Reverse I5-SpeR

<400> 124
actagtgctt tccatggtcc attcggt 27

<210> 125
<211> 115
<212> PRT
<213> Felis catus

<400> 125

Ile Ala Val Gln Ser Pro Met Asn Arg Leu Val Ala Glu Thr Leu Ala
1 5 10 15

Leu Leu Ser Thr His Arg Thr Leu Leu Ile Gly Asp Gly Asn Leu Met
20 25 30

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

Phe Gln Gly Ile Asp Thr Leu Lys Asn Arg Thr Val Pro Gly Asp Ala
50 55 60

Val Glu Lys Leu Phe Arg Asn Leu Ser Leu Ile Lys Glu His Ile Asp
65 70 75 80

Arg Gln Lys Lys Lys Cys Gly Gly Glu Arg Trp Arg Val Lys Lys Phe
85 90 95

Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr

100 105 110

Met Glu Ser
115

<210> 126
<211> 20
<212> PRT
<213> artificial sequence

<220>
<223> 18 aa linker GSED

<400> 126

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Asp
1 5 10 15

Glu Asp Gly Ser
20

<210> 127
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> 15 aa linker GSED

<400> 127

Thr Ser Asp Glu Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 128
<211> 370
<212> PRT
<213> artificial sequence

<220>
<223> CMV-Ntt830-fel-IL-5

<400> 128

Met Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu

```
1               5                   10                  15

Arg Arg Arg Arg Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala
            20                  25                  30

Asp Ala Asn Phe Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys
        35                  40                  45

Thr Leu Ala Ala Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly
    50                  55                  60

Ser Glu Arg Cys Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys
65                  70                  75                  80

Pro Pro Lys Ile Asp Arg Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
                85                  90                  95

Gly Ser Gly Gly Gly Asp Glu Asp Gly Ser Ile Ala Val Gln Ser Pro
            100                 105                 110

Met Asn Arg Leu Val Ala Glu Thr Leu Ala Leu Leu Ser Thr His Arg
        115                 120                 125

Thr Leu Leu Ile Gly Asp Gly Asn Leu Met Ile Pro Thr Pro Glu His
    130                 135                 140

Asn Asn His Gln Leu Cys Ile Glu Glu Val Phe Gln Gly Ile Asp Thr
145                 150                 155                 160

Leu Lys Asn Arg Thr Val Pro Gly Asp Ala Val Glu Lys Leu Phe Arg
                165                 170                 175

Asn Leu Ser Leu Ile Lys Glu His Ile Asp Arg Gln Lys Lys Lys Cys
            180                 185                 190

Gly Gly Glu Arg Trp Arg Val Lys Lys Phe Leu Asp Tyr Leu Gln Val
        195                 200                 205
```

```
Phe Leu Gly Val Ile Asn Thr Glu Trp Thr Met Glu Ser Thr Ser Asp
    210                 215                 220

Glu Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Tyr Tyr Gly Lys
225                 230                 235                 240

Arg Leu Leu Leu Pro Asp Ser Val Thr Glu Tyr Asp Lys Lys Leu Val
                245                 250                 255

Ser Arg Ile Gln Ile Arg Val Asn Pro Leu Pro Lys Phe Asp Ser Thr
            260                 265                 270

Val Trp Val Thr Val Arg Lys Val Pro Ala Ser Ser Asp Leu Ser Val
        275                 280                 285

Ala Ala Ile Ser Ala Met Phe Ala Asp Gly Ala Ser Pro Val Leu Val
    290                 295                 300

Tyr Gln Tyr Ala Ala Ser Gly Val Gln Ala Asn Asn Lys Leu Leu Tyr
305                 310                 315                 320

Asp Leu Ser Ala Met Arg Ala Asp Ile Gly Asp Met Arg Lys Tyr Ala
                325                 330                 335

Val Leu Val Tyr Ser Lys Asp Asp Ala Leu Glu Thr Asp Glu Leu Val
            340                 345                 350

Leu His Val Asp Val Glu His Gln Arg Ile Pro Thr Ser Gly Val Leu
        355                 360                 365

Pro Val
    370
```

<210> 129
<211> 1122
<212> DNA
<213> artificial sequence

<220>
<223> CMV-Ntt830-fel-IL-5

<400> 129
ccatgggcca gtatattaag gccaactcca aatttatcgg gattaccgag cgtcgacgtc 60

gtccgcgtcg tggttcccgc tccgccccct cctccgcgga tgctaacttt agagtcttgt 120

cgcagcagct ttcgcgactt aataagacgt tagcagctgg tcgtccaact attaaccacc 180

caacctttgt agggagtgaa cgctgtaaac ctgggtacac gttcacatct atcaccctaa 240

agccaccaaa aatagaccgt ggatctggag gaggtggtag tggtggaggt ggatctggag 300

gaggtgacga ggatggatcc attgcagttc agagcccgat gaatcgtctg gttgcagaaa 360

ccctggcact gctgagcacc catcgtaccc tgctgattgg tgatggtaat ctgatgattc 420

cgacaccgga acataataat catcagctgt gtatcgaaga agtgtttcag ggcattgata 480

ccctgaaaaa tcgtaccgtt ccgggtgatg cagttgaaaa actgtttcgt aatctgagcc 540

tgatcaaaga acatatcgat cgccagaaaa aaaagtgtgg tggtgaacgt tggcgtgtga 600

aaaaattcct ggattatctg caggtttttc tgggcgtgat taataccgaa tggaccatgg 660

aaagcactag tgacgaggat ggaggaggtg gaagcggagg aggtggatct tattatggta 720

aaaggttgtt attacctgat tcagtcacgg aatatgataa gaaacttgtt tcgcgcattc 780

aaattcgagt taatcctttg ccgaaatttg attcaaccgt gtgggtgaca gtccgtaaag 840

ttcctgcctc ttcggactta tccgttgccg ccatttctgc tatgtttgcg gacggagcct 900

caccggtact ggtttatcag tacgctgcat ctggagtcca agctaacaac aaactgttgt 960

atgatctttc ggcgatgcgc gctgatatag gcgacatgag aaagtacgcc gttctcgtgt 1020

attcaaaaga cgatgcactc gagacagacg agttagtact tcatgttgac gtcgagcacc 1080

aacgtattcc cacatctggg gtgctcccag tttgataagc tt 1122

<210> 130
<211> 62
<212> DNA
<213> artificial sequence

<220>
<223> Reverse 2xIL5-gsKpnR

<400> 130
ctccggaacc accgccaccg ctaccaccac caccgctttc catggtccat tcggtattaa 60

tc 62

<210> 131
<211> 44
<212> DNA
<213> artificial sequence

<220>
<223> Forward 2xIL5-gsKpnF

<400> 131
ttccggaggt ggcggtagca ttgcagttca gagcccgatg aatc 44

<210> 132
<211> 500
<212> PRT
<213> artificial sequence

<220>
<223> CMV-Ntt830-2xfel-IL-5

<400> 132

Met Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
1 5 10 15

Arg Arg Arg Arg Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala
20 25 30

Asp Ala Asn Phe Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys
35 40 45

Thr Leu Ala Ala Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly
50 55 60

Ser Glu Arg Cys Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys
65 70 75 80

Pro Pro Lys Ile Asp Arg Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

```
                85                  90                  95

Gly Ser Gly Gly Gly Asp Glu Asp Gly Ser Ile Ala Val Gln Ser Pro
            100                 105                 110

Met Asn Arg Leu Val Ala Glu Thr Leu Ala Leu Leu Ser Thr His Arg
        115                 120                 125

Thr Leu Leu Ile Gly Asp Gly Asn Leu Met Ile Pro Thr Pro Glu His
    130                 135                 140

Asn Asn His Gln Leu Cys Ile Glu Glu Val Phe Gln Gly Ile Asp Thr
145                 150                 155                 160

Leu Lys Asn Arg Thr Val Pro Gly Asp Ala Val Glu Lys Leu Phe Arg
                165                 170                 175

Asn Leu Ser Leu Ile Lys Glu His Ile Asp Arg Gln Lys Lys Lys Cys
            180                 185                 190

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

Phe Leu Gly Val Ile Asn Thr Glu Trp Thr Met Glu Ser Gly Gly Gly
    210                 215                 220

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Ala Val Gln
225                 230                 235                 240

Ser Pro Met Asn Arg Leu Val Ala Glu Thr Leu Ala Leu Leu Ser Thr
                245                 250                 255

His Arg Thr Leu Leu Ile Gly Asp Gly Asn Leu Met Ile Pro Thr Pro
            260                 265                 270

Glu His Asn Asn His Gln Leu Cys Ile Glu Glu Val Phe Gln Gly Ile
        275                 280                 285
```

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Asp Thr Leu Lys Asn Arg Thr Val Pro Gly Asp Ala Val Glu Lys Leu
    290                 295                 300

Phe Arg Asn Leu Ser Leu Ile Lys Glu His Ile Asp Arg Gln Lys Lys
305                 310                 315                 320

Lys Cys Gly Gly Glu Arg Trp Arg Val Lys Lys Phe Leu Asp Tyr Leu
                325                 330                 335

Gln Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr Met Glu Ser Thr
            340                 345                 350

Ser Asp Glu Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Tyr Tyr
        355                 360                 365

Gly Lys Arg Leu Leu Leu Pro Asp Ser Val Thr Glu Tyr Asp Lys Lys
    370                 375                 380

Leu Val Ser Arg Ile Gln Ile Arg Val Asn Pro Leu Pro Lys Phe Asp
385                 390                 395                 400

Ser Thr Val Trp Val Thr Val Arg Lys Val Pro Ala Ser Ser Asp Leu
                405                 410                 415

Ser Val Ala Ala Ile Ser Ala Met Phe Ala Asp Gly Ala Ser Pro Val
            420                 425                 430

Leu Val Tyr Gln Tyr Ala Ala Ser Gly Val Gln Ala Asn Asn Lys Leu
        435                 440                 445

Leu Tyr Asp Leu Ser Ala Met Arg Ala Asp Ile Gly Asp Met Arg Lys
    450                 455                 460

Tyr Ala Val Leu Val Tyr Ser Lys Asp Asp Ala Leu Glu Thr Asp Glu
465                 470                 475                 480

Leu Val Leu His Val Asp Val Glu His Gln Arg Ile Pro Thr Ser Gly
```

485 490 495

Val Leu Pro Val
500

<210> 133
<211> 1512
<212> DNA
<213> artificial sequence

<220>
<223> CMV-Ntt830-2xfel-IL-5

<400> 133
ccatgggcca gtatattaag gccaactcca aatttatcgg gattaccgag cgtcgacgtc 60

gtccgcgtcg tggttcccgc tccgccccct cctccgcgga tgctaacttt agagtcttgt 120

cgcagcagct ttcgcgactt aataagacgt tagcagctgg tcgtccaact attaaccacc 180

caacctttgt agggagtgaa cgctgtaaac ctgggtacac gttcacatct atcaccctaa 240

agccaccaaa aatagaccgt ggatctggag gaggtggtag tggtggaggt ggatctggag 300

gaggtgacga ggatggatcc attgcagttc agagcccgat gaatcgtctg gttgcagaaa 360

ccctggcact gctgagcacc catcgtaccc tgctgattgg tgatggtaat ctgatgattc 420

cgacaccgga acataataat catcagctgt gtatcgaaga agtgtttcag ggcattgata 480

ccctgaaaaa tcgtaccgtt ccgggtgatg cagttgaaaa actgtttcgt aatctgagcc 540

tgatcaaaga acatatcgat cgccagaaaa aaaagtgtgg tggtgaacgt tggcgtgtga 600

aaaaattcct ggattatctg caggtttttc tgggcgtgat taataccgaa tggaccatgg 660

aaagcggtgg tggtggtagc ggtggcggtg gttccggagg tggcggtagc attgcagttc 720

agagcccgat gaatcgtctg gttgcagaaa ccctggcact gctgagcacc catcgtaccc 780

tgctgattgg tgatggtaat ctgatgattc cgacaccgga acataataat catcagctgt 840

gtatcgaaga agtgtttcag ggcattgata ccctgaaaaa tcgtaccgtt ccgggtgatg 900

cagttgaaaa actgtttcgt aatctgagcc tgatcaaaga acatatcgat cgccagaaaa 960

aaaagtgtgg tggtgaacgt tggcgtgtga aaaaattcct ggattatctg caggtttttc 1020

tgggcgtgat taataccgaa tggaccatgg aaagcactag tgacgaggat ggaggaggtg 1080

gaagcggagg aggtggatct tattatggta aaaggttgtt attacctgat tcagtcacgg 1140

aatatgataa gaaacttgtt tcgcgcattc aaattcgagt taatcctttg ccgaaatttg 1200

attcaaccgt gtgggtgaca gtccgtaaag ttcctgcctc ttcggactta tccgttgccg 1260

ccatttctgc tatgtttgcg gacggagcct caccggtact ggtttatcag tacgctgcat 1320

ctggagtcca agctaacaac aaactgttgt atgatctttc ggcgatgcgc gctgatatag 1380

gcgacatgag aaagtacgcc gttctcgtgt attcaaaaga cgatgcactc gagacagacg 1440

agttagtact tcatgttgac gtcgagcacc aacgtattcc cacatctggg gtgctcccag 1500

tttgataagc tt 1512

<210> 134
<211> 152
<212> PRT
<213> artificial sequence

<220>
<223> canine IL-1b

<400> 134

Ala Ala Met Gln Ser Val Asp Cys Lys Leu Gln Asp Ile Ser His Lys
1 5 10 15

Tyr Leu Val Leu Ser Asn Ser Tyr Glu Leu Arg Ala Leu His Leu Asn
20 25 30

Gly Glu Asn Val Asn Lys Gln Val Val Phe His Met Ser Phe Val His
35 40 45

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

Lys Asn Leu Tyr Leu Ser Cys Val Met Lys Asp Gly Lys Pro Thr Leu
65 70 75 80

Gln Leu Glu Lys Val Asp Pro Lys Val Tyr Pro Lys Arg Lys Met Glu

85 90 95

Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Lys Asn Thr Val Glu Phe
100 105 110

Glu Ser Ser Gln Tyr Pro Asn Trp Tyr Ile Ser Thr Ser Gln Val Glu
115 120 125

Gly Met Pro Val Phe Leu Gly Asn Thr Arg Gly Gly Gln Asp Ile Thr
130 135 140

Asp Phe Thr Met Glu Phe Ser Ser
145 150

<210> 135
<211> 407
<212> PRT
<213> artificial sequence

<220>
<223> CMV-Ntt830-cIL-1b

<400> 135

Met Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
1 5 10 15

Arg Arg Arg Arg Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala
20 25 30

Asp Ala Asn Phe Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys
35 40 45

Thr Leu Ala Ala Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly
50 55 60

Ser Glu Arg Cys Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys
65 70 75 80

Pro Pro Lys Ile Asp Arg Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

```
                85                  90                  95

Gly Ser Gly Gly Gly Asp Glu Asp Gly Ser Ala Ala Met Gln Ser Val
            100                 105                 110

Asp Cys Lys Leu Gln Asp Ile Ser His Lys Tyr Leu Val Leu Ser Asn
        115                 120                 125

Ser Tyr Glu Leu Arg Ala Leu His Leu Asn Gly Glu Asn Val Asn Lys
    130                 135                 140

Gln Val Val Phe His Met Ser Phe Val His Gly Asp Glu Ser Asn Asn
145                 150                 155                 160

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

Cys Val Met Lys Asp Gly Lys Pro Thr Leu Gln Leu Glu Lys Val Asp
            180                 185                 190

Pro Lys Val Tyr Pro Lys Arg Lys Met Glu Lys Arg Phe Val Phe Asn
        195                 200                 205

Lys Ile Glu Ile Lys Asn Thr Val Glu Phe Glu Ser Ser Gln Tyr Pro
    210                 215                 220

Asn Trp Tyr Ile Ser Thr Ser Gln Val Glu Gly Met Pro Val Phe Leu
225                 230                 235                 240

Gly Asn Thr Arg Gly Gly Gln Asp Ile Thr Asp Phe Thr Met Glu Phe
                245                 250                 255

Ser Ser Thr Ser Asp Glu Asp Gly Gly Gly Gly Ser Gly Gly Gly Gly
            260                 265                 270

Ser Tyr Tyr Gly Lys Arg Leu Leu Leu Pro Asp Ser Val Thr Glu Tyr
        275                 280                 285
```

```
Asp Lys Lys Leu Val Ser Arg Ile Gln Ile Arg Val Asn Pro Leu Pro
    290                 295                 300

Lys Phe Asp Ser Thr Val Trp Val Thr Val Arg Lys Val Pro Ala Ser
305                 310                 315                 320

Ser Asp Leu Ser Val Ala Ala Ile Ser Ala Met Phe Ala Asp Gly Ala
                325                 330                 335

Ser Pro Val Leu Val Tyr Gln Tyr Ala Ala Ser Gly Val Gln Ala Asn
            340                 345                 350

Asn Lys Leu Leu Tyr Asp Leu Ser Ala Met Arg Ala Asp Ile Gly Asp
        355                 360                 365

Met Arg Lys Tyr Ala Val Leu Val Tyr Ser Lys Asp Asp Ala Leu Glu
    370                 375                 380

Thr Asp Glu Leu Val Leu His Val Asp Val Glu His Gln Arg Ile Pro
385                 390                 395                 400

Thr Ser Gly Val Leu Pro Val
                405
```

<210> 136
<211> 1233
<212> DNA
<213> artificial sequence

<220>
<223> CMV-Ntt830-cIL-1b

<400> 136

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ccatgggcca gtatattaag gccaactcca aatttatcgg gattaccgag cgtcgacgtc       60

gtccgcgtcg tggttcccgc tccgccccct cctccgcgga tgctaacttt agagtcttgt      120

cgcagcagct ttcgcgactt aataagacgt tagcagctgg tcgtccaact attaaccacc      180

caacctttgt agggagtgaa cgctgtaaac ctgggtacac gttcacatct atcaccctaa      240
```

agccaccaaa aatagaccgt ggatctggag gaggtggtag tggtggaggt ggatctggag 300

gaggtgacga ggatggatcc gcagccatgc aatcggtgga ctgcaagtta caggacataa 360

gccacaaata cctggtgctg tctaactctt atgagcttcg ggctctccac ctcaatgggg 420

aaaatgtgaa caaacaagtg gtgttccaca tgagctttgt gcacggggat gaaagtaata 480

acaagatacc tgtggtcttg ggcatcaaac aaaagaatct gtacctgtcc tgtgtgatga 540

aggatggaaa gcccacccta cagctagaga aggtagaccc caaagtctac ccaaagagga 600

agatggaaaa gcgatttgtc ttcaacaaga tagaaatcaa gaacacagtg gaatttgagt 660

cttctcagta ccctaactgg tacatcagca cctctcaagt cgaaggaatg cctgtcttcc 720

taggaaatac cagaggtggc caggatataa ctgacttcac gatggaattc tcttccacta 780

gtgacgagga tggaggaggt ggaagcggag gaggtggatc ttattatggt aaaaggttgt 840

tattacctga ttcagtcacg gaatatgata agaaacttgt ttcgcgcatt caaattcgag 900

ttaatccttt gccgaaattt gattcaaccg tgtgggtgac agtccgtaaa gttcctgcct 960

cttcggactt atccgttgcc gccatttctg ctatgtttgc ggacggagcc tcaccggtac 1020

tggtttatca gtacgctgca tctggagtcc aagctaacaa caaactgttg tatgatcttt 1080

cggcgatgcg cgctgatata ggcgacatga gaaagtacgc cgttctcgtg tattcaaaag 1140

acgatgcact cgagacagac gagttagtac ttcatgttga cgtcgagcac caacgtattc 1200

ccacatctgg ggtgctccca gtttgataag ctt 1233

<210> 137
<211> 48
<212> DNA
<213> artificial sequence

<220>
<223> Forward CM-BamSpeF

<400> 137
tggatcctct actagtggag gaggtggaag cggaggaggt ggatctta 48

<210> 138
<211> 11
<212> PRT

<213> artificial sequence

<220>
<223> 11 amino acid GST linker

<400> 138

Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1   5   10

<210> 139
<211> 363
<212> PRT
<213> artificial sequence

<220>
<223> CMV-Ntt830-fel-IL-5*

<400> 139

Met Gly Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
1   5   10   15

Arg Arg Arg Arg Pro Arg Arg Gly Ser Arg Ser Ala Pro Ser Ser Ala
            20   25   30

Asp Ala Asn Phe Arg Val Leu Ser Gln Gln Leu Ser Arg Leu Asn Lys
        35   40   45

Thr Leu Ala Ala Gly Arg Pro Thr Ile Asn His Pro Thr Phe Val Gly
    50   55   60

Ser Glu Arg Cys Lys Pro Gly Tyr Thr Phe Thr Ser Ile Thr Leu Lys
65   70   75   80

Pro Pro Lys Ile Asp Arg Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
                85   90   95

Gly Ser Gly Gly Gly Gly Ser Ile Ala Val Gln Ser Pro Met Asn Arg
            100   105   110

Leu Val Ala Glu Thr Leu Ala Leu Leu Ser Thr His Arg Thr Leu Leu

```
        115                 120                 125

Ile Gly Asp Gly Asn Leu Met Ile Pro Thr Pro Glu His Asn Asn His
    130                 135                 140

Gln Leu Cys Ile Glu Glu Val Phe Gln Gly Ile Asp Thr Leu Lys Asn
145                 150                 155                 160

Arg Thr Val Pro Gly Asp Ala Val Glu Lys Leu Phe Arg Asn Leu Ser
                165                 170                 175

Leu Ile Lys Glu His Ile Asp Arg Gln Lys Lys Lys Cys Gly Gly Glu
            180                 185                 190

Arg Trp Arg Val Lys Lys Phe Leu Asp Tyr Leu Gln Val Phe Leu Gly
        195                 200                 205

Val Ile Asn Thr Glu Trp Thr Met Glu Ser Thr Ser Gly Gly Gly Gly
    210                 215                 220

Ser Gly Gly Gly Gly Tyr Tyr Gly Lys Arg Leu Leu Leu Pro Asp Ser
225                 230                 235                 240

Val Thr Glu Tyr Asp Lys Lys Leu Val Ser Arg Ile Gln Ile Arg Val
                245                 250                 255

Asn Pro Leu Pro Lys Phe Asp Ser Thr Val Trp Val Thr Val Arg Lys
            260                 265                 270

Val Pro Ala Ser Ser Asp Leu Ser Val Ala Ala Ile Ser Ala Met Phe
        275                 280                 285

Ala Asp Gly Ala Ser Pro Val Leu Val Tyr Gln Tyr Ala Ala Ser Gly
    290                 295                 300

Val Gln Ala Asn Asn Lys Leu Leu Tyr Asp Leu Ser Ala Met Arg Ala
305                 310                 315                 320
```

Asp Ile Gly Asp Met Arg Lys Tyr Ala Val Leu Val Tyr Ser Lys Asp
325 330 335

Asp Ala Leu Glu Thr Asp Glu Leu Val Leu His Val Asp Val Glu His
340 345 350

Gln Arg Ile Pro Thr Ser Gly Val Leu Pro Val
355 360

<210> 140
<211> 1101
<212> DNA
<213> artificial sequence

<220>
<223> CMV-Ntt830-fel-IL-5*

<400> 140
ccatgggcca gtatattaag gccaactcca aatttatcgg gattaccgag cgtcgacgtc 60

gtccgcgtcg tggttcccgc tccgcccccc cctccgcgga tgctaacttt agagtcttgt 120

cgcagcagct ttcgcgactt aataagacgt tagcagctgg tcgtccaact attaaccacc 180

caacctttgt agggagtgaa cgctgtaaac ctgggtacac gttcacatct atcaccctaa 240

agccaccaaa aatagaccgt ggatctggag gaggtggtag tggtggaggt ggatctggag 300

gaggtggatc cattgcagtt cagagcccga tgaatcgtct ggttgcagaa accctggcac 360

tgctgagcac ccatcgtacc ctgctgattg gtgatggtaa tctgatgatt ccgacaccgg 420

aacataataa tcatcagctg tgtatcgaag aagtgtttca gggcattgat accctgaaaa 480

atcgtaccgt tccgggtgat gcagttgaaa aactgtttcg taatctgagc ctgatcaaag 540

aacatatcga tcgccagaaa aaaaagtgtg gtggtgaacg ttggcgtgtg aaaaaattcc 600

tggattatct gcaggttttt ctgggcgtga ttaataccga atggaccatg gaaagcacta 660

gtggaggagg tggaagcgga ggaggtggat attatggtaa aaggttgtta ttacctgatt 720

cagtcacgga atatgataag aaacttgttt cgcgcattca aattcgagtt aatcctttgc 780

cgaaatttga ttcaaccgtg tgggtgacag tccgtaaagt tcctgcctct tcggacttat 840

ccgttgccgc catttctgct atgtttgcgg acggagcctc accggtactg gtttatcagt 900

acgctgcatc tggagtccaa gctaacaaca aactgttgta tgatctttcg gcgatgcgcg 960

ctgatatagg cgacatgaga aagtacgccg tcctcgtgta ttcaaaagac gatgcactcg 1020

agacagacga gttagtactt catgttgacg tcgagcacca acgtattccc acatctgggg 1080

tgctcccagt ttgataagct t 1101

<210> 141
<211> 115
<212> PRT
<213> artificial sequence

<220>
<223> fel IL-5

<400> 141

Ile Ala Val Gln Ser Pro Met Asn Arg Leu Val Ala Glu Thr Leu Ala
1 5 10 15

Leu Leu Ser Thr His Arg Thr Leu Leu Ile Gly Asp Gly Asn Leu Met
20 25 30

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

Phe Gln Gly Ile Asp Thr Leu Lys Asn Arg Thr Val Pro Gly Asp Ala
50 55 60

Val Glu Lys Leu Phe Arg Asn Leu Ser Leu Ile Lys Glu His Ile Asp
65 70 75 80

Arg Gln Lys Lys Lys Cys Gly Gly Glu Arg Trp Arg Val Lys Lys Phe
85 90 95

Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr
100 105 110

Ile Glu Gly

115

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<211> 109
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<213> artificial sequence

<220>
<223> fel IL-5

<400> 142

Ile Ala Val Gln Ser Pro Met Asn Arg Leu Val Ala Glu Thr Leu Ala
1 5 10 15

Leu Leu Ser Thr His Arg Thr Leu Leu Ile Gly Asp Gly Asn Leu Met
20 25 30

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

Phe Gln Gly Ile Asp Thr Leu Lys Asn Arg Thr Val Pro Gly Asp Ala
50 55 60

Val Glu Lys Leu Phe Arg Asn Leu Ser Leu Ile Lys Glu His Ile Asp
65 70 75 80

Arg Gln Lys Lys Asn Phe Gly Gly Lys Lys Trp Lys Val Lys Asn Phe
85 90 95

Leu Asn Tyr Leu Gln Phe Phe Leu Gly Leu Leu Asn Thr
100 105

<210> 143
<211> 152
<212> PRT
<213> artificial sequence

<220>
<223> canine IL-1b

<400> 143

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Ala Ala Met Gln Ser Val Asp Cys Lys Leu Gln Gly Ile Ser His Lys
1               5                   10                  15


Tyr Leu Val Leu Ser Asn Ser Tyr Glu Leu Arg Ala Leu His Leu Asn
            20                  25                  30


Gly Glu Asn Val Asn Lys Gln Val Val Phe His Met Ser Phe Val His
        35                  40                  45


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


Lys Asn Leu Tyr Leu Ser Cys Val Met Lys Asp Gly Lys Pro Thr Leu
65                  70                  75                  80


Gln Leu Glu Lys Val Asp Pro Lys Val Tyr Pro Lys Arg Lys Met Glu
                85                  90                  95


Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Lys Asn Thr Val Glu Phe
            100                 105                 110


Glu Ser Ser Gln Tyr Pro Asn Trp Tyr Ile Ser Thr Ser Gln Val Glu
        115                 120                 125


Gly Met Pro Val Phe Leu Gly Asn Thr Arg Gly Gly Gln Asp Ile Thr
    130                 135                 140


Asp Phe Thr Met Glu Phe Ser Ser
145                 150


<210>  144
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<223>  canine IL-1b

<400>  144
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Ala Ala Leu Pro Ser Val Asp Cys Thr Leu Gln Asp Ile Asn His Lys
1               5                  10                  15

Tyr Leu Val Leu Ser Asn Ser Tyr Glu Leu Arg Ala Leu His Leu Asn
            20                  25                  30

Gly Glu Asn Val Asn Lys Gln Val Val Phe His Met Ser Phe Val His
        35                  40                  45

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

Lys Asn Leu Tyr Leu Ser Cys Val Met Lys Asp Gly Lys Pro Thr Leu
65                  70                  75                  80

Gln Leu Glu Lys Val Asp Pro Lys Val Tyr Pro Lys Arg Lys Met Glu
                85                  90                  95

Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Lys Asn Thr Val Glu Phe
            100                 105                 110

Glu Ser Ser Gln Tyr Pro Asn Trp Tyr Ile Ser Thr Ser Gln Val Glu
        115                 120                 125

Gly Met Pro Val Phe Leu Gly Asn Thr Lys Gly Gly Gln Asp Ile Thr
    130                 135                 140

Asp Phe Thr Met Glu Phe Ser Ser
145                 150
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<213> artificial sequence

<220>
<223> fel IlL-1b

<400> 145

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Ala Ala Ile Gln Ser Gln Asp Tyr Thr Phe Arg Asp Ile Ser Gln Lys
1               5                   10                  15

Ser Leu Val Leu Ser Gly Ser Tyr Glu Leu Arg Ala Leu His Leu Asn
            20                  25                  30

Gly Gln Asn Met Asn Gln Gln Val Val Phe Arg Met Ser Phe Val His
        35                  40                  45

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

Asn Asn Leu Tyr Leu Ser Cys Val Met Lys Asp Gly Lys Pro Thr Leu
65                  70                  75                  80

Gln Leu Glu Met Leu Asp Pro Lys Val Tyr Pro Lys Lys Lys Met Glu
                85                  90                  95

Lys Arg Phe Val Phe Asn Lys Thr Glu Ile Lys Gly Asn Val Glu Phe
            100                 105                 110

Glu Ser Ser Gln Phe Pro Asn Trp Tyr Ile Ser Thr Ser Gln Ala Glu
        115                 120                 125

Glu Met Pro Val Phe Leu Gly Asn Thr Lys Gly Gly Gln Asp Ile Thr
    130                 135                 140

Asp Phe Ile Met Glu Ser Ala Ser
145                 150
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