

1003545104_1.txt
SEQUENCE LISTING

<110> Merus N.V.
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<141> 2019-12-27
<150> EP 18215995.4
<151> 2018-12-31
<160> 102
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<210> 1
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<400> 1

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

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

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

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Ala Arg Asp His Gly Ser Arg His Phe Trp Ser Tyr Trp Gly Phe Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 2

<211> 127

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<220>

<223> heavy chain variable region of the chicken Fab region PDB 4GLR

<400> 2

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

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

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

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

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

Leu Gln Leu Asn Asn Leu Arg Ala Glu Asp Thr Gly Thr Tyr Tyr Cys
 85 90 95

Ala Lys Pro Ala Leu Asp Ser Asp Gln Cys Gly Phe Pro Glu Ala Gly
 100 105 110

Cys Ile Asp Ala Trp Gly His Gly Thr Glu Val Thr Val Ser Ser
 115 120 125

<210> 3

<211> 126

<212> PRT

<213> *Anas platyrhynchos*

<400> 3

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

Ser Leu Thr Leu Val Cys Lys Gly Ser Gly Phe Thr Phe Ser Ser Asn
 20 25 30

Glu Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Gly Ile Thr Thr Gly Gly Tyr Thr Gly Tyr Ala Pro Ala Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asn Asn Gly Gln Ser Thr Leu Thr Leu
 65 70 75 80

Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
 85 90 95

Lys Ile Thr Gly Tyr Ala Asn Cys Ala Gly Tyr Gly Cys Ala Ala Asp
 100 105 110

Ile Asp Leu Trp Gly His Gly Thr Glu Val Thr Val Ser Ser
 115 120 125

<210> 4

<211> 124

<212> PRT

<213> *Struthio camelus*

<400> 4

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

Ser Leu Arg Leu Ser Cys Lys Gly Thr Gly Phe Thr Leu Ser Ser Phe
 20 25 30

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

Ala Gly Ile Ser Ser Ser Gly Ser Asp Thr Tyr Tyr Ala Asp Ala Val
50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Gly Gln Ser Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Gly Leu Lys Ala Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Lys Cys Ala Thr Asp Trp Gly Ser Cys Gly Pro Trp Asn Leu Asp
100 105 110

Ala Trp Gly Arg Gly Ala Ser Val Thr Val Ser Ser
115 120

<210> 5
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> human kappa light chain IgVk1-39*01/IGJk1*01

<400> 5

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

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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 6
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> common light chain variable region - IGKV1-39/jk1

<400> 6
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctacttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

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aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccaac gttcggccaa 300
gggaccaagg tggagatcaa a 321

<210> 7
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> common light chain variable region - IGKV1-39/jk1

<400> 7

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

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

<210> 8
<211> 324
<212> DNA
<213> Artificial Sequence

<220>

<223> common light chain constant region

<400> 8

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tggaagggtg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac      180
agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag      240
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag      300
agcttcaaca ggggagagtg ttag                                           324

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<210> 9

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> common light chain constant region

<400> 9

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Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1           5           10          15

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Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
          20          25          30

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Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
          35          40          45

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```

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
          50          55          60

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Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65          70          75          80

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Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
          85          90          95

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Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
          100         105

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

<220>
 <223> common light chain variable domain - IGKV1-39/jk5

<400> 10

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> 11
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 <223> common light chain variable domain V gene segment - IGKV1-39

<400> 11

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
85 90 95

<210> 12
<211> 100
<212> PRT
<213> Anas platyrhynchos

<400> 12

Asn Ile Lys Met Val Ala Ser Gly Pro Lys Glu Gly Lys Ile Leu Gly
1 5 10 15

Ser Leu Pro Leu Thr Cys Thr Val Ile Gly Ala Pro Leu Asp Ser Pro
20 25 30

Arg Tyr Asp Trp Asn Tyr Val Arg Leu Ala Pro Thr Gly Glu Leu Gln
35 40 45

Phe Leu Ala Trp Val Tyr Pro Phe Gly Asn Asn Thr Gly Tyr Ala Pro
50 55 60

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

Val Ser Leu Gln Leu His Ala Leu Thr Ala Val Asp Thr Ala Thr Tyr
85 90 95

Phe Cys Ala Arg
100

<210> 13
<211> 98
<212> PRT
<213> Struthio camelus

<400> 13

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

Ser Leu Arg Leu Ser Cys Lys Gly Thr Gly Phe Thr Phe Ser Ser Phe
20 25 30

Asn Met Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Gly Gln Ser Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Ala Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Lys

<210> 14
<211> 101
<212> PRT
<213> Gallus gallus

<400> 14

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

Ala Leu Ser Leu Val Cys Lys Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

Asn Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Phe Val
 35 40 45

Ala Gly Ile Asp Asn Thr Gly Arg Tyr Thr Gly Tyr Gly Ser Ala Val
 50 55 60

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

Leu Gln Leu Asn Asn Leu Arg Ala Glu Asp Thr Gly Thr Tyr Tyr Cys
 85 90 95

Ala Lys Ala Ala Gly
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<210> 15
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chVH-FW primer

<400> 15
 gtcctcgcaa ctgcggccca gccggccatg gccgccgtga cgttggacga gtcc 54

<210> 16
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chVH-RV primer

<400> 16
 ggaggagacg gtgacctcgg tccc 24

<210> 17
 <211> 870
 <212> DNA
 <213> Homo sapiens

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<400> 17

atgcagatcc cacaggcgcc ctggccagtc gtctgggcgg tgctacaact gggctggcgg	60
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ctgctcgtgg tgaccgaagg ggacaacgcc accttcacct gcagcttctc caacacatcg	180
gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc	240
gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg	300
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tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagagag cctgcgggca	420
gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcacc	480
aggccagccg gccagttcca aaccctgggtg gttggtgtcg tgggcggcct gctgggcagc	540
ctggtgctgc tagtctgggt cctggccgtc atctgtctcc gggccgcacg agggacaata	600
ggagccaggc gcaccggcca gcccctgaag gaggaccct cagccgtgcc tgtgttctct	660
gtggactatg gggagctgga tttccagtgg cgagagaaga ccccgagcc ccccggtccc	720
tgtgtccctg agcagacgga gtatgccacc attgtctttc ctagcggaat gggcacctca	780
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gatggacact gctcttgcc cctctgatga	870

<210> 18

<211> 462

<212> DNA

<213> Artificial Sequence

<220>

<223> human PD-1 codon-optimized for expression in chicken

<400> 18

ggatccccag gatggttcct ggatagcccc gacagacat ggaaccacc aacattcagc	60
cccgctctgc tgggtggttac cgagggcgat aacgccacct tcacatgcag cttcagcaac	120
accagcgaga gcttcgtgct gaactggtac agaagtagcc ccagcaacca gaccgacaag	180
ctggctgctt tccccgagga tagaagccag ccaggccagg actgcagatt cagagtgaca	240
cagctgcca acggcagaga cttccacatg tctgttgtgc gcgccagaag aaacgacagc	300
ggcacatatc tgtgcggcgc cattagcctg gtcctaaagg ctcagatcaa agagagcctg	360

agagccgagc tgagagtgc agagcgcaga gctgaagtgc ccacagctca cccatctcca 420
tctccaagac cagccggcca gttccagaca ctggtgctcg ag 462

<210> 19
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer

<400> 19
gtcctcgcaa ctgcggccca gccggccatg gcc 33

<210> 20
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer

<400> 20
gccgtgacgt tggacgagtc c 21

<210> 21
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH1-02 (DP-75)

<400> 21

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

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

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

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Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg

<210> 22
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH1-02 (DP-8)

<400> 22

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

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

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Trp Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg

<210> 23
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH1-08 (DP-15)

<400> 23

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

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

Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg

<210> 24
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH1-46 (DP-7)

<400> 24

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg

<210> 25

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

<223> human VH1-03 (DP-25)

<400> 25

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

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

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

Gly Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe
50 55 60

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

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

Ala Arg

<210> 26
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH1-18 (DP-14)

<400> 26

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

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

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

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

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg

<210> 27
<211> 98

<212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH1-45 (DP-4)

<400> 27

Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Thr Gly Ser
 1 5 10 15

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

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

Gly Trp Ile Thr Pro Phe Asn Gly Asn Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

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

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

Ala Arg

<210> 28
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH1-58 (DP-2)

<400> 28

Gln Met Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Thr
 1 5 10 15

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

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

Gly Trp Ile Val Val Gly Ser Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Glu Arg Val Thr Ile Thr Arg Asp Met Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Ala

<210> 29
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH1-69 (DP-10)

<400> 29

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg

<210> 30
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH1-e (DP-88)

<400> 30

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Arg

<210> 31
<211> 98
<212> PRT
<213> Artificial Sequence

<220>

<223> human VH1-24 (DP-5)

<400> 31

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

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

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

Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr
 65 70 75 80

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

Ala Thr

<210> 32

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

<223> human VH1-f (DP-3)

<400> 32

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

Thr Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Tyr Met His Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Gly Leu Val Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Glu Lys Phe
50 55 60

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

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

Ala Thr

<210> 33
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH7-81

<400> 33

Gln Val Gln Leu Val Gln Ser Gly His Glu Val Lys Gln Pro Gly Ala
1 5 10 15

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

Gly Met Asn Trp Val Pro Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Phe Asn Thr Tyr Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Met Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Met Ala Met Tyr Tyr Cys
85 90 95

Ala Arg

<210> 34
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH5-51 (DP-73)

<400> 34

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30

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

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg

<210> 35
 <211> 100
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH2-05

<400> 35

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

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

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg
100

<210> 36
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH2-70 (DP-28)

<400> 36

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Met Cys Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
50 55 60

1003545104_1.txt

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile
100

<210> 37
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH2-26 (DP-26)

<400> 37

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

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

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

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile
100

<210> 38
 <211> 97
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH4-04

<400> 38

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
 20 25 30

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

Gly Arg Ile Tyr Thr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60

Ser Arg Val Thr Met 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 Ala
 85 90 95

Arg

<210> 39
 <211> 97
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH4-59 (DP-71)

<400> 39

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu 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 Ala
85 90 95

Arg

<210> 40

<211> 99

<212> PRT

<213> Artificial Sequence

<220>

<223> human VH4-61 (DP-66)

<400> 40

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg

<210> 41
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH4-39 (DP-79)

<400> 41

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg

<210> 42
<211> 99
<212> PRT
<213> Artificial Sequence

<220>

<223> human VH4-31 (DP-65)

<400> 42

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

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

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg

<210> 43

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

<223> human VH4-28 (DP-68)

<400> 43

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Asp
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Ser
20 25 30

1003545104_1.txt

Asn Trp Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Val Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg

<210> 44
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH4-34 (DP-63)

<400> 44

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His 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 Ala
85 90 95

Arg

<210> 45
 <211> 101
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH6-01 (DP-74)

<400> 45

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15

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

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
 35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
 50 55 60

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

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
 85 90 95

Tyr Tyr Cys Ala Arg
 100

<210> 46
 <211> 100
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH3-15 (DP-38)

<400> 46

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
 20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr Asp Tyr Ala Ala
 50 55 60

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

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

Tyr Cys Thr Thr
 100

<210> 47

<211> 100

<212> PRT

<213> Artificial Sequence

<220>

<223> human VH3-49

<400> 47

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 Thr Ala Ser Gly Phe Thr Phe Gly Asp Tyr
 20 25 30

Ala Met Ser Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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Gly Phe Ile Arg Ser Lys Ala Tyr Gly Gly Thr Thr Glu Tyr Ala Ala
50 55 60

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

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

Tyr Cys Thr Arg
100

<210> 48
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH3-72 (DP-29)

<400> 48

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp His
20 25 30

Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr Ala Ala
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65 70 75 80

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

Tyr Cys Ala Arg
100

<210> 49
 <211> 100
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH3-73

<400> 49

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Ser
 20 25 30

Ala Met His Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu Trp Val
 35 40 45

Gly Arg Ile Arg Ser Lys Ala Asn Ser Tyr Ala Thr Ala Tyr Ala Ala
 50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 65 70 75 80

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

Tyr Cys Thr Arg
 100

<210> 50
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH3-16

<400> 50

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ser
20 25 30

Asp Met Asn Trp Ala Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Val Ser Trp Asn Gly Ser Arg Thr His Tyr Val Asp Ser Val
50 55 60

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

Leu Gln Lys Asn Arg Arg Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys
85 90 95

Val Arg

<210> 51

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

<223> human VH3-35 (DP-59)

<400> 51

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ser
20 25 30

Asp Met Asn Trp Val His Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Val Ser Trp Asn Gly Ser Arg Thr His Tyr Ala Asp Ser Val
50 55 60

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

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

Val Arg

<210> 52
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH3-09 (DP-31)

<400> 52

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

Ala 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 Asp

<210> 53
<211> 98

<212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH3-20 (DP-32)

<400> 53

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr 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 His Cys
 85 90 95

Ala Arg

<210> 54
 <211> 99
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH3-43 (DP-33)

<400> 54

Glu Val Gln Leu Val Glu Ser Gly Gly Val Val Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

1003545104_1.txt

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

Ser Leu Ile Ser Trp Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Asp

<210> 55
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH3-07 (DP-54)

<400> 55

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val 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

1003545104_1.txt

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

Ala Arg

<210> 56
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH3-30 (DP-49)

<400> 56

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg

<210> 57
<211> 98
<212> PRT
<213> Artificial Sequence

<220>

<223> human VH3-33 (DP-50)

<400> 57

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg

<210> 58

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

<223> human VH3-74 (DP-53)

<400> 58

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Arg Ile Asn Ser Asp Gly Ser Ser Thr Ser Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg

<210> 59
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH3-13 (DP-48)

<400> 59

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys
50 55 60

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

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg

<210> 60
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH3-11 (DP-35)

<400> 60

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Tyr Ile Ser Ser Ser Gly Ser Thr Ile Tyr 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 Val Tyr Tyr Cys
 85 90 95

Ala Arg

<210> 61
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH3-21 (DP-77)

<400> 61

1003545104_1.txt

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr 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 Val Tyr Tyr Cys
85 90 95

Ala Arg

<210> 62

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

<223> human VH3-48 (DP-51)

<400> 62

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr 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 Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg

<210> 63
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH3-23 (DP-47)

<400> 63

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys

<210> 64
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH3-64

<400> 64

Glu Val Gln Leu Val Glu Ser Gly Glu Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ser Ser Asn Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg

<210> 65
 <211> 96
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH3-38

<400> 65

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Arg Gly
 1 5 10 15

1003545104_1.txt

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Asn
20 25 30

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

Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg Lys Gly
50 55 60

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

Met Asn Asn Leu Arg Ala Glu Gly Thr Ala Val Tyr Tyr Cys Ala Arg
85 90 95

<210> 66
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> human VH3-53 (DP-42)

<400> 66

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Arg

<210> 67
 <211> 97
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VH3-66

<400> 67

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Asn
 20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Val Ile Tyr Ser Cys Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
 50 55 60

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

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

Arg

<210> 68
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> chicken JH gene segment

<400> 68

Thr Ala Gly Ser Ile Asp Ala Trp Gly His Gly Thr Glu Val Ile Val
1 5 10 15

Ser Ser

<210> 69

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> human JH gene segment

<400> 69

Ala Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
1 5 10 15

Ser

<210> 70

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> human JH gene segment

<400> 70

Tyr Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser
1 5 10 15

Ser

<210> 71

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> human JH gene segment

<400> 71

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

<210> 72

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> human JH gene segment

<400> 72

Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
1				5					10					15

<210> 73

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> human JH gene segment

<400> 73

Asn	Trp	Phe	Asp	Pro	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
1				5					10					15	

<210> 74

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> human JH gene segment

<400> 74

Tyr	Tyr	Tyr	Tyr	Tyr	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val
1				5					10						15

Thr	Val	Ser	Ser
			20

<210> 75
 <211> 710
 <212> DNA
 <213> Gallus gallus

<400> 75
 acgcgctaac gaagccggag ccctccttat gcaaattagc ccctccagag ggccataaaa 60
 gcgccggctc tccgacggag gagcaccagt cggctccgca accatgagcc cactcgtctc 120
 ctccctcctg ctcttggccg ccctgccagg tgagggcgct gtggggctct atggggctct 180
 atggggctct agcggggctc tgcgggctca atggggggcca aaggggggggt ctgcgggctc 240
 tatggggggg tcaacggggg gtctcacggg gggccggctc cgcgaggccg tgtggcggcg 300
 gctccgtcag cgctctctgt ccttccccac agggctgatg gcggccgtga cgttggacga 360
 gtccgggggc ggcctccaga cgcccgaag agcgctcagc ctctgtctga aggcctccgg 420
 gttcaccttc agcagttaca acatgggttg ggtgacgacag gcgcccggca aggggctgga 480
 gttcgtcgct ggtattgaca aacttggttag atacacaggc tacgggtcgg cggatgaaggg 540
 ccgtgccacc atctcgaggg acaacgggca gagcacagtg aggctgcagc tgaacaacct 600
 cagggtgag gacaccggca cctactactg cgccaaagct gctggtcacg gtgacaccga 660
 tccccagcac ggggtggcaca aaaccaccg ttgcaaccga aggcggtgaa 710

<210> 76
 <211> 120
 <212> PRT
 <213> Gallus gallus

<400> 76
 Met Ser Pro Leu Val Ser Ser Leu Leu Leu Leu Ala Ala Leu Pro Gly
 1 5 10 15
 Leu Met Ala Ala Val Thr Leu Asp Glu Ser Gly Gly Gly Leu Gln Thr
 20 25 30
 Pro Gly Arg Ala Leu Ser Leu Val Cys Lys Ala Ser Gly Phe Thr Phe
 35 40 45

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Ser Ser Tyr Asn Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Phe Val Ala Gly Ile Asp Asn Thr Gly Arg Tyr Thr Gly Tyr Gly
65 70 75 80

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

Thr Val Arg Leu Gln Leu Asn Asn Leu Arg Ala Glu Asp Thr Gly Thr
100 105 110

Tyr Tyr Cys Ala Lys Ala Ala Gly
115 120

<210> 77
<211> 215
<212> DNA
<213> Gallus gallus

<400> 77
gttggatggc caaaaaacgg ttgttttttt ttttttttaa ccaaaatggg cggtttttcgc 60
ccgaaaagag tgggtggagt ttttgggtga aaaaaggcgg attttggggc attgtggtac 120
tgctggtagc atcgacgcat ggggccacgg gaccgaagtc atcgtctcct ccggtgagtc 180
ttcaaccccc ccctaaattg ccgcggcgat tttgg 215

<210> 78
<211> 18
<212> PRT
<213> Gallus gallus

<400> 78

Thr Ala Gly Ser Ile Asp Ala Trp Gly His Gly Thr Glu Val Ile Val
1 5 10 15

Ser Ser

<210> 79
<211> 18

<212> PRT
 <213> Artificial Sequence

<220>
 <223> forward primer chVH-FW annotation

<400> 79

Val	Leu	Ala	Thr	Ala	Ala	Gln	Pro	Ala	Met	Ala	Ala	Val	Thr	Leu	Asp
1				5				10				15			

Glu Ser

<210> 80
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> past of vector MV1511

<400> 80	
ggattgttat tactcgcggc ccagccggcc atggcgatgc ctgcttgccg aatatcatgg	60
tgg	63

<210> 81
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> part of the functional chicken VH

<400> 81	
cagcgtctc tgtccttccc cacagggctg atggcggccg tgacgttgga cgagtcggg	60
ggc	63

<210> 82
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> reverse complement of chVH-RV reverse primer

<220>
 <221> CDS
 <222> (1)..(24)

<400> 82
 ggg acc gag gtc acc gtc tcc tcc 24
 Gly Thr Glu Val Thr Val Ser Ser
 1 5

<210> 83
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 83
 Gly Thr Glu Val Thr Val Ser Ser
 1 5

<210> 84
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> part of vector MV1511

<400> 84
 aagtagcggc cctattgacg tcaatgacgg tcaccgtctc gagcgcctcc accaagggcc 60
 cat 63

<210> 85
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> part of chicken JH gene segment

<400> 85
 gcatcgacgc atggggccac gggaccgaag tcacgtctc ctccggtgag tcttcaaccc 60
 ccc 63

<210> 86
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nonsense sequence

<400> 86
 aaaaaaaaaa aaaaa

15

<210> 87
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> common light chain variable region IgVk3-15/IGJk1

<400> 87

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

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

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

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65 70 75 80

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

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

<210> 88

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

<220>
<223> common light chain variable region IgVk3-20/IGJk1

<400> 88

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

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

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

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

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

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

<210> 89
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> common light chain variable region IgVl3-21/IGJl3

<400> 89

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

Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ile Gly Arg Lys Ser Val

20

25

30

Tyr Trp Tyr Gln Gln Lys Ser Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Gly Ser Ser Asp His
 85 90 95

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> 90

<211> 95

<212> PRT

<213> Artificial Sequence

<220>

<223> Variable gene region sequence IgVk3-15

<400> 90

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

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

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

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65 70 75 80

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

<210> 91
<211> 96
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable gene region sequence IgVk3-20

<400> 91

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

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

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

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

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

<210> 92
<211> 225
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region of the chicken Fab region PDB 4GLR
and a human constant region CH1

<400> 92

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

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

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

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

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

Leu Gln Leu Asn Asn Leu Arg Ala Glu Asp Thr Gly Thr Tyr Tyr Cys
85 90 95

Ala Lys Pro Ala Leu Asp Ser Asp Gln Cys Gly Phe Pro Glu Ala Gly
100 105 110

Cys Ile Asp Ala Trp Gly His Gly Thr Glu Val Thr Val Ser Ser Ala
115 120 125

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

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

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

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

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

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

Val
225

<210> 93
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> human kappa light chain IgVk1-39/IGJk5/Ckappa

<400> 93

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 Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

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Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 94
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> human kappa light chain IgVk3-15/IGJk1/Ckappa

<400> 94

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

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

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

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 95
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> human kappa light chain IgVk3-20/IGJk1/Ckappa

<400> 95

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

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

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

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

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

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 96

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> human lambda light chain IgV13-21/IGJ13/Clambda

<400> 96

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

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

Tyr Trp Tyr Gln Gln Lys Ser Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Gly Ser Ser Asp His
 85 90 95

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys
 100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
 115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
 130 135 140

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

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
 165 170 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
 180 185 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
195 200 205

Ala Pro Thr Glu Cys Ser
210

<210> 97
<211> 96
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable gene region sequence IgV13-21

<400> 97

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

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

Tyr Trp Tyr Gln Gln Lys Ser Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Gly Ser Ser Asp His
85 90 95

<210> 98
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Human control MF1025 VH sequence

<400> 98

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Ala Asp Trp Trp Ala Thr Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 99

<211> 359

<212> PRT

<213> Mus musculus

<400> 99

Met Glu Pro Ile Ser Val Ser Ile Tyr Thr Ser Asp Asn Tyr Ser Glu
 1 5 10 15

Glu Val Gly Ser Gly Asp Tyr Asp Ser Asn Lys Glu Pro Cys Phe Arg
 20 25 30

Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr Ile Tyr Phe
 35 40 45

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Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val
50 55 60

Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu
65 70 75 80

His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp
85 90 95

Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys Lys
100 105 110

Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile
115 120 125

Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr
130 135 140

Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr Val
145 150 155 160

Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe
165 170 175

Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile
180 185 190

Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe
195 200 205

Gln His Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu Ser
210 215 220

Cys Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln
225 230 235 240

Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe Phe
245 250 255

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Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe Ile
260 265 270

Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val His
275 280 285

Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu
290 295 300

Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Ser Ser Ala
305 310 315 320

Gln His Ala Leu Asn Ser Met Ser Arg Gly Ser Ser Leu Lys Ile Leu
325 330 335

Ser Lys Gly Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser Glu
340 345 350

Ser Ser Ser Phe His Ser Ser
355

<210> 100
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> VH region of CXCR4-1

<400> 100

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

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

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

Val Ala Gly Ile Tyr Ser Ser Gly Ser Ser Thr Ala Tyr Gly Ala Ala

50

55

60

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

Arg Leu Gln Leu Asn Asn Leu Arg Ala Glu Asp Thr Gly Thr Tyr Tyr
 85 90 95

Cys Ala Lys Asp Ala Gly Ser Cys Trp Tyr Gly Arg Arg Ser Gly Phe
 100 105 110

Asn Cys Asp Pro Tyr Gly Gly Asn Ile Asp Ala Trp Gly His Gly Thr
 115 120 125

Glu Val Ile Val Ser Ser
 130

<210> 101
 <211> 134
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH region of CXCR4-2

<400> 101

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

Ala Leu Ser Leu Val Cys Lys Ala Ser Gly Phe Ser Phe Ser Ser Tyr
 20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Gly Ile Tyr Ser Ile Gly Arg Asp Ala Gly Tyr Gly Ala Ala Val
 50 55 60

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

1003545104_1.txt

Leu Gln Leu Asn Asn Leu Arg Ala Glu Asp Thr Gly Thr Tyr Tyr Cys
85 90 95

Ala Lys Glu Ser Gly Ser Ala Cys Arg Tyr Ala Ala Arg His Gly Tyr
100 105 110

Ile Cys Ala Gly Tyr Leu Gly Ser Ile Asp Ala Trp Gly His Gly Thr
115 120 125

Glu Val Ile Val Ser Ser
130

<210> 102
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> VH region of CXCR4-3

<400> 102

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

Ala Leu Ser Leu Val Cys Lys Ala Ser Gly Phe Ser Ile Gly Ser Tyr
20 25 30

Gly Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Phe Val
35 40 45

Ala Gly Ile Ser Thr Ile Gly Gly Val Thr Trp Tyr Gly Ala Ala Val
50 55 60

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

Leu Gln Leu Asn Asn Leu Arg Ala Glu Asp Thr Gly Thr Tyr Phe Cys
85 90 95

Ala Lys Ala Ser Asp Ser Pro Ser Cys Arg Tyr Gly Ser Arg Ser Gly

1003545104_1.txt

100

105

110

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

His Gly Thr Glu Val Ile Val Ser Ser
130 135