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<151> 2011-03-02

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20 25 30

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

Gly Xaa Ile Asn Thr Lys Xaa Gly Glu Ala Xaa Tyr Xaa Glu Glu Phe
50 55 60

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

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

Ala Arg Trp Asp Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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


Tyr Xaa Ala Ser Xaa Xaa Xaa Xaa Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
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Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Tyr Thr Tyr Pro Leu
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Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
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Lys Ala Ser Lys Asn Val Gly Thr Asn Val Ala

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Lys Ala Ser Gln Ile Met Gly Pro Asn Val Ala
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Tyr Leu Ala Ser Asn Leu Ser Gly
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Tyr Leu Ala Ser Tyr Pro Gln Ile
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Tyr Ser Ala Ser Tyr Arg Lys Arg
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caccaatatt acacctatcc tctattcacg 30

<210> 99
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<220>
<223> PR1A3 VH

<400> 99

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

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 100
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<212> PRT
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<223> pEM1496 huPR1A3 VH

<400> 100

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

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 101
<211> 121
<212> PRT
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<220>
<223> CH7A

<400> 101

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

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 102
<211> 98
<212> PRT
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<220>

<223> IGHV7-4-1*02

<400> 102

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

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

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

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

Ala Arg

<210> 103
<211> 110
<212> PRT
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<220>
<223> PR1A3 VL

<400> 103

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

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

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

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

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

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

Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Met Lys Arg Thr
100 105 110

<210> 104
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> pEM1495 huPR1A3 VL

<400> 104

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 Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

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

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

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

Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Tyr Tyr Thr Tyr Pro Leu
85 90 95

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

<210> 105
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> CL1A

<400> 105

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 Lys Ala Ser Gln Asn Val Gly Thr Asn
20 25 30

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

Tyr Ser Ala Ser Tyr Arg Tyr 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 His Gln Tyr Tyr Thr Tyr Pro Leu
85 90 95

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

<210> 106
<211> 95
<212> PRT
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<220>
<223> IMGT_hVK_1_39

<400> 106

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> 107
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH7 rF9

<400> 107

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

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 108
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> CLA1 rH11

<400> 108

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 Lys Ala Ser Gln Thr Val Ser Ala Asn
20 25 30

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

Tyr Leu Ala Ser Tyr Arg Tyr Arg 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 His Gln Tyr Tyr Thr Tyr Pro Leu
85 90 95

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
100 105 110

<210> 109

<400> 109
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<210> 110

<400> 110
000

<210> 111
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<212> DNA
<213> Artificial Sequence

<220>
<223> PR1A3 VH

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cctggaaagg gtttaaagtg gatgggctgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgccttc tctttggaga cctctgccac cactgcctat 240

ttgcagatca acaacctcaa aaatgaggac acggctaaat atttctgtgc tcgatgggat 300

ttctatgact atgttgaagc tatggactac tggggccaag ggaccaccgt gaccgtctcc 360

tca 363

<210> 112
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> pEM1496

<400> 112
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ctggacaagg gcttgagtgg atgggatgga taaacaccaa aactggagag gcaacatatg 180

ttgaagagtt taagggacgg tttgtcttct ccttggacac ctctgtcagc acggcatatc 240

tgcagatcag cagcctaaag gctgacgaca ctgccgtgta ttactgtgcg agatgggact 300

tctatgatta cgtggaggct atggactact ggggccaagg gaccacggtc accgtctcct 360

ca 362

<210> 113
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH7A

<400> 113
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tcctgcaagg cttctggata caccttcact gagtttggaa tgaactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttctatgatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

<210> 114
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> IGHV7-4-1*02

<400> 114
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tcctgcaagg cttctggata caccttcact agctatgcta tgaattgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacacca acactgggaa cccaacgtat 180

gcccagggct tcacaggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaggac actgccgtgt attactgtgc gaga 294

<210> 115
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> PR1A3 VL

<400> 115
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gtcacctgca aggccagtca gaatgtgggt actaatgttg cctggtatca acagaaacca 120

ggacaatccc ctaaagcact gatttactcg gcatcctacc ggtacagtgg agtccctgat 180

cgcttcacag gcagtggatc tgggacagat ttcactctca ccatcagcaa tgtacagtct 240

gaagacttgg cggagtattt ctgtcaccaa tattacacct atcctctatt cacgttcggc 300

tcggggacaa agttggaaat gaaacgtacg 330

<210> 116
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> pEM1495

<400> 116
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atcacctgta aggccagtca gaatgtgggt actaatgttg cctggtacca gcagaagcca 120

ggtaaggctc caaagctgct gatctactcg gcatcctacc ggtacagtgg tgtgccaagc 180

agattcagcg gtagcggtag cggtaccgac ttcaccttca ccatcagcag cctccagcca 240

gaggacatcg ccacctacta ctgccaccaa tattacacct atcctctatt cagcttcggc 300

caagggacca aggtggaaat caaacgt 327

<210> 117
<211> 324

<212> DNA
<213> Artificial Sequence

<220>
<223> CL1A

<400> 117
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atcacttgca aggccagtca gaatgtgggt actaatgttg cctggtatca gcagaaacca 120

gggaaagcac ctaagctcct gatctattcg gcatcctacc gctacagtgg agtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300

cagggcacca agctcgagat caag 324

<210> 118
<211> 285
<212> DNA
<213> Artificial Sequence

<220>
<223> IMGT_hVK_1_39

<400> 118
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atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccct 285

<210> 119
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> CH7 rF9

<400> 119
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tcctgcaagg cttctggata caccttcact gagtatggta tgaactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg ataaacacga aatctggaga ggcaacctat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttctatgatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tcagctagc 369

<210> 120
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> CLA1 rH11

<400> 120
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atcacttgca aggccagtca gactgtgagt gctaatgttg cgtggtatca gcagaaacca 120

gggaaagcac ctaagctcct gatctacttg gcatcctacc gctacagagg agtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300

cagggcacca agctcgagat caagcgtacg 330

<210> 121
<211> 987
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG1

<400> 121
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gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 120

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 180

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 240

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagcaga gcccaaatct 300

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 360

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 420

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 480

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 540

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 600

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 660

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 720

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 780

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 840

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 900

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 960

agcctctccc tgtctccggg taaatga 987

<210> 122
<211> 328
<212> PRT
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<220>

<223> IgG1

<400> 122

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Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
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Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
        35                  40                  45

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

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

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

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
            100                 105                 110

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

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

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

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

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

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

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
225                 230                 235                 240

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
                245                 250                 255
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eolf-seql

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

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

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

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

Ser Leu Ser Leu Ser Pro Gly Lys
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<211> 42
<212> DNA
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<220>
<223> Primer MS-43

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<210> 124
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer MS-52

<400> 124
gaagaccgat gggcctttgg tgctag 26

<210> 125
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer MS-55

<400> 125
gcaacatatg ttgaagagtt taagggacgg 30

<210> 126
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> MS-56

<400> 126
atgaactggg tgcgacaggc ccctg 25

<210> 127
<211> 56
<212> DNA
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<220>
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<223> m is a or c

<220>
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<222> (27)..(28)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (30)..(30)
<223> w is a or t

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<210> 128
<211> 81
<212> DNA
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<220>
<223> Primer EAB-680

<400> 128
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ccactcaagc ccttgtccag g 81

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<211> 50
<212> DNA
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<220>
<223> Primer EAB-685

<400> 129
cagctatgac catgattacg ccaagcttgc atgcaaattc tatttcaagg 50

<210> 130
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<220>
<223> Primer EAB-686

<400> 130
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<210> 131
<211> 34

<212> DNA
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<220>
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<400> 131
gctctttgtg acgggcgagc tcaggccctg atgg 34

<210> 132
<211> 35
<212> DNA
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<220>
<223> Primer EAB-688

<400> 132
ggagtcccat caaggttcag tggcagtgga tctgg 35

<210> 133
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer EAB-681

<400> 133
cctggtttct gctgatacca cgcaacatta gtacccacat tctgactggc cttgcaagtg 60

atggtgactc 70

<210> 134
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer EAB-682

<400> 134
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ttaggtgctt tccctgg 77

<210> 135
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer AC7

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<222> (37)..(37)
<223> m is a or c

<220>
<221> misc_feature
<222> (38)..(39)
<223> n is a, c, g, or t

<400> 135
ccagtagtcc atagcctcca cgtaatcata gaagtcmnnt ctcgcacagt aatacacggc 60

agtg 64

<210> 136
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer AC8

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<222> (34)..(34)
<223> m is a or c

<220>
<221> misc_feature
<222> (35)..(36)
<223> n is a, c, g, or t

<400> 136
ccagtagtcc atagcctcca cgtaatcata gaamnnccat ctcgcacagt aatacacggc 60

agtg 64

<210> 137
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer AC9

<220>
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<222> (31)..(31)
<223> m is a or c

<220>
<221> misc_feature
<222> (32)..(33)
<223> n is a, c, g, or t

<400> 137
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agtg 64

<210> 138
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<212> DNA
<213> Artificial Sequence

<220>
<223> Primer AC10

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<222> (28)..(28)
<223> m is a or c

<220>
<221> misc_feature
<222> (29)..(30)
<223> n is a, c, g, or t

<400> 138
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agtg 64

<210> 139
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer AC11

<220>
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<223> m is a or c

<220>
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<222> (26)..(27)
<223> n is a, c, g, or t

<400> 139
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agtg 64

<210> 140
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer AC12

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<222> (38)..(39)
<223> n is a, c, g, or t

<400> 140
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acag 64

<210> 141
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer AC13

<220>
<221> misc_feature
<222> (34)..(34)
<223> m is a or c

<220>
<221> misc_feature
<222> (35)..(36)
<223> n is a, c, g, or t

<400> 141
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acag 64

<210> 142
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer AC14

<220>
<221> misc_feature
<222> (31)..(31)
<223> m is a or c

<220>
<221> misc_feature
<222> (32)..(33)
<223> n is a, c, g, or t

<400> 142
cgtggtccct tggccccagt agtccatagc mnncacgtaa tcatagaagt cccatctcgc 60

acag 64

<210> 143
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer AC15

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<223> m is a or c

<220>
<221> misc_feature
<222> (29)..(30)
<223> n is a, c, g, or t

<400> 143
cgtggtccct tggccccagt agtccatmnn ctccacgtaa tcatagaagt cccatctcgc 60

acag 64

<210> 144
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<220>
<223> Primer AC16

<220>
<221> misc_feature
<222> (25)..(25)
<223> m is a or c

<220>
<221> misc_feature
<222> (26)..(27)
<223> n is a, c, g, or t

<400> 144
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acag 64

<210> 145
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<212> DNA
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<220>
<223> Primer AC17

<400> 145
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acagtaatac acggcag 77

<210> 146
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<212> DNA
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<220>
<223> Primer EAB-749

<400> 146
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<210> 147
<211> 30
<212> DNA
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<223> Primer EAB-750

<400> 147
cgtggaggct atggactact ggggccaagg 30

<210> 148
<211> 29

<212> DNA
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<220>
<223> Primer EAB-751

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gactactggg gccaagggac cacggtcac 29

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<220>
<223> Primer EAB-752

<400> 149
ggtcagggcg cctgagttcc acg 23

<210> 150
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer AC1

<220>
<221> misc_feature
<222> (37)..(37)
<223> m is a or c

<220>
<221> misc_feature
<222> (38)..(39)
<223> n is a, c, g, or t

<400> 150
ggtgccctgg ccaaacgtga atagaggata ggtgtamnnt tggtgacagt agtaagttgc 60

<210> 151
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer AC2

<220>
<221> misc_feature
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<223> m is a or c

<220>
<221> misc_feature
<222> (35)..(36)
<223> n is a, c, g, or t

<400> 151
ggtgccctgg ccaaacgtga atagaggata ggtmnnatat tggtgacagt agtaagttgc 60

<210> 152
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer AC3

<220>
<221> misc_feature
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<223> m is a or c

<220>
<221> misc_feature
<222> (32)..(33)
<223> n is a, c, g, or t

<400> 152
ggtgccctgg ccaaacgtga atagaggata mnngtaatat tggtgacagt agtaagttgc 60

<210> 153
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<223> Primer AC4

<220>
<221> misc_feature
<222> (28)..(28)
<223> m is a or c

<220>
<221> misc_feature
<222> (29)..(30)
<223> n is a, c, g, or t

<400> 153
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<210> 154
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer AC5

<220>
<221> misc_feature
<222> (22)..(22)
<223> m is a or c

<220>
<221> misc_feature
<222> (23)..(24)
<223> n is a, c, g, or t

<400> 154
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<210> 155
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<212> DNA
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<220>
<223> Primer AC6

<400> 155
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<210> 156
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer EAB-746

<400> 156
cgcttgatct cgagcttggt gccctggcca aacgtg 36

<210> 157

<400> 157
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<210> 158
<211> 428
<212> PRT
<213> Artificial Sequence

<220>
<223> pETR6592

<400> 158

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Val Leu Leu Leu Val His Asn Leu Pro Gln Gln Leu Phe Gly Tyr Ser
20 25 30

Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Val Gly Tyr
35 40 45

Ala Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Asn Ser Gly Arg
50 55 60

Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65 70 75 80

Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp Leu Val
85 90 95

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

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Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys Asp Ala
        115                 120                 125

Met Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr Leu Trp
    130                 135                 140

Trp Ile Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser
145                 150                 155                 160

Asn Gly Asn Arg Thr Leu Thr Leu Leu Ser Val Thr Arg Asn Asp Thr
                165                 170                 175

Gly Pro Tyr Glu Cys Glu Ile Gln Asn Pro Val Ser Ala Asn Arg Ser
            180                 185                 190

Asp Pro Val Thr Leu Asn Val Thr Tyr Gly Pro Asp Thr Pro Thr Ile
        195                 200                 205

Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly Ala Asn Leu Asn Leu Ser
    210                 215                 220

Cys His Ser Ala Ser Asn Pro Ser Pro Gln Tyr Ser Trp Arg Ile Asn
225                 230                 235                 240

Gly Ile Pro Gln Gln His Thr Gln Val Leu Phe Ile Ala Lys Ile Thr
                245                 250                 255

Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe Val Ser Asn Leu Ala Thr
            260                 265                 270

Gly Arg Asn Asn Ser Ile Val Lys Ser Ile Thr Val Ser Ala Leu Ser
        275                 280                 285

Pro Val Val Ala Lys Pro Gln Ile Lys Ala Ser Lys Thr Thr Val Thr
    290                 295                 300

Gly Asp Lys Asp Ser Val Asn Leu Thr Cys Ser Thr Asn Asp Thr Gly
305                 310                 315                 320

Ile Ser Ile Arg Trp Phe Phe Lys Asn Gln Ser Leu Pro Ser Ser Glu
                325                 330                 335

Arg Met Lys Leu Ser Gln Gly Asn Ile Thr Leu Ser Ile Asn Pro Val
            340                 345                 350

Lys Arg Glu Asp Ala Gly Thr Tyr Trp Cys Glu Val Phe Asn Pro Ile
        355                 360                 365

Ser Lys Asn Gln Ser Asp Pro Ile Met Leu Asn Val Asn Tyr Asn Ala
    370                 375                 380
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eolf-seql

Leu Pro Gln Glu Asn Leu Ile Asn Val Asp Leu Glu Val Leu Phe Gln
385 390 395 400

Gly Pro Gly Ser Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu
405 410 415

Trp His Glu Ala Arg Ala His His His His His His
420 425

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cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttctatgatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

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<211> 363
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<220>
<223> Primer 1C8

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tcctgcaagg cttctggata caccttcact gagtttggaa tgaactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttctatcatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

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<220>
<223> 3E1

<400> 161
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tcctgcaagg cttctggata caccttcact gagtttggaa tgaactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttcgtggatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

<210> 162
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> 2D7

<400> 162
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cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttctattggt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

<210> 163
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Affinity Matured Heavy Chain

<400> 163
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tcctgcaagg cttctggata caccttcact gagtttggaa tgaactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

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tca 363

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<400> 164
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cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttcgcttatt actttcagac tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

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cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggat 300

ttcgcgtatt accttgaggc tatggactac tggggccaag ggaccacgat caccgtctcc 360

tca 363

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<212> DNA
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<220>
<223> H3 Full (5) 19

<400> 166
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cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgctgtgt attactgtgc gagatgggac 300

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tca 363

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<212> DNA
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<220>
<223> H3 Full (5) 8

<400> 167
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cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggat 300

ttctttgagt attttaagac tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

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<212> DNA
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<220>
<223> H3 Full (5) 28

<400> 168
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cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

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ttttttatt acgtgcagac tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

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<220>
<223> H3 Full (5) 27

<400> 169
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cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

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tca 363

<210> 170
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<220>
<223> H4E9 Heavy Chain

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cctggacaag ggcttgagtg gatgggatgg ataaatacca aaactggaga ggcaacttat 180

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ttctatgatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

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<212> DNA
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<220>
<223> pAC14 (B9)

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cctggacaag ggcttgagtg gatgggatgg ataaacacca aaagtggaga ggcaacctat 180

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ttctatgatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

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<220>
<223> pAC15 (F9)

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tcctgcaagg cttctggata caccttcact gagtatggta tgaactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg ataaacacga aatctggaga ggcaacctat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttctatgatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

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cctggacaag ggcttgagtg gatgggatac ataaacacca aaaatggaga ggcaaactat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttctatgatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

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cctggacaag ggcttgagtg gatgggatgg ataaacacca aaaatggaga ggcaacctat 180

attgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttctatgatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

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<211> 363
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<220>
<223> H1/H2 (5) 13

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tcctgcaagg cttctggata caccttcact gagtttggta tgaactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatat ataaacacca aaaatggaga ggcaaactat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggacg cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttctatgatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

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<212> DNA
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<220>
<223> H1/H2 (5) 14

<400> 176
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cctggacaag ggcttgagtg gatgggatat ataaacacca aaaatggaga ggcaaactat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttctatgatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

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<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> H3 Full (5) 19

<400> 177
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cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

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gcctttgagt acgtgaaggc gctggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

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<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> pAC21 (3A1)

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gggaaagcac ctaagctcct gatctatttg gcctccaacc gctccggtgg agtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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cagggcacca agctcgagat caagcgtacg 330

<210> 179
<211> 330
<212> DNA
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<220>
<223> pAC19 (2C6)

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gggaaagcac ctaagcccct gatctacctg gcatcctacc cccagattgg agtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttcg caacttacta ctgtcaccaa tattacacct atcccctatt cacgtttggc 300

cagggcacca agctcgagat caagcgtacg 330

<210> 180
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> pAC18 (2F1)

<400> 180
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60

atcacttgca aggccagtgc ggctgtgggt acgtatgttg cgtggtatca gcagaaacca 120

gggaaagcac ctaagctcct gatctattcg gcatcctacc gcaaaagggg agtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300

cagggcacca agctcgagat caagcgtacg 330

<210> 181
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> pAC23 (2F11)

<400> 181
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60

atcacttgca aggccagtca gatagcgagt actaatgttg cctggtatca gcagaaacca 120

gggaaagcac ctaagctcct gatctattgg gcatcctacc gctatagtgg agtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300

cagggcacca agctcgagat caagcgtacg 330

<210> 182
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> H4E9 light chain

<400> 182
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60

atcacttgca aggccagtca gaatgtgggt actaatgttg cctggtatca gcagaaacca 120

gggaaagcac ctaagcccct gatctattcg gcatcctacc gctacagtgg agtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300

cagggcacca agctcgagat caagcgtacg 330

<210> 183
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> L2D2

<400> 183
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60

atcacttgca aggccagtca caatgtgggt accaacgttg cgtggtatca gcagaaacca 120

gggaaagcac ctaagctcct gatctattcg gcatcccacc ggtacagtgg agtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300

cagggcacca agctcgagat caagcgtacg 330

<210> 184
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> pAC6 (C1)

<400> 184
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60

atcacttgca aggccagtca gattatgggt cctaatgttg cgtggtatca gcagaaacca 120

gggaaagcac ctaagctcct gatctatttg gcatcctacc acgaaagtgg agtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300

cagggcacca agctcgagat caagcgtacg 330

<210> 185
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> pAC7 (E10)

<400> 185
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60

atcacttgca aggccagtca aattgtgggt actaatgttg cgtggtatca gcagaaacca 120

gggaaagcac ctaagctcct gatctattcg gcatcccacc gtcccagtgg agtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300

cagggcacca agctcgagat caagcgtacg 330

<210> 186
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> pAC12 (H7)

<400> 186
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60

atcacttgca aggccagtca gaaggtgctt actaatgttg cgtggtatca gcagaaacca 120

gggaaagcac ctaagctcct gatctatttg gcatcctacc gctacagtgg agtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300

cagggcacca agctcgagat caagcgtacg 330

<210> 187
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> pAC13 (H11)

<400> 187
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60

atcacttgca aggccagtca gactgtgagt gctaatgttg cgtggtatca gcagaaacca 120

gggaaagcac ctaagctcct gatctacttg gcatcctacc gctacagagg agtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300

cagggcacca agctcgagat caagcgtacg 330

<210> 188
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> PMS22

<400> 188

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

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 189
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> 1C8

<400> 189

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

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr His Tyr Val Glu Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 190
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> 3E1

<400> 190

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

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

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

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

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

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

Ala Arg Trp Asp Phe Val Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 191
<211> 121

<212> PRT
<213> Artificial Sequence

<220>
<223> 2D7

<400> 191

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

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr Trp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 192
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Affinity Matured Heavy Chain

<400> 192

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

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

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

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

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

```
Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

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

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 193
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Affinity Matured Heavy Chain

<400> 193

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

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

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 194
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Affinity Matured Heavy Chain

<400> 194

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

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

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

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

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

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

Ala Arg Trp Asp Phe Ala Tyr Tyr Leu Glu Ala Met Asp Tyr Trp Gly
            100   105   110

Gln Gly Thr Thr Ile Thr Val Ser Ser
        115   120

<210> 195
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> H3 Full (5) 19

<400> 195

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

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

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

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

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

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

Ala Arg Trp Asp Ala Phe Glu Tyr Val Lys Ala Leu Asp Tyr Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 196
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> H3 Full (5) 8

<400> 196

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

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

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

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

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

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

Ala Arg Trp Asp Phe Phe Glu Tyr Phe Lys Thr Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 197
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> H3 Full (5) 28

<400> 197

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

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

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 198
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> H3 Full (5) 27

<400> 198

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

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

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

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

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

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

Ala Arg Trp Asp Phe Ser Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 199
<211> 121
<212> PRT
<213> Artificial Sequence

<220>

<223> H4E9 Heavy Chain

<400> 199

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

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 200
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> pAC14 (B9)

<400> 200

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

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

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

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

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

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 201
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> pAC15 (F9)

<400> 201

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

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 202
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> H1/H2 (5) 2

<400> 202

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

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

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

Gly Tyr Ile Asn Thr Lys Asn Gly Glu Ala Asn Tyr Val Glu Glu Phe
50 55 60

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 203
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> H1/H2 (5) 11

<400> 203

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

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 204
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> H1/H2 (5) 13

<400> 204

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

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

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

Gly Tyr Ile Asn Thr Lys Asn Gly Glu Ala Asn Tyr Val Glu Glu Phe
50 55 60

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 205
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> H1/H2 (5) 14

<400> 205

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

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

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

Gly Tyr Ile Asn Thr Lys Asn Gly Glu Ala Asn Tyr Val Glu Glu Phe
50 55 60

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 206
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> H3 Full (5) 19

<400> 206

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

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

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

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

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

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

Ala Arg Trp Asp Ala Phe Glu Tyr Val Lys Ala Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 207
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> pAC21 (3A1)

<400> 207

```
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 Lys Ala Ser Ala Asn Val Gly Asn Asn
            20                  25                  30

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

Tyr Leu Ala Ser Asn Arg Ser Gly 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 His Gln Tyr Tyr Thr Tyr Pro Leu
                85                  90                  95

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
            100                 105                 110
```

<210> 208
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> pAC19 (2C6)

<400> 208

```
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 Lys Ala Ser Lys Asn Val Gly Thr Asn
            20                  25                  30

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

Tyr Leu Ala Ser Tyr Pro Gln Ile 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 His Gln Tyr Tyr Thr Tyr Pro Leu
                85                  90                  95

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
            100                 105                 110
```

<210> 209
<211> 110

<212> PRT
<213> Artificial Sequence

<220>
<223> pAC18 (2F1)

<400> 209

```
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 Lys Ala Ser Ala Ala Val Gly Thr Tyr
            20                  25                  30

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

Tyr Ser Ala Ser Tyr Arg Lys Arg 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 His Gln Tyr Tyr Thr Tyr Pro Leu
                85                  90                  95

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
            100                 105                 110
```

<210> 210
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> pAC23 (2F11)

<400> 210

```
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 Lys Ala Ser Gln Ile Ala Ser Thr Asn
            20                  25                  30

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

Tyr Trp Ala Ser Tyr Arg Tyr 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 His Gln Tyr Tyr Thr Tyr Pro Leu
                85                  90                  95
```

```
Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
            100                 105                 110


<210>  211
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  H4E9 light chain

<400>  211

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 Lys Ala Ser Gln Asn Val Gly Thr Asn
            20                  25                  30


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


Tyr Ser Ala Ser Tyr Arg Tyr 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 His Gln Tyr Tyr Thr Tyr Pro Leu
                85                  90                  95


Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
            100                 105                 110


<210>  212
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  L2D2

<400>  212

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 Lys Ala Ser His Asn Val Gly Thr Asn
            20                  25                  30


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


Tyr Ser Ala Ser His Arg Tyr 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 His Gln Tyr Tyr Thr Tyr Pro Leu
85 90 95

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
100 105 110

<210> 213
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> pAC6 (C1)

<400> 213

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 Lys Ala Ser Gln Ile Met Gly Pro Asn
20 25 30

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

Tyr Leu Ala Ser Tyr His Glu 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 His Gln Tyr Tyr Thr Tyr Pro Leu
85 90 95

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
100 105 110

<210> 214
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> pAC7 (E10)

<400> 214

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 Lys Ala Ser Gln Ile Val Gly Thr Asn
20 25 30

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

Tyr Ser Ala Ser His Arg Pro 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 His Gln Tyr Tyr Thr Tyr Pro Leu
                85                  90                  95

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
            100                 105                 110
```

<210> 215
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> pAC12 (H7)

<400> 215

```
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 Lys Ala Ser Gln Lys Val Leu Thr Asn
            20                  25                  30

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

Tyr Leu Ala Ser Tyr Arg Tyr 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 His Gln Tyr Tyr Thr Tyr Pro Leu
                85                  90                  95

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
            100                 105                 110
```

<210> 216
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> pAC13 (H11)

<400> 216

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 Lys Ala Ser Gln Thr Val Ser Ala Asn
20 25 30

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

Tyr Leu Ala Ser Tyr Arg Tyr Arg 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 His Gln Tyr Tyr Thr Tyr Pro Leu
85 90 95

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
100 105 110

<210> 217
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> PR1A3 (Y98A) Heavy Chain CDR3

<400> 217

Trp Asp Phe Ala Asp Tyr Val Glu Ala Met Asp Tyr
1 5 10

<210> 218
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> PR1A3 (D99Y) Heavy Chain CDR3

<400> 218

Trp Asp Phe Tyr Tyr Tyr Val Glu Ala Met Asp Tyr
1 5 10

<210> 219
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> PR1A3 (D99H) Heavy Chain CDR3

<400> 219

eolf-seql
Trp Asp Phe Tyr His Tyr Val Glu Ala Met Asp Tyr
1 5 10

<210> 220
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> PR1A3 (V101F) Heavy Chain CDR3

<400> 220

Trp Asp Phe Tyr Asp Tyr Phe Glu Ala Met Asp Tyr
1 5 10

<210> 221
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> PR1A3 (E101aQ) Heavy Chain CDR3

<400> 221

Trp Asp Phe Tyr Asp Tyr Val Gln Ala Met Asp Tyr
1 5 10

<210> 222
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> PR1A3 (A103T) Heavy Chain CDR3

<400> 222

Trp Asp Phe Tyr Asp Tyr Val Glu Thr Met Asp Tyr
1 5 10

<210> 223
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> PR1A3 (Y98A / D99Y) Heavy Chain CDR3

<400> 223

Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr
1 5 10

<210> 224
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> PR1A3 (W95Y) Heavy Chain CDR3

<400> 224

Tyr Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr
1 5 10

<210> 225
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH7A (Y98A) Heavy Chain Construct

<400> 225

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

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

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

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

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

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

Ala Arg Trp Asp Phe Ala Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 226
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH7A (D99Y) Heavy Chain Construct

<400> 226

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

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 227
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH7A (D99H) Heavy Chain Construct

<400> 227

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

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr His Tyr Val Glu Ala Met Asp Tyr Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 228
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH7A (V101F) Heavy Chain Construct

<400> 228

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

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Phe Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 229
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH7A (E102Q) Heavy Chain Construct

<400> 229

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

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Gln Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 230
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH7A (A103T) Heavy Chain Construct

<400> 230

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

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Thr Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 231
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH7A (Y98A / D99Y) Heavy Chain Construct

<400> 231

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

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

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

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

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

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

Ala Arg Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 232
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH7A (W95Y) Heavy Chain Construct

<400> 232

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

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

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

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

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

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

Ala Arg Tyr Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 233
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A (Y98A)

<400> 233

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 Glu Phe
20 25 30

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

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

Lys Gly Arg Val Thr Phe 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 Trp Asp Phe Ala Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 234
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A (D99Y)

<400> 234

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 Glu Phe
20 25 30

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

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

Lys Gly Arg Val Thr Phe 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 Trp Asp Phe Tyr Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 235
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A (D99H)

<400> 235

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 Glu Phe
20 25 30

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

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

Lys Gly Arg Val Thr Phe 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 Trp Asp Phe Tyr His Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 236
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A (V101F)

<400> 236

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 Glu Phe
20 25 30

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

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

Lys Gly Arg Val Thr Phe 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 Trp Asp Phe Tyr Asp Tyr Phe Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 237
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A (E102Q)

<400> 237

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 Glu Phe
20 25 30

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 238
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A (A103T)

<400> 238

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 Glu Phe
20 25 30

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

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

Lys Gly Arg Val Thr Phe 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 Trp Asp Phe Tyr Asp Tyr Val Glu Thr Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 239
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A (Y98A / D99Y)

<400> 239

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 Glu Phe
20 25 30

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

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

Lys Gly Arg Val Thr Phe 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 Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 240
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A (W95Y)

<400> 240

```
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 Glu Phe
            20                  25                  30

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

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

Lys Gly Arg Val Thr Phe 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 Tyr Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 241
<211> 121

<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1B (Y98A)

<400> 241

```
Gln Val Lys Leu Gln 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 Glu Phe
            20                  25                  30


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


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


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


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 242
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1B (D99Y)

<400> 242

```
Gln Val Lys Leu Gln 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 Glu Phe
            20                  25                  30


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


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


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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 243
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1B (D99H)

<400> 243

Gln Val Lys Leu Gln 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 Glu Phe
20 25 30

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

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

Lys 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 Trp Asp Phe Tyr His Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 244
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1B (V101F)

<400> 244

Gln Val Lys Leu Gln 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 Glu Phe
            20   25   30

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

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

Lys 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 Trp Asp Phe Tyr Asp Tyr Phe Glu Ala Met Asp Tyr Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 245
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1B (E102Q)

<400> 245

Gln Val Lys Leu Gln 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 Glu Phe
            20   25   30

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 246
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1B (A103T)

<400> 246

Gln Val Lys Leu Gln 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 Glu Phe
            20   25   30

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

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

Lys 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 Trp Asp Phe Tyr Asp Tyr Val Glu Thr Met Asp Tyr Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 247
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1B (Y98A / D99Y)

<400> 247

Gln Val Lys Leu Gln 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 Glu Phe
            20   25   30

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 248
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1B (W95Y)

<400> 248

Gln Val Lys Leu Gln 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 Glu Phe
20 25 30

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 249
<211> 363
<212> DNA
<213> Artificial Sequence

<220>

<223> CH7A (Y98A) Heavy Chain Construct

<400> 249
caggtgcagc tggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata caccttcact gagtttggaa tgaactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttcgctgatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

<210> 250
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH7A (D99Y) Heavy Chain Construct

<400> 250
caggtgcagc tggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata caccttcact gagtttggaa tgaactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttctattatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

<210> 251
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH7A (D99H) Heavy Chain Construct

<400> 251
caggtgcagc tggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata caccttcact gagtttggaa tgaactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttctatcatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

<210> 252
<211> 364

<212> DNA
<213> Artificial Sequence

<220>
<223> CH7A (V101F) Heavy Chain Construct

<400> 252
ccaggtgcag ctggtgcaat ctgggtctga gttgaagaag cctggggcct cagtgaaggt 60

ttcctgcaag gcttctggat acaccttcac tgagtttgga atgaactggg tgcgacaggc 120

ccctggacaa gggcttgagt ggatgggatg gataaacacc aaaactggag aggcaacata 180

tgttgaagag tttaagggac ggtttgtctt ctccttggac acctctgtca gcacggcata 240

tctgcagatc agcagcctaa aggctgaaga cactgccgtg tattactgtg cgagatggga 300

cttctatgat tacttcgagg ctatggacta ctggggccaa gggaccacgg tcaccgtctc 360

ctca 364

<210> 253
<211> 364
<212> DNA
<213> Artificial Sequence

<220>
<223> CH7A (E102Q) Heavy Chain Construct

<400> 253
ccaggtgcag ctggtgcaat ctgggtctga gttgaagaag cctggggcct cagtgaaggt 60

ttcctgcaag gcttctggat acaccttcac tgagtttgga atgaactggg tgcgacaggc 120

ccctggacaa gggcttgagt ggatgggatg gataaacacc aaaactggag aggcaacata 180

tgttgaagag tttaagggac ggtttgtctt ctccttggac acctctgtca gcacggcata 240

tctgcagatc agcagcctaa aggctgaaga cactgccgtg tattactgtg cgagatggga 300

cttctatgat tacgtgcagg ctatggacta ctggggccaa gggaccacgg tcaccgtctc 360

ctca 364

<210> 254
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH7A (A103T) Heavy Chain Construct

<400> 254
caggtgcagc tggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata caccttcact gagtttggaa tgaactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttctatgatt acgtggagac tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

<210> 255
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH7A (Y98A / D99Y) Heavy Chain Construct

<400> 255
caggtgcagc tggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata caccttcact gagtttggaa tgaactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300

ttcgcttatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

<210> 256
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH7A (W95Y) Heavy Chain Construct

<400> 256
caggtgcagc tggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata caccttcact gagtttggaa tgaactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg ataaacacca aaactggaga ggcaacatat 180

gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatacgac 300

ttctatgatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc 360

tca 363

<210> 257
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1

<400> 257

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 Glu Phe
20 25 30

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

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

Lys Gly Arg Val Thr Phe Thr Leu 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 Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 258
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A2

<400> 258

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 259
<211> 121

<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A3

<400> 259

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 Glu Phe
20 25 30

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 260
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A4

<400> 260

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 Glu Phe
20 25 30

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

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

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

```
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Lys Tyr Phe Cys
                85                  90                  95

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 261
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A

<400> 261

```
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 Glu Phe
            20                  25                  30

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

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

Lys Gly Arg Val Thr Phe 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 Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 262
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1B

<400> 262

```
Gln Val Lys Leu Gln 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 Glu Phe
            20   25   30

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 263
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1C

<400> 263

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 264
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1D

<400> 264

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 265
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1E

<400> 265

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 Glu Phe
20 25 30

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

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

Lys Gly Arg Phe 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 Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 266
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1F

<400> 266

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 Glu Phe
20 25 30

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

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

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 267
<211> 121
<212> PRT
<213> Artificial Sequence

<220>

<223> CH1A1G

<400> 267

```
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 Glu Phe
            20                  25                  30

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

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

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 268
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1

<400> 268
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaaggtg 60

tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120

ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccttc accctggaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttctacgatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agc 363

<210> 269
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A2

<400> 269
caggtcaaac tgcagcagag cggccctgag ctgaagaaac ccggcgagac agtgaagatc 60

agctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggca 120

ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccatg accaccgaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttctacgatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agc 363

<210> 270
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A3

<400> 270
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ctggcgccag cgtgaaggtg 60

tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt caagcaggcc 120

cctggcaagg gcctgaagtg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccatg accaccgaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttctacgatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agc 363

<210> 271
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A4

<400> 271
aggtgcagct ggtgcagtct ggcgccgaag tgaagaaacc tggcgccagc gtgaaggtgt 60

cctgcaaggc cagcggctac accttcaccg agttcggcat gaactgggtc cgacaggcac 120

caggccaggg cctcgaatgg atgggctgga tcaacaccaa gaccggcgag gccacctacg 180

tggaagagtt caagggcaga ttcgccttca gcctggaaac cagcgccacc accgcctacc 240

tgcagatcaa caacctgaag aacgaggata ccgccaagta cttctgcgcc agatgggact 300

tctacgatta cgtggaagcc atggactact ggggccaggg caccaccgtg accgtgtcta 360

gc 362

<210> 272
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A

<400> 272
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaaggtg 60

tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120

ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttctacgatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agc 363

<210> 273
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1B

<400> 273
caggtgaagc tgcagcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaaggtg 60

tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120

ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccatg accacggaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttctacgatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agc 363

<210> 274
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1C

<400> 274
caggtgcagc tggtgcagtc tggccccgaa ctgaagaaac ctggagctag tgtgaaggtg 60

tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120

ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccatg accacggaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttctacgatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agc 363

<210> 275
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1D

<400> 275
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tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120

ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccatg accacggaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttctacgatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agc 363

<210> 276
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1E

<400> 276
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaaggtg 60

tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120

ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag attcaccatg accacggaca ccagcaccag caccgcctac 240

atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

ttctacgatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360

agc 363

<210> 277
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1F

<400> 277
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaaggtg 60

tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120

ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccatg accacggaca ccagcaccag caccgcctac 240

ctggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

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agc 363

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ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180

gtggaagagt tcaagggcag agtgaccatg accacggaca ccagcaccag caccgcctac 240

atggaaatcc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300

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agc 363

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<212> PRT
<213> Artificial Sequence

<220>
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Phe
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Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Lys 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
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Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
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Gln Gly Thr Thr Val Thr Val Ser Ser
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cctgggcaag ggctcgagtg gatgggatgg ataaacacga agacaggcga ggccacctac 180

gtagaagagt tcaaaggaag ggtcacgatg accacagata cttctacctc tactgcgtat 240

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

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

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

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

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

Ala Arg Trp Asp Phe Tyr Asp Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120