

SEQUENCE LISTING

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<120> BI-FUNCTIONAL HUMANIZED ANTI-C5 ANTIBODIES AND FACTOR H FUSION
PROTEINS AND USES THEREOF

<130> 046483-6180-00WO

<150> US 62/837,853

<151> 2019-04-24

<160> 84

<170> PatentIn version 3.5

<210> 1

<211> 482

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanized 2G1 VH-11801

<400> 1

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ttgagtggat gggagatatt agtcctaact atggttatac tatctacaac cagaaattca	300
aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga	360
gcctgagatc tgacgacacg gccgtgtatt actgtgcgag aaggacatt cgttactccg	420
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ca	482

<210> 2

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized 2G1 VH-11801 (amino acid)

<400> 2

Met Asp Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile
35 40 45

Thr Asp Tyr Asn Leu Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asp Ile Ser Pro Asn Tyr Gly Tyr Thr Ile Tyr Asn
65 70 75 80

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 3

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 Humanized 2G1 VH-11801 (amino acid)

<400> 3

Gly Tyr Thr Ile Thr Asp Tyr Asn Leu Asp

1 5 10

<210> 4
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 Humanized 2G1 VH-11801 (amino acid)

<400> 4

Asp Ile Ser Pro Asn Tyr Gly Tyr Thr Ile Tyr Asn Gln Lys Phe Lys
1 5 10 15

<210> 5
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 Humanized 2G1 VH-11801 (amino acid)

<400> 5

Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys Trp Tyr Phe Asp Val
1 5 10 15

<210> 6
<211> 428
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 2G1 VL-1901

<400> 6
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cccagtctcc atccttcctg tctgcatctg taggagacag agtcaccatc acttgcagga 180
caagtaagag cataagcaaa tatttagcct ggtatcagca aaaaccaggg aaagccccta 240
agctcctgat ctattctgga tccaccttgc aatctgggggt cccatcaagg ttcagcggca 300
gtggatctgg gacagaattc actctcacia tcagcagcct gcagcctgaa gattttgcaa 360
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<210> 7
 <211> 127
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized 2G1 VL-1901 (amino acid)

<400> 7

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser
 20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Lys Ser
 35 40 45

Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 50 55 60

Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Val Pro Ser
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
 85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Asn
 100 105 110

Glu Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 115 120 125

<210> 8
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR1 Humanized 2G1 VL-1901 (amino acid)

<400> 8

Arg Thr Ser Lys Ser Ile Ser Lys Tyr Leu Ala
1 5 10

<210> 9
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 Humanized 2G1 VL-1901 (amino acid)

<400> 9

Ser Gly Ser Thr Leu Gln Ser
1 5

<210> 10
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 Humanized 2G1 VL-1901 (amino acid)

<400> 10

Gln Gln His Asn Glu Tyr Pro Tyr Thr
1 5

<210> 11
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 Humanized 2G1 VL-1901 variant (Q->H mutation in CDR3) (amino acid)

<400> 11

His Gln His Asn Glu Tyr Pro Tyr Thr
1 5

<210> 12
<211> 428
<212> DNA
<213> Artificial Sequence

<220>

<223> Humanized 2G1 VL-1901 variant (Q->H mutation in CDR3)

<400> 12

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caagtaagag cataagcaaa tatttagcct ggtatcagca aaaaccaggg aaagccccta      240
agctcctgat ctattctgga tccaccttgc aatctgggggt cccatcaagg ttcagcggca      300
gtggatctgg gacagaattc actctcacia tcagcagcct gcagcctgaa gattttgcaa      360
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agatcaaa                                         428
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<210> 13

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized 2G1 VL-1901 variant (Q->H mutation in CDR3) (amino acid)

<400> 13

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Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1           5           10          15
```

```
Asp Thr Thr Gly Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser
          20          25          30
```

```
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Lys Ser
          35          40          45
```

```
Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
          50          55          60
```

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

Glu Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

<210> 14
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 Humanized 2G1 VL-1901 variant (T->H mutation in CDR1) (amino acid)

<400> 14

Arg His Ser Lys Ser Ile Ser Lys Tyr Leu Ala
1 5 10

<210> 15
<211> 428
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 2G1 VL-1901 variant (T->H mutation in CDR1)

<400> 15
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ctcagcttct cttcctcctg ctactctggc tcccagatac caccggagac atccagttga 120
cccagtctcc atccttcctg tctgcatctg taggagacag agtcaccatc acttgcaggc 180
atagtaagag cataagcaaa tatttagcct ggtatcagca aaaaccaggg aaagccccta 240
agctcctgat ctattctgga tccaccttgc aatctgggggt cccatcaagg ttcagcggca 300
gtggatctgg gacagaattc actctcacia tcagcagcct gcagcctgaa gattttgcaa 360
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agatcaaa 428

<210> 16
<211> 127
<212> PRT
<213> Artificial Sequence

<220>

<223> Humanized 2G1 VL-1901 variant (T->H mutation in CDR1) (amino acid)

<400> 16

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser
20 25 30

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

Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Asn
100 105 110

Glu Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

<210> 17

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 Humanized 2G1 VH-11801 variant (I->H mutation in CDR1) (amino acid)

<400> 17

Arg His Ser Lys Ser Ile Ser Lys Tyr Leu Ala
1 5 10

<210> 18
<211> 482
<212> DNA
<213> Artificial Sequence

<220>

<223> Humanized 2G1 VH-11801 variant (I->H mutation in CDR1)

<400> 18
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tgcagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc tgcaaggctt 180
ctggatacac acatacagac tacaatttgg actgggtgcg acaggcccct ggacaagggc 240
ttgagtggat gggagatatt agtcctaact atggttatac tatctacaac cagaaattca 300
aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga 360
gcctgagatc tgacgacacg gccgtgtatt actgtgcgag aaggacatt cgttactccg 420
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ca 482

<210> 19
<211> 144
<212> PRT
<213> Artificial Sequence

<220>

<223> Humanized 2G1 VH-11801 variant (I->H mutation in CDR1) (amino acid)

<400> 19

Met Asp Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr His
35 40 45

Thr Asp Tyr Asn Leu Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asp Ile Ser Pro Asn Tyr Gly Tyr Thr Ile Tyr Asn
65 70 75 80

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 20
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 Humanized 2G1 VH-11801 variant (N->H mutation in CDR1)
(amino acid)

<400> 20

Gly Tyr Thr Ile Thr Asp Tyr His Leu Asp
1 5 10

<210> 21
<211> 481
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 2G1 VH-11801 variant (N->H mutation in CDR1)

<400> 21
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tgcagtctgg agctgagggtg aagaagcctg gggcctcagt gaaggctctc tgcaaggctt 180
ctggatacac aatcacagac taccatttgg actgggtgctg acaggcccct ggacaagggc 240
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aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga 360
gcctgagatc tgacgacacg gccgtgtatt actgtgcgag aaggacatt cgttactccg 420
gtaattccta caaatggtac ttcgatgtct ggggccaagg gacaatggtc accgtctctt 480
c 481

<210> 22
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 2G1 VH-11801 variant (N->H mutation in CDR1) (amino acid)

<400> 22

Met Asp Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile
35 40 45

Thr Asp Tyr His Leu Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asp Ile Ser Pro Asn Tyr Gly Tyr Thr Ile Tyr Asn
65 70 75 80

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser

130

135

140

<210> 23
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR1 Humanized 2G1 VL-1901 variant (Y->H mutation in CDR1) (amino acid)

<400> 23

Arg Thr Ser Lys Ser Ile Ser Lys His Leu Ala
 1 5 10

<210> 24
 <211> 428
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanized 2G1 VL-1901 variant (Y->H mutation in CDR1)

<400> 24
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 cccagtctcc atccttcctg tctgcatctg taggagacag agtcaccatc acttgcagga 180
 caagtaagag cataagcaaa catttagcct ggtatcagca aaaaccaggg aaagccccta 240
 agtcctgat ctattctgga tccaccttgc aatctgggggt cccatcaagg ttcagcggca 300
 gtggatctgg gacagaattc actctcacia tcagcagcct gcagcctgaa gattttgcaa 360
 cttattactg tcaacaacat aatgaatacc cgtacacgtt tggccagggg accaagctgg 420
 agatcaaa 428

<210> 25
 <211> 127
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized 2G1 VL-1901 variant (Y->H mutation in CDR1) (amino acid)

<400> 25

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Lys Ser
35 40 45

Ile Ser Lys His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Asn
100 105 110

Glu Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

<210> 26

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 Humanized 2G1 VH-11801 variant (Y->H mutation in CDR2)

<400> 26

Asp Ile Ser Pro Asn His Gly Tyr Thr Ile Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 27

<211> 482

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanized 2G1 VH-11801 variant (Y->H mutation in CDR2)

<400> 27

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tgcagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc tgcaaggctt      180
ctggatacac aatcacagac tacaatttgg actgggtgcg acaggcccct ggacaagggc      240
ttgagtggat gggagatatt agtcctaacc atggttatac tatctacaac cagaaattca      300
aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga      360
gcctgagatc tgacgacacg gccgtgtatt actgtgcgag aaggacatt cgttactccg      420
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<210> 28

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized 2G1 VH-11801 variant (Y->H mutation in CDR2) (amino acid)

<400> 28

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Met Asp Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
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```

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Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
          20          25          30
```

```
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile
          35          40          45
```

```
Thr Asp Tyr Asn Leu Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
          50          55          60
```

```
Glu Trp Met Gly Asp Ile Ser Pro Asn His Gly Tyr Thr Ile Tyr Asn
65          70          75          80
```

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

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

<220>
<223> CDR3 Humanized 2G1 VL-1901 variant (E->H mutation in CDR3) (amino acid)

<400> 29

Gln Gln His Asn His Tyr Pro Tyr Thr
1 5

<210> 30
<211> 428
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 2G1 VL-1901 variant (E->H mutation in CDR3)

<400> 30
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cccagtctcc atccttcctg tctgcatctg taggagacag agtcaccatc acttgcagga 180
caagtaagag cataagcaaa tatttagcct ggtatcagca aaaaccaggg aaagccccta 240
agctcctgat ctattctgga tccaccttgc aatctgggggt cccatcaagg ttcagcggca 300
gtggatctgg gacagaattc actctcacia tcagcagcct gcagcctgaa gattttgcaa 360

cttattactg tcaacaacat aatcattacc cgtacacgtt tggccagggg accaagctgg 420
agatcaaa 428

<210> 31
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 2G1 VL-1901 variant (E->H mutation in CDR3) (amino acid)

<400> 31

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Lys Ser
35 40 45

Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Asn
100 105 110

His Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

<210> 32
<211> 327
<212> PRT
<213> Artificial Sequence

<220>

<223> Human IgG4 Constant Heavy chain region (amino acid)

<400> 32

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

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

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

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Pro Gly Lys
325

<210> 33
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG4 Constant Heavy chain region with S228P mutation (amino acid)

<400> 33

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

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser

35

40

45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

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

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Pro Gly Lys
325

<210> 34
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 Humanized 2G1 VH-11801 variant (T->H mutation in CDR2)

<400> 34

Asp Ile Ser Pro Asn Tyr Gly Tyr His Ile Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 35
<211> 482
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized 2G1 VH-11801 variant (T->H mutation in CDR2)

<400> 35
cagcatatga tcagtgtcct ctccaaagtc cttgaacata gactctaacc atggactgga 60
cctgggtctt tctcttcctc ctgtcagtaa ctgcaggtgt ccactcccag gttcagctgg 120
tgcagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc tgcaaggctt 180

ctggatacac aatcacagac tacaatttgg actgggtgcg acaggcccct ggacaagggc 240
 ttgagtggat gggagatatt agtcctaact atggttatca tatctacaac cagaaattca 300
 aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga 360
 gcctgagatc tgacgacacg gccgtgtatt actgtgcgag aaggacatt cgttactccg 420
 gtaattccta caaatggtac ttcgatgtct ggggccaagg gacaatggtc accgtctctt 480
 ca 482

<210> 36
 <211> 144
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized 2G1 VH-11801 variant (T->H mutation in CDR2) (amino acid)

<400> 36

Met Asp Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
 1 5 10 15

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile
 35 40 45

Thr Asp Tyr Asn Leu Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Met Gly Asp Ile Ser Pro Asn Tyr Gly Tyr His Ile Tyr Asn
 65 70 75 80

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
 85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
 115 120 125

Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 37
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 IWW-VH (amino acid)

<400> 37

Gly Tyr Thr Ile Thr Asp Tyr His Ile Asp
1 5 10

<210> 38
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 IWW-VH (amino acid)

<400> 38

Asp Ile Ser Trp Asn Tyr Gly Tyr Thr Ile Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 39
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 IWW-VH (amino acid)

<400> 39

Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys Trp Tyr Phe Asp Trp
1 5 10 15

<210> 40
<211> 482

<212> DNA
<213> Artificial Sequence

<220>
<223> IWW-VH

<400> 40
cagcatatga tcagtgtcct ctccaaagtc cttgaacata gactctaacc atggactgga 60
cctgggtctt tctcttcctc ctgtcagtaa ctgcaggtgt ccactcccag gttcagctgg 120
tgcaagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc tgcaaggctt 180
ctggatacac aatcacagac taccatatcg actgggtgcg acaggcccct ggacaagggc 240
ttgagtggat gggagatatt agttggaact atgggttatac tatctacaac cagaaattca 300
aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga 360
gcctgagatc tgacgacacg gccgtgtatt actgtgagag aaggacatt cgttactccg 420
gtaattccta caaatggtac ttcgattggt ggggccaagg gacaatggtc accgtctctt 480
ca 482

<210> 41
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> IWW-VH (amino acid)

<400> 41

Met Asp Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile
35 40 45

Thr Asp Tyr His Ile Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asp Ile Ser Trp Asn Tyr Gly Tyr Thr Ile Tyr Asn
65 70 75 80

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Trp Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 42
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 IFW-VH (amino acid)

<400> 42

Gly Tyr Thr Ile Thr Asp Tyr His Ile Asp
1 5 10

<210> 43
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 IFW-VH (amino acid)

<400> 43

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

Asp

<210> 44
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> CDR3 IFW-VH (amino acid)

<400> 44

Arg	Asp	Ile	Arg	Tyr	Ser	Gly	Asn	Ser	Tyr	Lys	Trp	Tyr	Phe	Asp	Trp
1				5					10					15	

<210> 45

<211> 482

<212> DNA

<213> Artificial Sequence

<220>

<223> IFW-VH

<400> 45

cagcatatga tcagtgtcct ctccaaagtc cttgaacata gactctaacc atggactgga	60
cctgggtctt tctcttcctc ctgtcagtaa ctgcaggtgt ccactcccag gttcagctgg	120
tgcagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc tgcaaggctt	180
ctggatacac aatcacagac taccatatcg actgggtgcg acaggcccct ggacaagggc	240
ttgagtggat gggagatatt agtttcaact atggttatac tatctacaac cagaaattca	300
aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga	360
gcctgagatc tgacgacacg gccgtgtatt actgtgcgag aaggacatt cgttactccg	420
gtaattccta caaatggtag ttcgattggg ggggccaagg gacaatggtc accgtctctt	480
ca	482

<210> 46

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> IFW-VH (amino acid)

<400> 46

Met	Asp	Trp	Thr	Trp	Val	Phe	Leu	Phe	Leu	Leu	Ser	Val	Thr	Ala	Gly
1				5					10					15	

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile
35 40 45

Thr Asp Tyr His Ile Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asp Ile Ser Phe Asn Tyr Gly Tyr Thr Ile Tyr Asn
65 70 75 80

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Trp Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 47
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 FME-VH (amino acid)

<400> 47

Gly Tyr Thr Ile Thr Asp Tyr His Phe Asp
1 5 10

<210> 48
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 FME-VH (amino acid)

<400> 48

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

Asp

<210> 49
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 FME-VH (amino acid)

<400> 49

Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys Trp Tyr Phe Asp Glu
1 5 10 15

<210> 50
<211> 482
<212> DNA
<213> Artificial Sequence

<220>
<223> FME-VH

<400> 50
cagcatatga tcagtgtcct ctccaaagtc cttgaacata gactctaacc atggactgga 60
cctgggtctt tctcttcctc ctgtcagtaa ctgcaggtgt ccactcccag gttcagctgg 120
tgcagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc tgcaaggctt 180
ctggatacac aatcacagac taccatttcg actgggtgcg acaggcccct ggacaagggc 240
ttgagtggat gggagatatt agtatgaact atggttatac tatctacaac cagaaattca 300
aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga 360
gcctgagatc tgacgacacg gccgtgtatt actgtgcgag aaggacatt cgttactccg 420
gtaattccta caaatggtac ttcgatgagt ggggcccaagg gacaatggtc accgtctctt 480
ca 482

<210> 51
<211> 144
<212> PRT
<213> Artificial Sequence

<220>

<223> FME-VH (amino acid)

<400> 51

Met Asp Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile
35 40 45

Thr Asp Tyr His Phe Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asp Ile Ser Met Asn Tyr Gly Tyr Thr Ile Tyr Asn
65 70 75 80

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Glu Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 52

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 FMW-VH (amino acid)

<400> 52

Gly Tyr Thr Ile Thr Asp Tyr His Phe Asp
1 5 10

<210> 53
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 FMW-VH (amino acid)

<400> 53

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

Asp

<210> 54
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 FMW-VH (amino acid)

<400> 54

Arg	Asp	Ile	Arg	Tyr	Ser	Gly	Asn	Ser	Tyr	Lys	Trp	Tyr	Phe	Asp	Trp
1				5					10					15	

<210> 55
<211> 482
<212> DNA
<213> Artificial Sequence

<220>
<223> FMW-VH

<400> 55

cagcatatga tcagtgtcct ctccaaagtc cttgaacata gactctaacc atggactgga	60
cctgggtctt tctcttcctc ctgtcagtaa ctgcaggtgt ccactcccag gttcagctgg	120
tgcagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc tgcaaggctt	180
ctggatacac aatcacagac taccatttcg actgggtgcg acaggcccct ggacaagggc	240
ttgagtggat gggagatatt agtatgaact atggttatac tatctacaac cagaaattca	300
aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga	360

gcctgagatc tgacgacacg gccgtgtatt actgtgagag aaggacatt cggtactccg 420
gtaattccta caaatggtac ttcgattggt ggggccaagg gacaatggtc accgtctctt 480
ca 482

<210> 56
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> FMW-VH (amino acid)

<400> 56

Met Asp Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile
35 40 45

Thr Asp Tyr His Phe Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asp Ile Ser Met Asn Tyr Gly Tyr Thr Ile Tyr Asn
65 70 75 80

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Trp Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 57
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 FMEH-VH (amino acid)

<400> 57

Asp	Ile	Ser	Met	Asn	Tyr	Gly	Tyr	His	Ile	Tyr	Asn	Gln	Lys	Phe	Lys
1				5					10					15	

Asp

<210> 58
<211> 482
<212> DNA
<213> Artificial Sequence

<220>
<223> FMEH-VH

<400> 58
cagcatatga tcagtgtcct ctccaaagtc cttgaacata gactctaacc atggactgga 60
cctgggtctt tctcttcctc ctgtcagtaa ctgcaggtgt ccactcccag gttcagctgg 120
tgcagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc tgcaaggctt 180
ctggatacac aatcacagac taccatttcg actgggtgcg acaggcccct ggacaagggc 240
ttgagtggat gggagatatt agtatgaact atggttatca tatctacaac cagaaattca 300
aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga 360
gcctgagatc tgacgacacg gccgtgtatt actgtgcgag aaggacatt cgttactccg 420
gtaattccta caaatggtac ttcgatgagt ggggccaagg gacaatggtc accgtctctt 480
ca 482

<210> 59
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> FMEH-VH (amino acid)

<400> 59

Met Asp Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile
35 40 45

Thr Asp Tyr His Phe Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asp Ile Ser Met Asn Tyr Gly Tyr His Ile Tyr Asn
65 70 75 80

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Glu Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 60

<211> 984

<212> DNA

<213> Artificial Sequence

<220>

<223> Human IgG4 Fc PLA domain mutation

<400> 60

gctagcacca agggcccatc ggtcttcccc ctggcgcctt gctccaggag cacctccgag 60

agcacagccg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg 120

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180

ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg cacgaagacc 240

tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagag agttgagtcc	300
aaatatgggtc ccccatgccc accatgcccga gcacctgagt tcctgggggg accatcagtc	360
ttcctgttcc ccccaaaacc caaggacact ctcatgatct cccggacccc tgaggtcacg	420
tgcgtggtgg tggacgtgag ccaggaagac cccgaggtcc agttcaactg gtacgtggat	480
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagttcaa cagcacgtac	540
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaacggcaa ggagtacaag	600
tgcaagggtct ccaacaaagg cctcccgtcc tccatcgaga aaaccatctc caaagccaaa	660
gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccaggagga gatgaccaag	720
aaccaggtca gcctgacctg cctgggtcaaa ggcttctacc ccagcgacat cgccgtggag	780
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	840
gacggctcct tcttcctcta cagcaggctc accgtggaca agagcaggtg gcaggagggg	900
aatgtcttct catgctccgt gctgcatgag gctctgcacg cccactacac acagaagagc	960
ctctccctgt ctctgggtaa atga	984

<210> 61
 <211> 327
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human IgG4 Fc PLA domain mutation (amino acid)
 <400> 61

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

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

Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
		35					40					45			

Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
	50					55					60				

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

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

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Leu His Glu Ala Leu His Ala His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325

<210> 62
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 IWWH-VH (amino acid)

<400> 62

Asp Ile Ser Trp Asn Tyr Gly Tyr His Ile Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 63
<211> 482
<212> DNA
<213> Artificial Sequence

<220>
<223> IWWH-VH

<400> 63
cagcatatga tcagtgtcct ctccaaagtc cttgaacata gactctaacc atggactgga 60
cctgggtctt tctcttcctc ctgtcagtaa ctgcaggtgt ccactcccag gttcagctgg 120
tgcagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc tgcaaggctt 180
ctggatacac aatcacagac taccatatcg actgggtgcg acaggcccct ggacaagggc 240
ttgagtggat gggagatatt agttggaact atggttatca tatctacaac cagaaattca 300
aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga 360
gcctgagatc tgacgacacg gccgtgtatt actgtgcgag aaggacatt cgttactccg 420

gtaattccta caaatggtac ttcgattggt ggggccaaagg gacaatgggc accgtctctt 480

ca 482

<210> 64

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> IWWH-VH (amino acid)

<400> 64

Met Asp Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile
35 40 45

Thr Asp Tyr His Ile Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asp Ile Ser Trp Asn Tyr Gly Tyr His Ile Tyr Asn
65 70 75 80

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Trp Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 65

<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 IFWH-VH (amino acid)

<400> 65

Asp Ile Ser Phe Asn Tyr Gly Tyr His Ile Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 66
<211> 482
<212> DNA
<213> Artificial Sequence

<220>
<223> IFWH-VH

<400> 66
cagcatatga tcagtgtcct ctccaaagtc cttgaacata gactctaacc atggactgga 60
cctgggtctt tctcttcctc ctgtcagtaa ctgcaggtgt ccactcccag gttcagctgg 120
tgcagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc tgcaaggctt 180
ctggatacac aatcacagac taccatatcg actgggtgcg acaggcccct ggacaagggc 240
ttgagtggat gggagatatt agtttcaact atggttatca tatctacaac cagaaattca 300
aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga 360
gcctgagatc tgacgacacg gccgtgtatt actgtgcgag aaggacatt cgttactccg 420
gtaattccta caaatggtac ttcgattggt ggggcccaagg gacaatggtc accgtctctt 480
ca 482

<210> 67
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> IFWH-VH (amino acid)

<400> 67

Met Asp Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile
35 40 45

Thr Asp Tyr His Ile Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asp Ile Ser Phe Asn Tyr Gly Tyr His Ile Tyr Asn
65 70 75 80

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Trp Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 68

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 FMWH-VH (amino acid)

<400> 68

Asp Ile Ser Met Asn Tyr Gly Tyr His Ile Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 69
<211> 482
<212> DNA
<213> Artificial Sequence

<220>
<223> FMWH-VH

<400> 69
cagcatatga tcagtgtcct ctccaaagtc cttgaacata gactctaacc atggactgga 60
cctgggtctt tctcttcctc ctgtcagtaa ctgcaggtgt ccactcccag gttcagctgg 120
tgcagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc tgcaaggctt 180
ctggatacac aatcacagac taccatttcg actgggtgcg acaggcccct ggacaagggc 240
ttgagtggat gggagatatt agtatgaact atggttatca tatctacaac cagaaattca 300
aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga 360
gcctgagatc tgacgacacg gccgtgtatt actgtgcgag aaggacatt cgttactccg 420
gtaattccta caaatggtac ttcgattggg ggggccaagg gacaatggtc accgtctctt 480
ca 482

<210> 70
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> FMWH-VH (amino acid)

<400> 70

Met Asp Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile
35 40 45

Thr Asp Tyr His Phe Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asp Ile Ser Met Asn Tyr Gly Tyr His Ile Tyr Asn
65 70 75 80

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Trp Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 71
<211> 2384
<212> DNA
<213> Artificial Sequence

<220>
<223> VH sequence of FMEH-IgG4PLA-FH1-5

<400> 71
cagcatatga tcagtgtcct ctccaaagtc cttgaacata gactctaacc atggactgga 60
cctgggtctt tctcttcctc ctgtcagtaa ctgcaggtgt ccactcccag gttcagctgg 120
tgcagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc tgcaaggctt 180
ctggatacac aatcacagac taccatttcg actgggtgcg acaggcccct ggacaagggc 240
ttgagtggat gggagatatt agtatgaact atggttatca tatctacaac cagaaattca 300
aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga 360
gcctgagatc tgacgacacg gccgtgtatt actgtgcgag aaggacatt cgttactccg 420
gtaattccta caaatggtag ttcgatgagt ggggccaagg gacaatggtc accgtctctt 480
cagctagcac caagggccca tcggtcttcc ccctggcgcc ctgctccagg agcacctccg 540
agagcacagc cgccctgggc tgcctgggtca aggactactt ccccgaaccg gtgacgggtg 600
cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc ctacagtcct 660
caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg ggcacgaaga 720
cctacacctg caacgtagat cacaagccca gcaacaccaa ggtggacaag agagttgagt 780

ccaaatatgg tcccccatgc ccaccatgcc cagcacctga gttcctgggg ggaccatcag	840
tcttcctgtt ccccccaaaa cccaaggaca ctctcatgat ctcccggacc cctgaggtca	900
cgtgcgtggg ggtggacgtg agccaggaag accccgaggt ccagttcaac tggtagctgg	960
atggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagttc aacagcacgt	1020
accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaacggc aaggagtaca	1080
agtgcaagggt ctccaacaaa ggcctcccgt cctccatcga gaaaaccatc tccaaagcca	1140
aagggcagcc ccgagagcca caggtgtaca ccctgcccc atcccaggag gagatgacca	1200
agaaccagggt cagcctgacc tgcctgggtca aaggcttcta cccagcgac atcgccgtgg	1260
agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc gtgctggact	1320
ccgacggctc cttcttcctc tacagcaggc tcaccgtgga caagagcagg tggcaggagg	1380
ggaatgtctt ctcatgctcc gtgctgcatg aggctctgca cgcccactac acacagaaga	1440
gcctctccct gtctctgggt aaagaggatt gtaatgaact gcctccaaga aggaacacag	1500
aaattttgac cgggtcctgg tccgatcaaa cctaccctga aggaactcaa gctatataca	1560
agtcagacc tggttataga tctactgggca acattatcat ggtatgtcgc aaaggagaat	1620
gggtggctct gaatcccctc agaaaatgcc agaaacggcc atgtggacac cccggcgata	1680
ccccattcgg gacatttacc ttgactggag gcaatgtatt cgagtatggc gtgaaagctg	1740
tctatacctg taacgaagggt taccaattgt tgggagaaat aaattacaga gaatgtgata	1800
ccgatggatg gaccaacgat attcccatat gcgaggttgt taagtgcttg cctgtcactg	1860
caccagaaaa cgggaaaatc gtatctagcg caatggagcc agaccgcgaa taccatttcg	1920
ggcaggcagt gaggtttgtt tgcaattccg gttataagat agaaggggat gaggagatgc	1980
actgtagcga cgatggtttt tgggtccaagg aaaagcccaa gtgcgtcgaa ataagttgca	2040
agtcacctga cgtcataaac gggagcccca tatcccaaaa gataatttac aaggagaacg	2100
aacgatttca atataagtgt aatatgggggt atgaatactc cgagagaggt gatgccgtct	2160
gtaccgaaag tggatggcga ccactcccct catgcgaaga gaagtcctgt gataatccat	2220
acatccctaa tgggtgattat tcccccttc gaataaagca tcggacagga gacgagatca	2280
catatcagtg tcgcaacgga ttctatccag ccaccagagg caacactgca aagtgtacat	2340
ctacaggatg gatacctgcc ccacgatgta cttgaagcc ctga	2384

<210> 72
<211> 777
<212> PRT
<213> Artificial Sequence

<220>
<223> VH sequence of FMEH-IgG4PLA-FH1-5 (amino acid)

<400> 72

Met Asp Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile
35 40 45

Thr Asp Tyr His Phe Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asp Ile Ser Met Asn Tyr Gly Tyr His Ile Tyr Asn
65 70 75 80

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Glu Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
145 150 155 160

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
165 170 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
180 185 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
195 200 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
210 215 220

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
225 230 235 240

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
245 250 255

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
275 280 285

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
290 295 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
340 345 350

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
370 375 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Leu His Glu Ala Leu His Ala His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Leu Gly Lys Glu Asp Cys Asn Glu Leu Pro Pro Arg
465 470 475 480

Arg Asn Thr Glu Ile Leu Thr Gly Ser Trp Ser Asp Gln Thr Tyr Pro
485 490 495

Glu Gly Thr Gln Ala Ile Tyr Lys Cys Arg Pro Gly Tyr Arg Ser Leu
500 505 510

Gly Asn Ile Ile Met Val Cys Arg Lys Gly Glu Trp Val Ala Leu Asn
515 520 525

Pro Leu Arg Lys Cys Gln Lys Arg Pro Cys Gly His Pro Gly Asp Thr
530 535 540

Pro Phe Gly Thr Phe Thr Leu Thr Gly Gly Asn Val Phe Glu Tyr Gly
545 550 555 560

Val Lys Ala Val Tyr Thr Cys Asn Glu Gly Tyr Gln Leu Leu Gly Glu
565 570 575

Ile Asn Tyr Arg Glu Cys Asp Thr Asp Gly Trp Thr Asn Asp Ile Pro
580 585 590

Ile Cys Glu Val Val Lys Cys Leu Pro Val Thr Ala Pro Glu Asn Gly
595 600 605

Lys Ile Val Ser Ser Ala Met Glu Pro Asp Arg Glu Tyr His Phe Gly
610 615 620

Gln Ala Val Arg Phe Val Cys Asn Ser Gly Tyr Lys Ile Glu Gly Asp
625 630 635 640

Glu Glu Met His Cys Ser Asp Asp Gly Phe Trp Ser Lys Glu Lys Pro
645 650 655

Lys Cys Val Glu Ile Ser Cys Lys Ser Pro Asp Val Ile Asn Gly Ser
660 665 670

Pro Ile Ser Gln Lys Ile Ile Tyr Lys Glu Asn Glu Arg Phe Gln Tyr
675 680 685

Lys Cys Asn Met Gly Tyr Glu Tyr Ser Glu Arg Gly Asp Ala Val Cys
690 695 700

Thr Glu Ser Gly Trp Arg Pro Leu Pro Ser Cys Glu Glu Lys Ser Cys
705 710 715 720

Asp Asn Pro Tyr Ile Pro Asn Gly Asp Tyr Ser Pro Leu Arg Ile Lys
725 730 735

His Arg Thr Gly Asp Glu Ile Thr Tyr Gln Cys Arg Asn Gly Phe Tyr
740 745 750

Pro Ala Thr Arg Gly Asn Thr Ala Lys Cys Thr Ser Thr Gly Trp Ile
755 760 765

Pro Ala Pro Arg Cys Thr Leu Lys Pro
770 775

<210> 73
<211> 752
<212> DNA
<213> Artificial Sequence

<220>
<223> VL sequence of FMEH-IgG4-FH1-5

<400> 73
gtcagagccc tggggaggaa ctgctcagtt aggaccaga gggaaccatg gaagccccag 60
ctcagcttct cttcctcctg ctactctggc tcccagatac caccggagac atccagttga 120
cccagttctc atccttcctg tctgcatctg taggagacag agtcaccatc acttgcagga 180
caagtaagag cataagcaaa catttagcct ggtatcagca aaaaccaggg aaagccccta 240
agctcctgat ctattctgga tccaccttgc aatctggggt cccatcaagg ttcagcggca 300
gtggatctgg gacagaattc actctcacia tcagcagcct gcagcctgaa gattttgcaa 360
cttattactg tcaacaacat aatgaatacc cgtacacgtt tggccagggg accaagctgg 420
agatcaaacg tacggtggct gcaccatctg tcttcatctt cccgccatct gatgagcagt 480
tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc agagaggcca 540
aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag agtgtcacag 600
agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg agcaaagcag 660
actacgagaa acacaaagtc tacgcctgcg aagtcacca tcagggcctg agctcgccccg 720
tcacaaagag cttcaacagg ggagagtgtt ag 752

<210> 74
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> VL sequence of FMEH-IgG4-FH1-5 (amino acid)

<400> 74

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Lys Ser
35 40 45

Ile Ser Lys His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Asn
100 105 110

Glu Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 75
<211> 2384
<212> DNA
<213> Artificial Sequence

<220>
<223> VH sequence of IWWH-IgG4PLA-FH1-5

<400> 75
cagcatatga tcagtgtcct ctccaaagtc cttgaacata gactctaacc atggactgga

cctgggtctt tctcttcctc ctgtcagtaa ctgcaggtgt ccactcccag gttcagctgg	120
tgcaagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc tgcaaggctt	180
ctggatacac aatcacagac taccatatcg actgggtgcg acaggcccct ggacaagggc	240
ttgagtggat gggagatatt agttggaact atggttatca tatctacaac cagaaattca	300
aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga	360
gcctgagatc tgacgacacg gccgtgtatt actgtgagag aaggacatt cgttactccg	420
gtaattccta caaatggtac ttcgattggg ggggccaagg gacaatggc accgtctctt	480
cagctagcac caagggccca tcggtcttcc ccctggcgcc ctgctccagg agcacctccg	540
agagcacagc cgccctgggc tgcctgggtca aggactactt cccgaaccg gtgacgggtg	600
cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc ctacagtcct	660
caggactcta ctccctcagc agcgtgggtga ccgtgccctc cagcagcttg ggcacgaaga	720
cctacacctg caacgtagat cacaagccca gcaacaccaa ggtggacaag agagttgagt	780
ccaaatatgg tccccatgc ccaccatgcc cagcacctga gttcctgggg ggaccatcag	840
tcttctgtt cccccaaaa cccaaggaca ctctcatgat ctcccggacc cctgaggtca	900
cgtgcgtggg ggtggacgtg agccaggaag accccgaggt ccagttcaac tggtagctgg	960
atggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagttc aacagcacgt	1020
accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaacggc aaggagtaca	1080
agtgaagggt ctccaacaaa ggcctcccgt cctccatcga gaaaaccatc tccaaagcca	1140
aagggcagcc ccgagagcca caggtgtaca ccctgcccc atcccaggag gagatgacca	1200
agaaccaggt cagcctgacc tgcctgggtca aaggcttcta cccagcgac atcgccgtgg	1260
agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc gtgctggact	1320
ccgacggctc cttcttcctc tacagcaggc tcaccgtgga caagagcagg tggcaggagg	1380
ggaatgtctt ctcatgctcc gtgctgcatg aggctctgca cggccactac acacagaaga	1440
gcctctccct gtctctgggt aaagaggatt gtaatgaact gcctccaaga aggaacacag	1500
aaattttgac cgggtcctgg tccgatcaaa cctaccctga aggaactcaa gctatataca	1560
agtgcagacc tgggtataga tctactgggc acattatcat ggtatgtcgc aaaggagaat	1620
gggtggctct gaatcccctc agaaaatgcc agaaacggcc atgtggacac cccggcgata	1680

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ccccattcgg gacatttacc ttgactggag gcaatgtatt cgagtatggc gtgaaagctg      1740
tctataacctg taacgaaggt taccaattgt tgggagaaat aaattacaga gaatgtgata      1800
ccgatggatg gaccaacgat attcccatat gcgagggttg taagtgcttg cctgtcactg      1860
caccagaaaa cgggaaaatc gtatctagcg caatggagcc agaccgcgaa taccatttcg      1920
ggcaggcagt gaggtttgtt tgcaattccg gttataagat agaaggggat gaggagatgc      1980
actgtagcga cgatggtttt tgggtccaagg aaaagcccaa gtgcgtcgaa ataagttgca      2040
agtcacctga cgtcataaac gggagcccca tatcccaaaa gataatttac aaggagaacg      2100
aacgatttca atataagtgt aatatggggt atgaatactc cgagagaggt gatgccgtct      2160
gtaccgaaag tggatggcga ccactcccct catgcgaaga gaagtcctgt gataatccat      2220
acatccctaa tgggtgattat tcccccttc gaataaagca tcggacagga gacgagatca      2280
catatcagtg tcgcaacgga ttctatccag ccaccagagg caacactgca aagtgtacat      2340
ctacaggatg gatactgcc ccacgatgta ccttgaagcc ctga                        2384

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<210> 76
<211> 777
<212> PRT
<213> Artificial Sequence

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<220>
<223> VH sequence of IWWH-IgG4PLA-FH1-5 (amino acid)

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<400> 76

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Met Asp Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1           5           10          15

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

```

```

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile
          35          40          45

```

```

Thr Asp Tyr His Ile Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
          50          55          60

```

```

Glu Trp Met Gly Asp Ile Ser Trp Asn Tyr Gly Tyr His Ile Tyr Asn
65           70           75          80

```

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Trp Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
145 150 155 160

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
165 170 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
180 185 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
195 200 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
210 215 220

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
225 230 235 240

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
245 250 255

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
275 280 285

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
290 295 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
340 345 350

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
370 375 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Leu His Glu Ala Leu His Ala His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Leu Gly Lys Glu Asp Cys Asn Glu Leu Pro Pro Arg
465 470 475 480

Arg Asn Thr Glu Ile Leu Thr Gly Ser Trp Ser Asp Gln Thr Tyr Pro
485 490 495

Glu Gly Thr Gln Ala Ile Tyr Lys Cys Arg Pro Gly Tyr Arg Ser Leu
500 505 510

Gly Asn Ile Ile Met Val Cys Arg Lys Gly Glu Trp Val Ala Leu Asn
515 520 525

Pro Leu Arg Lys Cys Gln Lys Arg Pro Cys Gly His Pro Gly Asp Thr
530 535 540

Pro Phe Gly Thr Phe Thr Leu Thr Gly Gly Asn Val Phe Glu Tyr Gly
545 550 555 560

Val Lys Ala Val Tyr Thr Cys Asn Glu Gly Tyr Gln Leu Leu Gly Glu
565 570 575

Ile Asn Tyr Arg Glu Cys Asp Thr Asp Gly Trp Thr Asn Asp Ile Pro
580 585 590

Ile Cys Glu Val Val Lys Cys Leu Pro Val Thr Ala Pro Glu Asn Gly
595 600 605

Lys Ile Val Ser Ser Ala Met Glu Pro Asp Arg Glu Tyr His Phe Gly
610 615 620

Gln Ala Val Arg Phe Val Cys Asn Ser Gly Tyr Lys Ile Glu Gly Asp
625 630 635 640

Glu Glu Met His Cys Ser Asp Asp Gly Phe Trp Ser Lys Glu Lys Pro
645 650 655

Lys Cys Val Glu Ile Ser Cys Lys Ser Pro Asp Val Ile Asn Gly Ser
660 665 670

Pro Ile Ser Gln Lys Ile Ile Tyr Lys Glu Asn Glu Arg Phe Gln Tyr
675 680 685

Lys Cys Asn Met Gly Tyr Glu Tyr Ser Glu Arg Gly Asp Ala Val Cys
690 695 700

Thr Glu Ser Gly Trp Arg Pro Leu Pro Ser Cys Glu Glu Lys Ser Cys
705 710 715 720

Asp Asn Pro Tyr Ile Pro Asn Gly Asp Tyr Ser Pro Leu Arg Ile Lys
725 730 735

His Arg Thr Gly Asp Glu Ile Thr Tyr Gln Cys Arg Asn Gly Phe Tyr
740 745 750

Pro Ala Thr Arg Gly Asn Thr Ala Lys Cys Thr Ser Thr Gly Trp Ile
755 760 765

Pro Ala Pro Arg Cys Thr Leu Lys Pro
770 775

<210> 77
<211> 2384
<212> DNA
<213> Artificial Sequence

<220>
<223> VH sequence of IFWH-IgG4PLA-FH1-5

<400> 77
cagcatatga tcagtgtcct ctccaaagtc cttgaacata gactctaacc atggactgga 60
cctgggtctt tctcttcctc ctgtcagtaa ctgcaggtgt ccactcccag gttcagctgg 120
tgcagtctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc tgcaaggctt 180
ctggatacac aatcacagac taccatatcg actgggtgcg acaggcccct ggacaagggc 240
ttgagtggat gggagatatt agtttcaact atggttatca tatctacaac cagaaattca 300
aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga 360
gcctgagatc tgacgacacg gccgtgtatt actgtgagag aaggacatt cgttactccg 420
gtaattccta caaatggtac ttcgattggg ggggccaagg gacaatgggc accgtctctt 480
cagctagcac caagggccca tcggtcttcc ccctggcgcc ctgctccagg agcacctccg 540
agagcacagc cgccctgggc tgcctgggtc aggactactt ccccgaaccg gtgacggtgt 600
cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc ctacagtcct 660
caggactcta ctccctcagc agcgtgggtg ccgtgccctc cagcagcttg ggcacgaaga 720
cctacacctg caacgtagat cacaagccca gcaacaccaa ggtggacaag agagttgagt 780
ccaaatatgg tccccatgc ccaccatgcc cagcacctga gttcctgggg ggaccatcag 840
tcttcctgtt cccccaaaa cccaaggaca ctctcatgat ctcccgacc cctgaggtca 900

cgtgcgtggt ggtggacgtg agccaggaag accccgaggt ccagttcaac tggtagctgg	960
atggcgtgga ggtgcataat gccaaagaaa agccgcggga ggagcagttc aacagcacgt	1020
accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaacggc aaggagtaca	1080
agtgaaggt ctccaacaaa ggcctcccgt cctccatcga gaaaaccatc tccaaagcca	1140
aagggcagcc ccgagagcca caggtgtaca ccctgcccc atcccaggag gagatgacca	1200
agaaccaggt cagcctgacc tgcctgggtca aaggcttcta cccagcgcac atcgccgtgg	1260
agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc gtgctggact	1320
ccgacggctc cttcttcctc tacagcaggc tcaccgtgga caagagcagg tggcaggagg	1380
ggaatgtctt ctcatgctcc gtgctgcatg aggctctgca cgcccactac acacagaaga	1440
gcctctccct gtctctgggt aaagaggatt gtaatgaact gcctccaaga aggaacacag	1500
aaattttgac cgggtcctgg tccgatcaaa cctaccctga aggaactcaa gctatataca	1560
agtgcagacc tggttataga tctactgggca acattatcat ggtatgtcgc aaaggagaat	1620
gggtggctct gaatcccctc agaaaatgcc agaaacggcc atgtggacac cccggcgata	1680
ccccattcgg gacatttacc ttgactggag gcaatgtatt cgagtatggc gtgaaagctg	1740
tctatacctg taacgaaggt taccaattgt tgggagaaat aaattacaga gaatgtgata	1800
ccgatggatg gaccaacgat attcccatat gcgaggttgt taagtgcttg cctgtcactg	1860
caccagaaaa cgggaaaatc gtatctagcg caatggagcc agaccgcgaa taccatttcg	1920
ggcaggcagt gaggtttgtt tgcaattccg gttataagat agaaggggat gaggagatgc	1980
actgtagcga cgatggtttt tgggtccaagg aaaagcccaa gtgcgtcgaa ataagttgca	2040
agtcacctga cgtcataaac gggagcccca tatcccaaaa gataatttac aaggagaacg	2100
aacgatttca atataagtggt aatatgggggt atgaatactc cgagagaggt gatgccgtct	2160
gtaccgaaag tggatggcga ccactcccct catgcgaaga gaagtcctgt gataatccat	2220
acatcccctaa tgggtgattat tcccccttc gaataaagca tcggacagga gacgagatca	2280
catatcagtg tcgcaacgga ttctatccag ccaccagagg caacactgca aagtgtacat	2340
ctacaggatg gatacctgcc ccacgatgta ccttgaagcc ctga	2384

<212> PRT

<213> Artificial Sequence

<220>

<223> VH sequence of IFWH-IgG4PLA-FH1-5 (amino acid)

<400> 78

Met Asp Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ile
35 40 45

Thr Asp Tyr His Ile Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asp Ile Ser Phe Asn Tyr Gly Tyr His Ile Tyr Asn
65 70 75 80

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Trp Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
145 150 155 160

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
165 170 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
180 185 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
195 200 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
210 215 220

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
225 230 235 240

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
245 250 255

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
275 280 285

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
290 295 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
340 345 350

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
370 375 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Leu His Glu Ala Leu His Ala His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Leu Gly Lys Glu Asp Cys Asn Glu Leu Pro Pro Arg
465 470 475 480

Arg Asn Thr Glu Ile Leu Thr Gly Ser Trp Ser Asp Gln Thr Tyr Pro
485 490 495

Glu Gly Thr Gln Ala Ile Tyr Lys Cys Arg Pro Gly Tyr Arg Ser Leu
500 505 510

Gly Asn Ile Ile Met Val Cys Arg Lys Gly Glu Trp Val Ala Leu Asn
515 520 525

Pro Leu Arg Lys Cys Gln Lys Arg Pro Cys Gly His Pro Gly Asp Thr
530 535 540

Pro Phe Gly Thr Phe Thr Leu Thr Gly Gly Asn Val Phe Glu Tyr Gly
545 550 555 560

Val Lys Ala Val Tyr Thr Cys Asn Glu Gly Tyr Gln Leu Leu Gly Glu
565 570 575

Ile Asn Tyr Arg Glu Cys Asp Thr Asp Gly Trp Thr Asn Asp Ile Pro
580 585 590

Ile Cys Glu Val Val Lys Cys Leu Pro Val Thr Ala Pro Glu Asn Gly
595 600 605

Lys Ile Val Ser Ser Ala Met Glu Pro Asp Arg Glu Tyr His Phe Gly
610 615 620

Gln Ala Val Arg Phe Val Cys Asn Ser Gly Tyr Lys Ile Glu Gly Asp
625 630 635 640

Glu Glu Met His Cys Ser Asp Asp Gly Phe Trp Ser Lys Glu Lys Pro
645 650 655

Lys Cys Val Glu Ile Ser Cys Lys Ser Pro Asp Val Ile Asn Gly Ser
660 665 670

Pro Ile Ser Gln Lys Ile Ile Tyr Lys Glu Asn Glu Arg Phe Gln Tyr
675 680 685

Lys Cys Asn Met Gly Tyr Glu Tyr Ser Glu Arg Gly Asp Ala Val Cys
690 695 700

Thr Glu Ser Gly Trp Arg Pro Leu Pro Ser Cys Glu Glu Lys Ser Cys
705 710 715 720

Asp Asn Pro Tyr Ile Pro Asn Gly Asp Tyr Ser Pro Leu Arg Ile Lys
725 730 735

His Arg Thr Gly Asp Glu Ile Thr Tyr Gln Cys Arg Asn Gly Phe Tyr
740 745 750

Pro Ala Thr Arg Gly Asn Thr Ala Lys Cys Thr Ser Thr Gly Trp Ile
755 760 765

Pro Ala Pro Arg Cys Thr Leu Lys Pro
770 775

<210> 79
<211> 2384
<212> DNA
<213> Artificial Sequence

<220>
<223> VH sequence of FMWH-IgG4PLA-FH1-5

<400> 79
cagcatatga tcagtgtcct ctccaaagtc cttgaacata gactctaacc atggactgga 60
cctgggtctt tctcttcctc ctgtcagtaa ctgcaggtgt ccactcccag gttcagctgg 120

tgca gctctgg agctgaggtg aagaagcctg gggcctcagt gaaggtctcc tgcaaggctt	180
ctggatacac aatcacagac taccatttcg actgggtgcg acaggcccct ggacaagggc	240
ttgagtggat gggagatatt agtatgaact atggttatca tatctacaac cagaaattca	300
aggacagagt caccatgacc acagacacat ccacgagcac agcctacatg gagctgagga	360
gcctgagatc tgacgacacg gccgtgtatt actgtgagcg aaggacatt cgttactccg	420
gtaattccta caaatggtag ttcgattggg ggggccaagg gacaatgggc accgtctctt	480
cagctagcac caagggccca tcggtcttcc ccctggcgcc ctgctccagg agcacctccg	540
agagcacagc cgccctgggc tgcctgggtc aggactactt cccgaaccg gtgacgggtg	600
cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc ctacagtcct	660
caggactcta ctccctcagc agcgtgggtg ccgtgccctc cagcagcttg ggcacgaaga	720
cctacacctg caacgtagat cacaagccca gcaacaccaa ggtggacaag agagttgagt	780
ccaaatatgg tccccatgc ccaccatgcc cagcacctga gttcctgggg ggaccatcag	840
tcttctgtt cccccaaaa cccaaggaca ctctcatgat ctcccggacc cctgaggtca	900
cgtgcgtggg ggtggacgtg agccaggaag accccgaggt ccagttcaac tggtagctgg	960
atggcgtgga ggtgcataat gccaaagaca agccgcggga ggagcagttc aacagcacgt	1020
accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaacggc aaggagtaca	1080
agtgaagggt ctccaacaaa ggcctcccgt cctccatcga gaaaaccatc tccaaagcca	1140
aagggcagcc ccgagagcca caggtgtaca ccctgcccc atcccaggag gagatgacca	1200
agaaccaggt cagcctgacc tgcctgggtc aaggcttcta cccagcgac atcgccgtgg	1260
agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc gtgctggact	1320
ccgacggctc cttcttcctc tacagcaggc tcaccgtgga caagagcagg tggcaggagg	1380
ggaatgtctt ctcatgctcc gtgctgcatg aggctctgca cgcccactac acacagaaga	1440
gcctctccct gtctctgggt aaagaggatt gtaatgaact gcctccaaga aggaacacag	1500
aaattttgac cgggtcctgg tccgatcaaa cctaccctga aggaactcaa gctatataca	1560
agtgcagacc tggttataga tctactgggc acattatcat ggtatgtcgc aaaggagaat	1620
gggtggctct gaatcccctc agaaaatgcc agaaacggcc atgtggacac cccggcgata	1680
ccccattcgg gacatttacc ttgactggag gcaatgtatt cgagtatggc gtgaaagctg	1740

tctatacctg taacgaaggt taccaattgt tgggagaaat aaattacaga gaatgtgata	1800
ccgatggatg gaccaacgat attcccatat gcgaggttgt taagtgcttg cctgtcactg	1860
caccagaaaa cgggaaaatc gtatctagcg caatggagcc agaccgcgaa taccatttcg	1920
ggcaggcagt gaggtttgtt tgcaattccg gttataagat agaaggggat gaggagatgc	1980
actgtagcga cgatggtttt tgggtccaagg aaaagcccaa gtgcgtcgaa ataagttgca	2040
agtcacctga cgtcataaac gggagcccca tatcccaaaa gataatttac aaggagaacg	2100
aacgatttca atataagtgt aatatgggggt atgaatactc cgagagaggt gatgccgtct	2160
gtaccgaaag tggatggcga ccactcccct catgcgaaga gaagtcctgt gataatccat	2220
acatccctaa tggtgattat tcccccttc gaataaagca tcggacagga gacgagatca	2280
catatcagtg tcgcaacgga ttctatccag ccaccagagg caacactgca aagtgtacat	2340
ctacaggatg gatacctgcc ccacgatgta ccttgaagcc ctga	2384

<210> 80
 <211> 777
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH sequence of FMWH-IgG4PLA-FH1-5 (amino acid)

<400> 80

Met	Asp	Trp	Thr	Trp	Val	Phe	Leu	Phe	Leu	Leu	Ser	Val	Thr	Ala	Gly
1				5					10					15	

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

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Ile
		35					40					45			

Thr	Asp	Tyr	His	Phe	Asp	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu
	50						55				60				

Glu	Trp	Met	Gly	Asp	Ile	Ser	Met	Asn	Tyr	Gly	Tyr	His	Ile	Tyr	Asn
65					70					75					80

Gln Lys Phe Lys Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Ile Arg Tyr Ser Gly Asn Ser Tyr Lys
115 120 125

Trp Tyr Phe Asp Trp Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
145 150 155 160

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
165 170 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
180 185 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
195 200 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
210 215 220

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
225 230 235 240

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
245 250 255

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
275 280 285

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
290 295 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
340 345 350

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
370 375 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Leu His Glu Ala Leu His Ala His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Leu Gly Lys Glu Asp Cys Asn Glu Leu Pro Pro Arg
465 470 475 480

Arg Asn Thr Glu Ile Leu Thr Gly Ser Trp Ser Asp Gln Thr Tyr Pro
485 490 495

Glu Gly Thr Gln Ala Ile Tyr Lys Cys Arg Pro Gly Tyr Arg Ser Leu
500 505 510

Gly Asn Ile Ile Met Val Cys Arg Lys Gly Glu Trp Val Ala Leu Asn
515 520 525

Pro Leu Arg Lys Cys Gln Lys Arg Pro Cys Gly His Pro Gly Asp Thr
530 535 540

Pro Phe Gly Thr Phe Thr Leu Thr Gly Gly Asn Val Phe Glu Tyr Gly
545 550 555 560

Val Lys Ala Val Tyr Thr Cys Asn Glu Gly Tyr Gln Leu Leu Gly Glu
565 570 575

Ile Asn Tyr Arg Glu Cys Asp Thr Asp Gly Trp Thr Asn Asp Ile Pro
580 585 590

Ile Cys Glu Val Val Lys Cys Leu Pro Val Thr Ala Pro Glu Asn Gly
595 600 605

Lys Ile Val Ser Ser Ala Met Glu Pro Asp Arg Glu Tyr His Phe Gly
610 615 620

Gln Ala Val Arg Phe Val Cys Asn Ser Gly Tyr Lys Ile Glu Gly Asp
625 630 635 640

Glu Glu Met His Cys Ser Asp Asp Gly Phe Trp Ser Lys Glu Lys Pro
645 650 655

Lys Cys Val Glu Ile Ser Cys Lys Ser Pro Asp Val Ile Asn Gly Ser
660 665 670

Pro Ile Ser Gln Lys Ile Ile Tyr Lys Glu Asn Glu Arg Phe Gln Tyr
675 680 685

Lys Cys Asn Met Gly Tyr Glu Tyr Ser Glu Arg Gly Asp Ala Val Cys
690 695 700

Thr Glu Ser Gly Trp Arg Pro Leu Pro Ser Cys Glu Glu Lys Ser Cys
705 710 715 720

Asp Asn Pro Tyr Ile Pro Asn Gly Asp Tyr Ser Pro Leu Arg Ile Lys
725 730 735

His Arg Thr Gly Asp Glu Ile Thr Tyr Gln Cys Arg Asn Gly Phe Tyr
740 745 750

Pro Ala Thr Arg Gly Asn Thr Ala Lys Cys Thr Ser Thr Gly Trp Ile
755 760 765

Pro Ala Pro Arg Cys Thr Leu Lys Pro
770 775

<210> 81

<211> 1231

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino Acid sequence of P08603-1; Human Complement Factor H
Isoform 1, precursor

<400> 81

Met Arg Leu Leu Ala Lys Ile Ile Cys Leu Met Leu Trp Ala Ile Cys
1 5 10 15

Val Ala Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile
20 25 30

Leu Thr Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala
35 40 45

Ile Tyr Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met
50 55 60

Val Cys Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys
65 70 75 80

Gln Lys Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe
85 90 95

Thr Leu Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr
100 105 110

Thr Cys Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu

115

120

125

Cys Asp Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val
 130 135 140

Lys Cys Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser
 145 150 155 160

Ala Met Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe
 165 170 175

Val Cys Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys
 180 185 190

Ser Asp Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile
 195 200 205

Ser Cys Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys
 210 215 220

Ile Ile Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly
 225 230 235 240

Tyr Glu Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp
 245 250 255

Arg Pro Leu Pro Ser Cys Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile
 260 265 270

Pro Asn Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp
 275 280 285

Glu Ile Thr Tyr Gln Cys Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly
 290 295 300

Asn Thr Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys
 305 310 315 320

Thr Leu Lys Pro Cys Asp Tyr Pro Asp Ile Lys His Gly Gly Leu Tyr
 325 330 335

His Glu Asn Met Arg Arg Pro Tyr Phe Pro Val Ala Val Gly Lys Tyr
340 345 350

Tyr Ser Tyr Tyr Cys Asp Glu His Phe Glu Thr Pro Ser Gly Ser Tyr
355 360 365

Trp Asp His Ile His Cys Thr Gln Asp Gly Trp Ser Pro Ala Val Pro
370 375 380

Cys Leu Arg Lys Cys Tyr Phe Pro Tyr Leu Glu Asn Gly Tyr Asn Gln
385 390 395 400

Asn Tyr Gly Arg Lys Phe Val Gln Gly Lys Ser Ile Asp Val Ala Cys
405 410 415

His Pro Gly Tyr Ala Leu Pro Lys Ala Gln Thr Thr Val Thr Cys Met
420 425 430

Glu Asn Gly Trp Ser Pro Thr Pro Arg Cys Ile Arg Val Lys Thr Cys
435 440 445

Ser Lys Ser Ser Ile Asp Ile Glu Asn Gly Phe Ile Ser Glu Ser Gln
450 455 460

Tyr Thr Tyr Ala Leu Lys Glu Lys Ala Lys Tyr Gln Cys Lys Leu Gly
465 470 475 480

Tyr Val Thr Ala Asp Gly Glu Thr Ser Gly Ser Ile Thr Cys Gly Lys
485 490 495

Asp Gly Trp Ser Ala Gln Pro Thr Cys Ile Lys Ser Cys Asp Ile Pro
500 505 510

Val Phe Met Asn Ala Arg Thr Lys Asn Asp Phe Thr Trp Phe Lys Leu
515 520 525

Asn Asp Thr Leu Asp Tyr Glu Cys His Asp Gly Tyr Glu Ser Asn Thr
530 535 540

Gly Ser Thr Thr Gly Ser Ile Val Cys Gly Tyr Asn Gly Trp Ser Asp

545		550		555		560									
Leu	Pro	Ile	Cys	Tyr	Glu	Arg	Glu	Cys	Glu	Leu	Pro	Lys	Ile	Asp	Val
			565						570					575	
His	Leu	Val	Pro	Asp	Arg	Lys	Lys	Asp	Gln	Tyr	Lys	Val	Gly	Glu	Val
			580					585					590		
Leu	Lys	Phe	Ser	Cys	Lys	Pro	Gly	Phe	Thr	Ile	Val	Gly	Pro	Asn	Ser
		595					600					605			
Val	Gln	Cys	Tyr	His	Phe	Gly	Leu	Ser	Pro	Asp	Leu	Pro	Ile	Cys	Lys
	610					615					620				
Glu	Gln	Val	Gln	Ser	Cys	Gly	Pro	Pro	Pro	Glu	Leu	Leu	Asn	Gly	Asn
625					630					635					640
Val	Lys	Glu	Lys	Thr	Lys	Glu	Glu	Tyr	Gly	His	Ser	Glu	Val	Val	Glu
				645					650					655	
Tyr	Tyr	Cys	Asn	Pro	Arg	Phe	Leu	Met	Lys	Gly	Pro	Asn	Lys	Ile	Gln
			660					665					670		
Cys	Val	Asp	Gly	Glu	Trp	Thr	Thr	Leu	Pro	Val	Cys	Ile	Val	Glu	Glu
		675					680					685			
Ser	Thr	Cys	Gly	Asp	Ile	Pro	Glu	Leu	Glu	His	Gly	Trp	Ala	Gln	Leu
	690					695					700				
Ser	Ser	Pro	Pro	Tyr	Tyr	Tyr	Gly	Asp	Ser	Val	Glu	Phe	Asn	Cys	Ser
705					710					715					720
Glu	Ser	Phe	Thr	Met	Ile	Gly	His	Arg	Ser	Ile	Thr	Cys	Ile	His	Gly
				725					730					735	
Val	Trp	Thr	Gln	Leu	Pro	Gln	Cys	Val	Ala	Ile	Asp	Lys	Leu	Lys	Lys
			740					745					750		
Cys	Lys	Ser	Ser	Asn	Leu	Ile	Ile	Leu	Glu	Glu	His	Leu	Lys	Asn	Lys
		755					760					765			

Lys Glu Phe Asp His Asn Ser Asn Ile Arg Tyr Arg Cys Arg Gly Lys
770 775 780

Glu Gly Trp Ile His Thr Val Cys Ile Asn Gly Arg Trp Asp Pro Glu
785 790 795 800

Val Asn Cys Ser Met Ala Gln Ile Gln Leu Cys Pro Pro Pro Pro Gln
805 810 815

Ile Pro Asn Ser His Asn Met Thr Thr Thr Leu Asn Tyr Arg Asp Gly
820 825 830

Glu Lys Val Ser Val Leu Cys Gln Glu Asn Tyr Leu Ile Gln Glu Gly
835 840 845

Glu Glu Ile Thr Cys Lys Asp Gly Arg Trp Gln Ser Ile Pro Leu Cys
850 855 860

Val Glu Lys Ile Pro Cys Ser Gln Pro Pro Gln Ile Glu His Gly Thr
865 870 875 880

Ile Asn Ser Ser Arg Ser Ser Gln Glu Ser Tyr Ala His Gly Thr Lys
885 890 895

Leu Ser Tyr Thr Cys Glu Gly Gly Phe Arg Ile Ser Glu Glu Asn Glu
900 905 910

Thr Thr Cys Tyr Met Gly Lys Trp Ser Ser Pro Pro Gln Cys Glu Gly
915 920 925

Leu Pro Cys Lys Ser Pro Pro Glu Ile Ser His Gly Val Val Ala His
930 935 940

Met Ser Asp Ser Tyr Gln Tyr Gly Glu Glu Val Thr Tyr Lys Cys Phe
945 950 955 960

Glu Gly Phe Gly Ile Asp Gly Pro Ala Ile Ala Lys Cys Leu Gly Glu
965 970 975

Lys Trp Ser His Pro Pro Ser Cys Ile Lys Thr Asp Cys Leu Ser Leu

980

985

990

Pro Ser Phe Glu Asn Ala Ile Pro Met Gly Glu Lys Lys Asp Val Tyr
 995 1000 1005

Lys Ala Gly Glu Gln Val Thr Tyr Thr Cys Ala Thr Tyr Tyr Lys
 1010 1015 1020

Met Asp Gly Ala Ser Asn Val Thr Cys Ile Asn Ser Arg Trp Thr
 1025 1030 1035

Gly Arg Pro Thr Cys Arg Asp Thr Ser Cys Val Asn Pro Pro Thr
 1040 1045 1050

Val Gln Asn Ala Tyr Ile Val Ser Arg Gln Met Ser Lys Tyr Pro
 1055 1060 1065

Ser Gly Glu Arg Val Arg Tyr Gln Cys Arg Ser Pro Tyr Glu Met
 1070 1075 1080

Phe Gly Asp Glu Glu Val Met Cys Leu Asn Gly Asn Trp Thr Glu
 1085 1090 1095

Pro Pro Gln Cys Lys Asp Ser Thr Gly Lys Cys Gly Pro Pro Pro
 1100 1105 1110

Pro Ile Asp Asn Gly Asp Ile Thr Ser Phe Pro Leu Ser Val Tyr
 1115 1120 1125

Ala Pro Ala Ser Ser Val Glu Tyr Gln Cys Gln Asn Leu Tyr Gln
 1130 1135 1140

Leu Glu Gly Asn Lys Arg Ile Thr Cys Arg Asn Gly Gln Trp Ser
 1145 1150 1155

Glu Pro Pro Lys Cys Leu His Pro Cys Val Ile Ser Arg Glu Ile
 1160 1165 1170

Met Glu Asn Tyr Asn Ile Ala Leu Arg Trp Thr Ala Lys Gln Lys
 1175 1180 1185

Leu Tyr Ser Arg Thr Gly Glu Ser Val Glu Phe Val Cys Lys Arg
1190 1195 1200

Gly Tyr Arg Leu Ser Ser Arg Ser His Thr Leu Arg Thr Thr Cys
1205 1210 1215

Trp Asp Gly Lys Leu Glu Tyr Pro Thr Cys Ala Lys Arg
1220 1225 1230

<210> 82

<211> 1213

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino Acid sequence of P08603-1; Human Complement Factor H
Isoform 1

<400> 82

Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
1 5 10 15

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
20 25 30

Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
35 40 45

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

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
65 70 75 80

Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys
85 90 95

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
100 105 110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
115 120 125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met
130 135 140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
145 150 155 160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
165 170 175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
180 185 190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile
195 200 205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu
210 215 220

Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro
225 230 235 240

Leu Pro Ser Cys Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn
245 250 255

Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile
260 265 270

Thr Tyr Gln Cys Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly Asn Thr
275 280 285

Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu
290 295 300

Lys Pro Cys Asp Tyr Pro Asp Ile Lys His Gly Gly Leu Tyr His Glu
305 310 315 320

Asn Met Arg Arg Pro Tyr Phe Pro Val Ala Val Gly Lys Tyr Tyr Ser
325 330 335

Tyr Tyr Cys Asp Glu His Phe Glu Thr Pro Ser Gly Ser Tyr Trp Asp
340 345 350

His Ile His Cys Thr Gln Asp Gly Trp Ser Pro Ala Val Pro Cys Leu
355 360 365

Arg Lys Cys Tyr Phe Pro Tyr Leu Glu Asn Gly Tyr Asn Gln Asn Tyr
370 375 380

Gly Arg Lys Phe Val Gln Gly Lys Ser Ile Asp Val Ala Cys His Pro
385 390 395 400

Gly Tyr Ala Leu Pro Lys Ala Gln Thr Thr Val Thr Cys Met Glu Asn
405 410 415

Gly Trp Ser Pro Thr Pro Arg Cys Ile Arg Val Lys Thr Cys Ser Lys
420 425 430

Ser Ser Ile Asp Ile Glu Asn Gly Phe Ile Ser Glu Ser Gln Tyr Thr
435 440 445

Tyr Ala Leu Lys Glu Lys Ala Lys Tyr Gln Cys Lys Leu Gly Tyr Val
450 455 460

Thr Ala Asp Gly Glu Thr Ser Gly Ser Ile Thr Cys Gly Lys Asp Gly
465 470 475 480

Trp Ser Ala Gln Pro Thr Cys Ile Lys Ser Cys Asp Ile Pro Val Phe
485 490 495

Met Asn Ala Arg Thr Lys Asn Asp Phe Thr Trp Phe Lys Leu Asn Asp
500 505 510

Thr Leu Asp Tyr Glu Cys His Asp Gly Tyr Glu Ser Asn Thr Gly Ser
515 520 525

Thr Thr Gly Ser Ile Val Cys Gly Tyr Asn Gly Trp Ser Asp Leu Pro
530 535 540

Ile Cys Tyr Glu Arg Glu Cys Glu Leu Pro Lys Ile Asp Val His Leu
545 550 555 560

Val Pro Asp Arg Lys Lys Asp Gln Tyr Lys Val Gly Glu Val Leu Lys
565 570 575

Phe Ser Cys Lys Pro Gly Phe Thr Ile Val Gly Pro Asn Ser Val Gln
580 585 590

Cys Tyr His Phe Gly Leu Ser Pro Asp Leu Pro Ile Cys Lys Glu Gln
595 600 605

Val Gln Ser Cys Gly Pro Pro Pro Glu Leu Leu Asn Gly Asn Val Lys
610 615 620

Glu Lys Thr Lys Glu Glu Tyr Gly His Ser Glu Val Val Glu Tyr Tyr
625 630 635 640

Cys Asn Pro Arg Phe Leu Met Lys Gly Pro Asn Lys Ile Gln Cys Val
645 650 655

Asp Gly Glu Trp Thr Thr Leu Pro Val Cys Ile Val Glu Glu Ser Thr
660 665 670

Cys Gly Asp Ile Pro Glu Leu Glu His Gly Trp Ala Gln Leu Ser Ser
675 680 685

Pro Pro Tyr Tyr Tyr Gly Asp Ser Val Glu Phe Asn Cys Ser Glu Ser
690 695 700

Phe Thr Met Ile Gly His Arg Ser Ile Thr Cys Ile His Gly Val Trp
705 710 715 720

Thr Gln Leu Pro Gln Cys Val Ala Ile Asp Lys Leu Lys Lys Cys Lys
725 730 735

Ser Ser Asn Leu Ile Ile Leu Glu Glu His Leu Lys Asn Lys Lys Glu
740 745 750

Phe Asp His Asn Ser Asn Ile Arg Tyr Arg Cys Arg Gly Lys Glu Gly
755 760 765

Trp Ile His Thr Val Cys Ile Asn Gly Arg Trp Asp Pro Glu Val Asn
770 775 780

Cys Ser Met Ala Gln Ile Gln Leu Cys Pro Pro Pro Pro Gln Ile Pro
785 790 795 800

Asn Ser His Asn Met Thr Thr Thr Leu Asn Tyr Arg Asp Gly Glu Lys
805 810 815

Val Ser Val Leu Cys Gln Glu Asn Tyr Leu Ile Gln Glu Gly Glu Glu
820 825 830

Ile Thr Cys Lys Asp Gly Arg Trp Gln Ser Ile Pro Leu Cys Val Glu
835 840 845

Lys Ile Pro Cys Ser Gln Pro Pro Gln Ile Glu His Gly Thr Ile Asn
850 855 860

Ser Ser Arg Ser Ser Gln Glu Ser Tyr Ala His Gly Thr Lys Leu Ser
865 870 875 880

Tyr Thr Cys Glu Gly Gly Phe Arg Ile Ser Glu Glu Asn Glu Thr Thr
885 890 895

Cys Tyr Met Gly Lys Trp Ser Ser Pro Pro Gln Cys Glu Gly Leu Pro
900 905 910

Cys Lys Ser Pro Pro Glu Ile Ser His Gly Val Val Ala His Met Ser
915 920 925

Asp Ser Tyr Gln Tyr Gly Glu Glu Val Thr Tyr Lys Cys Phe Glu Gly
930 935 940

Phe Gly Ile Asp Gly Pro Ala Ile Ala Lys Cys Leu Gly Glu Lys Trp
945 950 955 960

Ser His Pro Pro Ser Cys Ile Lys Thr Asp Cys Leu Ser Leu Pro Ser
965 970 975

Phe Glu Asn Ala Ile Pro Met Gly Glu Lys Lys Asp Val Tyr Lys Ala
980 985 990

Gly Glu Gln Val Thr Tyr Thr Cys Ala Thr Tyr Tyr Lys Met Asp Gly
995 1000 1005

Ala Ser Asn Val Thr Cys Ile Asn Ser Arg Trp Thr Gly Arg Pro
1010 1015 1020

Thr Cys Arg Asp Thr Ser Cys Val Asn Pro Pro Thr Val Gln Asn
1025 1030 1035

Ala Tyr Ile Val Ser Arg Gln Met Ser Lys Tyr Pro Ser Gly Glu
1040 1045 1050

Arg Val Arg Tyr Gln Cys Arg Ser Pro Tyr Glu Met Phe Gly Asp
1055 1060 1065

Glu Glu Val Met Cys Leu Asn Gly Asn Trp Thr Glu Pro Pro Gln
1070 1075 1080

Cys Lys Asp Ser Thr Gly Lys Cys Gly Pro Pro Pro Pro Ile Asp
1085 1090 1095

Asn Gly Asp Ile Thr Ser Phe Pro Leu Ser Val Tyr Ala Pro Ala
1100 1105 1110

Ser Ser Val Glu Tyr Gln Cys Gln Asn Leu Tyr Gln Leu Glu Gly
1115 1120 1125

Asn Lys Arg Ile Thr Cys Arg Asn Gly Gln Trp Ser Glu Pro Pro
1130 1135 1140

Lys Cys Leu His Pro Cys Val Ile Ser Arg Glu Ile Met Glu Asn
1145 1150 1155

Tyr Asn Ile Ala Leu Arg Trp Thr Ala Lys Gln Lys Leu Tyr Ser
1160 1165 1170

Arg Thr Gly Glu Ser Val Glu Phe Val Cys Lys Arg Gly Tyr Arg
1175 1180 1185

Leu Ser Ser Arg Ser His Thr Leu Arg Thr Thr Cys Trp Asp Gly
1190 1195 1200

Lys Leu Glu Tyr Pro Thr Cys Ala Lys Arg
1205 1210

<210> 83

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino Acid sequence of P08603-2; Human Complement Factor H
Isoform 2, precursor

<400> 83

Met Arg Leu Leu Ala Lys Ile Ile Cys Leu Met Leu Trp Ala Ile Cys
1 5 10 15

Val Ala Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile
20 25 30

Leu Thr Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala
35 40 45

Ile Tyr Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met
50 55 60

Val Cys Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys
65 70 75 80

Gln Lys Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe
85 90 95

Thr Leu Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr
100 105 110

Thr Cys Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu
115 120 125

Cys Asp Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val
130 135 140

Lys Cys Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser
145 150 155 160

Ala Met Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe
165 170 175

Val Cys Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys
180 185 190

Ser Asp Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile
195 200 205

Ser Cys Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys
210 215 220

Ile Ile Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly
225 230 235 240

Tyr Glu Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp
245 250 255

Arg Pro Leu Pro Ser Cys Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile
260 265 270

Pro Asn Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp
275 280 285

Glu Ile Thr Tyr Gln Cys Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly
290 295 300

Asn Thr Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys
305 310 315 320

Thr Leu Lys Pro Cys Asp Tyr Pro Asp Ile Lys His Gly Gly Leu Tyr
325 330 335

His Glu Asn Met Arg Arg Pro Tyr Phe Pro Val Ala Val Gly Lys Tyr
340 345 350

Tyr Ser Tyr Tyr Cys Asp Glu His Phe Glu Thr Pro Ser Gly Ser Tyr

355

360

365

Trp Asp His Ile His Cys Thr Gln Asp Gly Trp Ser Pro Ala Val Pro
 370 375 380

Cys Leu Arg Lys Cys Tyr Phe Pro Tyr Leu Glu Asn Gly Tyr Asn Gln
 385 390 395 400

Asn Tyr Gly Arg Lys Phe Val Gln Gly Lys Ser Ile Asp Val Ala Cys
 405 410 415

His Pro Gly Tyr Ala Leu Pro Lys Ala Gln Thr Thr Val Thr Cys Met
 420 425 430

Glu Asn Gly Trp Ser Pro Thr Pro Arg Cys Ile Arg Val Ser Phe Thr
 435 440 445

Leu

<210> 84

<211> 431

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino Acid sequence of P08603-2; Human Complement Factor H
 Isoform 2

<400> 84

Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
 1 5 10 15

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
 20 25 30

Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
 35 40 45

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

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
65 70 75 80

Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys
85 90 95

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
100 105 110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
115 120 125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met
130 135 140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
145 150 155 160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
165 170 175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
180 185 190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile
195 200 205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu
210 215 220

Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro
225 230 235 240

Leu Pro Ser Cys Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn
245 250 255

Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile
260 265 270

Thr Tyr Gln Cys Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly Asn Thr
275 280 285

Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu
290 295 300

Lys Pro Cys Asp Tyr Pro Asp Ile Lys His Gly Gly Leu Tyr His Glu
305 310 315 320

Asn Met Arg Arg Pro Tyr Phe Pro Val Ala Val Gly Lys Tyr Tyr Ser
325 330 335

Tyr Tyr Cys Asp Glu His Phe Glu Thr Pro Ser Gly Ser Tyr Trp Asp
340 345 350

His Ile His Cys Thr Gln Asp Gly Trp Ser Pro Ala Val Pro Cys Leu
355 360 365

Arg Lys Cys Tyr Phe Pro Tyr Leu Glu Asn Gly Tyr Asn Gln Asn Tyr
370 375 380

Gly Arg Lys Phe Val Gln Gly Lys Ser Ile Asp Val Ala Cys His Pro
385 390 395 400

Gly Tyr Ala Leu Pro Lys Ala Gln Thr Thr Val Thr Cys Met Glu Asn
405 410 415

Gly Trp Ser Pro Thr Pro Arg Cys Ile Arg Val Ser Phe Thr Leu
420 425 430