

SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.

<120> ANTI-FC EPSILON-R1 ALPHA (FCER1A) ANTIBODIES, BISPECIFIC ANTIGEN-BINDING MOLECULES THAT BIND FCER1A AND CD3, AND USES THEREOF

<130> 118003-45320/10480W001

<140>

<141>

<150> 62/721,921

<151> 2018-08-23

<160> 63

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1

```
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtga ctccatcagt gattactatt ggatctggat ccggcagccc 120
ccaggaaagg gactggagtg gattggatat atctattaca gtgggagcac caactacaac 180
ccctccctca agagtcgagt caccatatca gtagccacgt ccaagaacca gttctccctg 240
aagttgaggt ctgtgaccgc cgcagacacg gccatgtatt actgtgagag acgaaataac 300
tggaaccacg tccgtgcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 360
```

<210> 2

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 2

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1             5             10            15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Asp Tyr
          20          25          30
Tyr Trp Ile Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
          35          40          45
Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
          50          55          60
```

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

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

<220>
 <223> synthetic

<400> 3
 ggtgactcca tcagtgatta ctat 24

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

<220>
 <223> synthetic

<400> 4
 Gly Asp Ser Ile Ser Asp Tyr Tyr
 1 5

<210> 5
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 5
 atctattaca gtgggagcac c 21

<210> 6
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 6

Ile Tyr Tyr Ser Gly Ser Thr
 1 5

<210> 7

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 7

gcgagacgaa ataactggaa ccacgtccgt gcttttgata tc

42

<210> 8

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 8

Ala Arg Arg Asn Asn Trp Asn His Val Arg Ala Phe Asp Ile

1

5

10

<210> 9

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 9

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
 acctgcactg tctctggtga ctccatcaat gattactact ggagctggct ccggcagccc 120
 ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180
 ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240
 aagctgagct ctgtgaccgc cgctgacacg gccgtgtatt actgtacgag acgaaataac 300
 tggaactacg tccgtgcttt tgatatctgg ggccaaggga caatgggtcac cgtctcttca 360

<210> 10

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 10

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

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 11

ggtgactcca tcaatgatta ctac

24

<210> 12

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 12

Gly Asp Ser Ile Asn Asp Tyr Tyr

1

5

<210> 13

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 13

atctattaca gtgggagcac c

21

<210> 14

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

<220>
 <223> synthetic

<400> 14
 Ile Tyr Tyr Ser Gly Ser Thr
 1 5

<210> 15
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 15
 acgagacgaa ataactggaa ctacgtccgt gcttttgata tc 42

<210> 16
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 16
 Thr Arg Arg Asn Asn Trp Asn Tyr Val Arg Ala Phe Asp Ile
 1 5 10

<210> 17
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 17
 caggtgcagg tgcaggagtc gggcccaaga ctggtgaagc cttcggagac cctgtccctc 60
 acctgcactg tctctggtgg ctccatgagt agttactatt ggatttggat ccggcagccc 120
 ccagggaagg aattggagtg gattgggtat atctattaca gtgggagcac caactacaac 180
 cctctccctca agagtcgagc caccatatca gtagacacgt ccaagaatca gttctccctg 240
 aacctgaact ctgtgaccgc cgcagacacg gccgtgtatt actgtgagag acgaaataac 300
 tggaactacg tccgtgcttt tgatatctgg ggccaaggga caatgggtcac cgtctcttca 360

<210> 18

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

<220>
 <223> synthetic

<400> 18
 Gln Val Gln Val Gln Glu Ser Gly Pro Arg Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Met Ser Ser Tyr
 20 25 30
 Tyr Trp Ile Trp Ile Arg Gln Pro Pro Gly Lys Glu Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Arg Asn Asn Trp Asn Tyr Val Arg Ala Phe Asp Ile Trp Gly Gln
 100 105 110
 Gly Thr Met Val Thr Val Ser Ser
 115 120

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

<220>
 <223> synthetic

<400> 19
 ggtggctcca tgagtagtta ctat

24

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

<220>
 <223> synthetic

<400> 20
 Gly Gly Ser Met Ser Ser Tyr Tyr
 1 5

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

<220>

<223> synthetic

<400> 21

atctattaca gtgggagcac c

21

<210> 22

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 22

Ile Tyr Tyr Ser Gly Ser Thr
1 5

<210> 23

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 23

gcgagacgaa ataactggaa ctacgtccgt gcttttgata tc

42

<210> 24

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 24

Ala Arg Arg Asn Asn Trp Asn Tyr Val Arg Ala Phe Asp Ile
1 5 10

<210> 25

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 25

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

```

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccgtca 180
aggttcagtg gcagtggatc tgggacagat ttctactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
caagggacac gactggagat taaa                                     324

```

<210> 26

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 26

```

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

```

<210> 27

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 27

cagagcatta gcagctat

18

<210> 28

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 28

```

Gln Ser Ile Ser Ser Tyr
 1           5

```

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

<220>
 <223> synthetic

<400> 29
 gctgcatcc

9

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

<220>
 <223> synthetic

<400> 30
 Ala Ala Ser
 1

<210> 31
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 31
 caacagagtt acagtacccc tccgatcacc

30

<210> 32
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 32
 Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
 1 5 10

<210> 33
 <211> 1344
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 33

```

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggatg ctccatcagt gattactatt ggatctggat ccggcagccc 120
ccaggaaagg gactggagtg gattggatat atctattaca gtgggagcac caactacaac 180
ccctccctca agagtcgagt caccatatca gtagccacgt ccaagaacca gttctccctg 240
aagttgaggt ctgtgaccgc cgcagacacg gccatgtatt actgtgagag acgaaataac 300
tggaaccacg tccgtgcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 360
gcctccacca agggcccacg ggtcttcccc ctggcgccct gctccaggag cacctccgag 420
agcacagccg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 480
tggaactcag gcgccctgac cagcggcgctg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg cacgaagacc 600
tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 660
aaatatggtc ccccatgccc accctgccc gcacctgagt tcctgggggg accatcagtc 720
ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg 780
tgcgtgggtg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat 840
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac 900
cgtgtgggtc gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag 960
tgcaagggtc ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa 1020
gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag 1080
aaccagggtc gcctgacctg cctgggtcaaa ggcttctacc ccagcgacat cgccgtggag 1140
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200
gacggctcct tcttctctca cagcaggctc accgtggaca agagcaggtg gcaggagggg 1260
aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagtcc 1320
ctctccctgt ctctgggtaa atga                                     1344

```

<210> 34

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 34

```

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

```

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

<210> 35

<211> 1344

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 35

```

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtga ctccatcaat gattactact ggagctggct ccggcagccc 120
ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180
ccctccctca agatcagagt caccatatca gtagacacgt ccaagaacca gttctccctg 240

```

```

aagctgagct ctgtgaccgc cgctgacacg gccgtgtatt actgtacgag acgaaataac 300
tggaactacg tccgtgcttt tgatatctgg ggccaaggga caatgggtcac cgtctcttca 360
gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 420
agcacagccg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtcg 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg cacgaagacc 600
tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 660
aaatatggtc ccccatgccc accctgccc aacaccaagg tcctgggggg accatcagtc 720
ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg 780
tgcgtgggtgg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat 840
ggcgtggagg tgcataatgc caagacaaag ccgcggggagg agcagttcaa cagcacgtac 900
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag 960
tgcaagggtct ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa 1020
gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag 1080
aaccaggtca gcctgacctg cctgggtcaaa ggcttctacc ccagcgacat cgccgtggag 1140
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200
gacggctcct tcttctctta cagcaggctc accgtggaca agagcaggtg gcaggagggg 1260
aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagtcc 1320
ctctccctgt ctctgggtaa atga 1344

```

<210> 36

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 36

```

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

```

195	200	205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro		
210	215	220
Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val		
225	230	235
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr		
245	250	255
Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu		
260	265	270
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys		
275	280	285
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser		
290	295	300
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys		
305	310	315
Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile		
325	330	335
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro		
340	345	350
Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu		
355	360	365
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn		
370	375	380
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Val Leu Asp Ser		
385	390	395
Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg		
405	410	415
Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu		
420	425	430
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys		
435	440	445

<210> 37

<211> 1344

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 37

```

cagggtgcagg tgcaggagtc gggcccaaga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatgagt agttactatt ggatttggat ccggcagccc 120
ccagggaagg aattggagtg gattgggtat atctattaca gtgggagcac caactacaac 180
ccctccctca agatcgagc caccatatca gtagacacgt ccaagaatca gttctccctg 240
aacctgaact ctgtgaccgc cgcagacacg gccgtgtatt actgtgagag acgaaataac 300
tggaactacg tccgtgcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 360
gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 420
agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacgaagacc 600
tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 660
aaatatggtc ccccatgccc accctgccc a gcacctgagt tcctgggggg accatcagtc 720

```

```

ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg 780
tgcgtgggtgg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat 840
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac 900
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag 960
tgcaagggtct ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa 1020
gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag 1080
aaccaggtca gcctgacctg cctgggtcaaa ggcttctacc ccagcgacat cgccgtggag 1140
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200
gacggctcct tcttctctta cagcaggctc accgtggaca agagcaggtg gcaggagggg 1260
aatgtcttct catgctccgt gatgcatgag gctctgcaca accactacac acagaagtcc 1320
ctctccctgt ctctgggtaa atga 1344

```

<210> 38

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 38

```

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

```

$\langle 220 \rangle$
 $\langle 223 \rangle$ synthetic

```
<210> 40
<211> 214
<212> PRT
<213> Artificial Sequence
```

$\langle 220 \rangle$
 $\langle 223 \rangle$ synthetic

<400> 40

```

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

```

<210> 41

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 41

```

gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg 60
agttgcgcag ctagtgggtt tacattcgac gattacagca tgcattgggt gaggcaagct 120
cctggtaaag gattggaatg ggtagcggg atatcatgga actcaggaag catcggtac 180
gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac 240
cttcaaatga actctcttag ggcagaagac acagcattgt attattgcgc aaaatacggc 300
agtggttatg gcaagtttta ttattatgga atggacgtgt ggggacaagg gacaacagtg 360
acagtgagta gc                                     372

```

<210> 42

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 42

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

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 43

gggtttacat tcgacgatta cagc

24

<210> 44

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 44

Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Ser
1				5			

<210> 45

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 45

atatcatgga actcaggaag catc

24

<210> 46

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 46

Ile Ser Trp Asn Ser Gly Ser Ile

1

5

<210> 47

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 47

gcaaaatacg gcagtgggta tggcaagttt tattattatg gaatggacgt g

51

<210> 48

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 48

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Met Asp

1

5

10

15

Val

<210> 49

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 49

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtga ctccatcagt gattactatt ggatctggat ccggcagccc 120
ccaggaaagg gactggagtg gattggatat atctattaca gtgggagcac caactacaac 180
ccctccctca agagtcgagt caccatatca gtagccacgt ccaagaacca gttctccctg 240

```

aagttgaggt ctgtgaccgc cgcagacacg gccatgtatt actgtgagag acgaaataac 300
tggaaccacg tccgtgcttt tgatatctgg ggccaaggga caatgggtcac cgtctcttca 360
gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 420
agcacagccg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg cacgaagacc 600
tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 660
aaatatggtc ccccatgccc accgtgccc aacaccaagg tggcaggacc atcagtcttc 720
ctgttcccc caaaaccaa ggacactctc atgatctccc ggaccctga ggtcacgtgc 780
gtgggtgggtg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc 840
gtggaggtgc ataatgcaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt 900
gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc 960
aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctcaa agccaaaggg 1020
cagccccgag agccacaggt gtacaccctg ccccatccc aggaggagat gaccaagaac 1080
caggtcagcc tgacctgcct ggtcaaaggc ttctaccca gcgacatcgc cgtggagtgg 1140
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
ggctccttct tcctctacag caggctcacc gtggacaaga gcaggtggca ggagggaat 1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagtccttc 1320
tccctgtctc tgggtaaata a 1341

```

<210> 50

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 50

```

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

```

195	200	205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro		
210	215	220
Pro Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe		
225	230	235
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro		
245	250	255
Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val		
260	265	270
Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr		
275	280	285
Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val		
290	295	300
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys		
305	310	315
Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser		
325	330	335
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro		
340	345	350
Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val		
355	360	365
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly		
370	375	380
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp		
385	390	395
Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp		
405	410	415
Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His		
420	425	430
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys		
435	440	445

<210> 51

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 51

```

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtga ctccatcaat gattactact ggagctggct ccggcagccc 120
ccagggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180
ccctccctca agatcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240
aagctgagct ctgtgaccgc cgctgacacg gccgtgtatt actgtacgag acgaaataac 300
tggaactacg tccgtgcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 360
gcctccacca agggcccatc ggtcttcccc ctggcgccct gctccaggag cacctccgag 420
agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacgaagacc 600
tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc 660
aaatatggtc ccccatgccc accgtgcca gcaccactg tggcaggacc atcagtcttc 720

```

```

ctgttcccc caaaacccaa ggacactctc atgatctccc ggaccctga ggtcacgtgc 780
gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc 840
gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt 900
gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc 960
aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctccaa agccaaaggg 1020
cagccccgag agccacaggt gtacaccctg ccccatccc aggaggagat gaccaagaac 1080
caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 1140
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
ggctccttct tcctctacag caggctcacc gtggacaaga gcaggtggca ggaggggaat 1260
gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacaca gaagtccttc 1320
tccctgtctc tgggtaaata a                                     1341

```

<210> 52

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 52

```

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

```

<210> 53
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 53						
caggtgcagg	tgcaggagtc	gggccaaga	ctggtgaagc	cttcggagac	cctgtccctc	60
acctgcactg	tctctggtgg	ctccatgagt	agttactatt	ggatttggat	ccggcagccc	120
ccaggggaagg	aattggagtg	gattgggtat	atctattaca	gtgggagcac	caactacaac	180
ccctccctca	agagtcgagc	caccatatca	gtagacacgt	ccaagaatca	gttctccctg	240
aacctgaact	ctgtgaccgc	cgcagacacg	gccgtgtatt	actgtgcgag	acgaaataac	300
tggaactacg	tccgtgcttt	tgatatctgg	ggccaaggga	caatggtcac	cgtctcttca	360
gcctccacca	agggcccatc	ggtcttcccc	ctggcgccct	gctccaggag	cacctccgag	420
agcacagccg	ccctgggctg	cctggtcaag	gactacttcc	ccgaaccggg	gacggtgtcg	480
tggaactcag	gcgccctgac	cagcggcgtg	cacaccttcc	cggctgtcct	acagtcctca	540
ggactctact	ccctcagcag	cgtggtgacc	gtgccctcca	gcagcttggg	cacgaagacc	600
tacacctgca	acgtagatca	caagcccagc	aacaccaagg	tggacaagag	agttgagtc	660
aaatatggtc	ccccatgccc	accgtgcccc	gcaccacctg	tggcaggacc	atcagtcttc	720
ctgttcccc	caaaacccaa	ggacactctc	atgatctccc	ggaccctga	ggtcacgtgc	780
gtggtggtgg	acgtgagcca	ggaagacccc	gaggtccagt	tcaactggta	cgtggatggc	840
gtggaggtgc	ataatgccaa	gacaaaagccg	cgggaggagc	agttcaacag	cacgtaccgt	900
gtggtcagcg	tcctcaccgt	cctgcaccag	gactggctga	acggcaagga	gtacaagtgc	960
aaggtctcca	acaaaggcct	ccgctcctcc	atcgagaaaa	ccatctccaa	agccaaagg	1020
cagccccgag	agccacaggt	gtacaccctg	cccccatccc	aggaggagat	gaccaagaac	1080
caggtcagcc	tgacctgcct	ggtcaaaggc	ttctacccca	gcgacatcgc	cgtggagtgg	1140
gagagcaatg	ggcagccgga	gaacaactac	aagaccacgc	ctcccgtgct	ggactccgac	1200

```

ggctccttct tcctctacag caggctcacc gtggacaaga gcaggtggca ggaggggaat 1260
gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacaca gaagtccttc 1320
tccctgtctc tgggtaaata a 1341

```

<210> 54

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 54

```

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

```

				325					330					335			
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro		
			340					345					350				
Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val		
		355					360					365					
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly		
	370					375					380						
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp		
385					390				395						400		
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp		
			405					410						415			
Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His		
		420					425						430				
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys				
	435						440					445					

<210> 55

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 55

```

gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg 60
agttgcgagc ctagtgggtt tacattcgac gattacagca tgcattgggt gaggcaagct 120
cctggtaaag gattggaatg ggtagcggg atatcatgga actcaggaag catcggatag 180
gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac 240
cttcaaatga actctcttag ggcagaagac acagcattgt attattgcgc aaaatacggc 300
agtggttatg gcaagtttta ttattatgga atggacgtgt ggggacaagg gacaacagt 360
acagtgaagta gcgccagcac aaaaggtcct agcgtttttc cacttgcccc atgttcaagg 420
tcaacctccg aaagtaccgc cgctcttggc tgtctcgtaa aagattattt tcccgaacct 480
gtaactgtct cctggaactc cggcgcactc acttccggcg tacatacctt ccccgctgtc 540
ctccaatctt ccggtctcta ctccctgtct tctgttgtca ctgttccatc atcctcactc 600
ggcacaaaaa catatacctg caacgttgat cacaagccaa gtaataccaa agttgataag 660
cgcgctgaat ccaaatacgg tccccctgc ccccatgtc ccgctccacc tgtggctggg 720
ccctctgttt tcctttttcc ccctaaacc aaagataccc tcatgatttc cagaaccccc 780
gaggtcacct gcgtcgtcgt tgatgtaagc caagaagatc ccgaagtcca gttcaattgg 840
tatgtagacg gtgttgaagt ccataatgca aaaacaaaac ccagagagga acagtttaat 900
tcaacctatc gtgtcgttag cgtactcacc gttcttcatc aagactggct caatggaaaa 960
gaatataaat gtaaagttag caacaaaggt ctgcccagtt caatcgaaaa aacaattagc 1020
aaagccaaag gccaacctcg cgaaccccaa gtctatacct tgcccccttc tcaggaagaa 1080
atgacaaaaa accaagtttc actcacatgc ctcgtaaaag gattctatcc atcagacatt 1140
gcagtagaat gggaatctaa cggccaacct gaaaataatt acaaaaccac tcctcctgtc 1200
ctcgattctg acggctcttt tttcctttac tccagattga ctgttgataa atcccgtgg 1260
caggaaggta acgttttttc ttgttctgtg atgcacgaag ccctccataa cagattcact 1320
caaaaatctc tttctctctc ccctggcaaa taa 1353

```

<210> 56

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 56

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

```

385          390          395          400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
          405          410          415
Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
          420          425          430
Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro
          435          440          445
Gly Lys
          450

```

```

<210> 57
<211> 208
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> hFceR1a ecto-mmH
      aa 1-180: hFceR1a (amino acid V26-Q205) from
      NP_001992
      aa 181-208: Myc-Myc-hexahistidine tag

```

```

<400> 57
Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro Pro Trp Asn Arg Ile
 1          5          10          15
Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe
          20          25          30
Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly Ser Leu Ser Glu Glu
          35          40          45
Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly
          50          55          60
Glu Tyr Lys Cys Gln His Gln Gln Val Asn Glu Ser Glu Pro Val Tyr
65          70          75          80
Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val
          85          90          95
Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys His Gly Trp Arg Asn
          100          105          110
Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp Gly Glu Ala Leu Lys
          115          120          125
Tyr Trp Tyr Glu Asn His Asn Ile Ser Ile Thr Asn Ala Thr Val Glu
          130          135          140
Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr
145          150          155          160
Glu Ser Glu Pro Leu Asn Ile Thr Val Ile Lys Ala Pro Arg Glu Lys
          165          170          175
Tyr Trp Leu Gln Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Gly
          180          185          190
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu His His His His His His
          195          200          205

```

```

<210> 58
<211> 208

```

<212> PRT

<213> Artificial Sequence

<220>

<223> mFfCeR1a ecto-mmH

aa 1-180: mf FceR1a (aa V29-Q208; L81W) from
translation of XM_005541313.2

aa 181-208: Myc-Myc-hexahistidine tag

<400> 58

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

<210> 59

<211> 207

<212> PRT

<213> Artificial Sequence

<220>

<223> hCD3 epsilon

<400> 59

Met	Gln	Ser	Gly	Thr	His	Trp	Arg	Val	Leu	Gly	Leu	Cys	Leu	Leu	Ser
1				5					10					15	
Val	Gly	Val	Trp	Gly	Gln	Asp	Gly	Asn	Glu	Glu	Met	Gly	Gly	Ile	Thr
			20					25					30		
Gln	Thr	Pro	Tyr	Lys	Val	Ser	Ile	Ser	Gly	Thr	Thr	Val	Ile	Leu	Thr

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

$\langle 210 \rangle$ 60

<211> 171

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> hCD3 delta

<400> 60

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

165

170

<210> 61
 <211> 164
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hCD3 zeta

<400> 61
 Met Lys Trp Lys Ala Leu Phe Thr Ala Ala Ile Leu Gln Ala Gln Leu
 1 5 10 15
 Pro Ile Thr Glu Ala Gln Ser Phe Gly Leu Leu Asp Pro Lys Leu Cys
 20 25 30
 Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala
 35 40 45
 Leu Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
 50 55 60
 Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
 65 70 75 80
 Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
 85 90 95
 Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
 100 105 110
 Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
 115 120 125
 Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
 130 135 140
 Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
 145 150 155 160
 Leu Pro Pro Arg

<210> 62
 <211> 182
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hCD3 gamma

<400> 62
 Met Glu Gln Gly Lys Gly Leu Ala Val Leu Ile Leu Ala Ile Ile Leu
 1 5 10 15
 Leu Gln Gly Thr Leu Ala Gln Ser Ile Lys Gly Asn His Leu Val Lys
 20 25 30
 Val Tyr Asp Tyr Gln Glu Asp Gly Ser Val Leu Leu Thr Cys Asp Ala
 35 40 45
 Glu Ala Lys Asn Ile Thr Trp Phe Lys Asp Gly Lys Met Ile Gly Phe

```

      50              55              60
Leu Thr Glu Asp Lys Lys Lys Trp Asn Leu Gly Ser Asn Ala Lys Asp
65              70              75              80
Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser Gln Asn Lys Ser Lys Pro
      85              90              95
Leu Gln Val Tyr Tyr Arg Met Cys Gln Asn Cys Ile Glu Leu Asn Ala
      100             105             110
Ala Thr Ile Ser Gly Phe Leu Phe Ala Glu Ile Val Ser Ile Phe Val
      115             120             125
Leu Ala Val Gly Val Tyr Phe Ile Ala Gly Gln Asp Gly Val Arg Gln
      130             135             140
Ser Arg Ala Ser Asp Lys Gln Thr Leu Leu Pro Asn Asp Gln Leu Tyr
145             150             155             160
Gln Pro Leu Lys Asp Arg Glu Asp Asp Gln Tyr Ser His Leu Gln Gly
      165             170             175
Asn Gln Leu Arg Arg Asn
      180

```

<210> 63

<211> 257

<212> PRT

<213> Artificial Sequence

<220>

<223> hFceR1a

<400> 63

```

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

```

[illegible]