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<130> G0224_WO

<150> GB1412658.5
<151> 2014-07-16

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<170> PatentIn version 3.5

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


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


Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


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


His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
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Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
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Gly Ser Asp Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Ala Pro
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Phe Leu Lys Met Asn Ser Leu Gln Ser Gly Asp Ser Ala Arg Tyr Tyr
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Cys Val Thr Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
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Ser His Lys Ser Pro
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Arg Pro

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Tyr Pro Arg Ser Ile Tyr Ile Arg Arg Arg His Pro Ser Pro Ser Leu
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Thr Thr

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Phe Asn

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Pro Ala

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Ser Pro Ala Ala His Phe Pro Arg Ser Ile Pro Arg Pro Gly Pro Ile

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Arg Thr

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Ala Pro Gly Pro Ser Ala Pro Ser His Arg Ser Leu Pro Ser Arg Ala
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Phe Gly

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Pro Arg Asn Ser Ile His Phe Leu His Pro Leu Leu Val Ala Pro Leu
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Gly Ala

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Met Pro Ser Leu Ser Gly Val Leu Gln Val Arg Tyr Leu Ser Pro Pro
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Asp Leu

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Ser Pro Gln Tyr Pro Ser Pro Leu Thr Leu Thr Leu Pro Pro His Pro
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Ser Leu

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Ile Ser

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Leu Pro Trp Arg Thr Ser Leu Leu Pro Ser Leu Pro Leu Arg Arg Arg
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Pro

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Pro Pro Leu Phe Ala Lys Gly Pro Val Gly Leu Leu Ser Arg Ser Phe
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Pro Pro

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Pro Tyr

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Pro

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Pro Asn Val Ala His Val Leu Pro Leu Leu Thr Val Pro Trp Asp Asn
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Leu Arg

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Cys Asn Pro Leu Leu Pro Leu Cys Ala Arg Ser Pro Ala Val Arg Thr
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Phe Pro

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Asp Leu Cys Leu Arg Asp Trp Gly Cys Leu Trp
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<210> 57
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Met Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp Gly Asp
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<210> 58
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Glu Asp Asp Glu
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Gly Arg Ser Val
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Gly Arg Ser Val Lys
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1 5 10 15

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<400> 62

Arg Leu Met Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp Glu
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Asp Asp

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<400> 63

Met Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp Glu Asp Asp
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<210> 64
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Glu Val Arg Ser Phe Cys Thr Arg Trp Pro Ala Glu Lys Ser Cys Lys
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Pro Leu Arg Gly
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Arg Ser Glu Gln
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<400> 69

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

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

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

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

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

Ser Ser His Asp Cys Asn Ala Phe Gly Gly Gly Thr Glu Val Val Val
100 105 110

Lys

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tgtaatgctt tcggcggagg gaccgaggtg gtggtcaaa 339

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


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


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


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


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            100                 105                 110


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Ser Ala Ser Thr Leu Ala Ser
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<210> 77
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<212> PRT
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<400> 77

Leu Gly Glu Phe Ser Cys Ser Ser His Asp Cys Asn Ala
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<210> 78
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<220>
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<400> 78

Gly Phe Ser Leu Ser Asn Tyr Ala Val Ser
1 5 10

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<220>
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<400> 79

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1 5 10 15

Gly

<210> 80
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3

<400> 80

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

Pro

<210> 81
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4450 VL region

<400> 81

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

Gly Thr Val Thr Ile Asn Cys Gln Ser Ser Gln Ser Ile Tyr Asn Asn
20 25 30

Asn Asp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
35 40 45

Leu Ile Tyr Glu Ala Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe
50 55 60

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

Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gly Gly Gly Ser Gly
85 90 95

Gly Asp Gly Ile Ala Phe Gly Gly Gly Thr Lys Val Val Val Glu
100 105 110

<210> 82
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4450 VL region

<400> 82
gccattgata tgacccagac tccatccccc gtgtctgcag ctgtgggagg cacagtcacc 60

atcaattgcc agtccagtca gagtatttat aataataatg acttagcctg gtatcagcag 120

aaaccagggc agcctcccaa gctcctgatc tacgaagcat ccaaactggc atctggggtc 180

ccatcgcggt tcaaaggcag tggatctggg acacagttca ctctcaccat cagtggcgtg 240

cagtgtgatg atgctgccac ttactactgt cagggcggtg gtagtggtgg tgatggcatt 300

gctttcggcg gagggaccaa ggtggtcgtc gaa 333

<210> 83
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4450 VH region

<400> 83

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

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

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

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

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

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

Gly His Ser Asp Val Asp Val Leu Asp Ile Trp Gly Pro Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 84
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4450 VH region

<400> 84
cagtcggtgg aggagtccgg gggtcgcctg gtcacgcctg gggcacccct gacactcacc 60

tgcacagtct ctggattctc cctcaataac tatgtaatgg tctgggtccg ccaggctcca 120

gggaaggggc tggaatggat cggaatcatt tatgttagtg gtaatgcata ctacgcgagc 180

tgggcaaaag gccgattcac catctccaga acctcgacca cggtggatct gaaagtgacc 240

agtctgacaa ccgaggacac ggccacctat ttctgtgcca gagatgctgg tcatagtgat 300

gtcgatgttt tggatatttg gggcccgggc accctcgtca ccgtctcgag t 351

<210> 85
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1

<400> 85

Gln Ser Ser Gln Ser Ile Tyr Asn Asn Asn Asp Leu Ala
1 5 10

<210> 86
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2

<400> 86

Glu Ala Ser Lys Leu Ala Ser
1 5

<210> 87

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

<220>
<223> CDRL3

<400> 87

Gln Gly Gly Gly Ser Gly Gly Asp Gly Ile Ala
1 5 10

<210> 88
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH1

<400> 88

Gly Phe Ser Leu Asn Asn Tyr Val Met Val
1 5 10

<210> 89
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH2

<400> 89

Ile Ile Tyr Val Ser Gly Asn Ala Tyr Tyr Ala Ser Trp Ala Lys Gly
1 5 10 15

<210> 90
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3

<400> 90

Asp Ala Gly His Ser Asp Val Asp Val Leu Asp Ile

1 5 10

<210> 91
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4120 VL region

<400> 91

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

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

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

Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Ser Ser Arg Phe Lys Gly
50 55 60

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

Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Ser Tyr Tyr Gly Thr Ser Ser
85 90 95

Gly Gly Ser Trp Ala Phe Gly Gly Gly Thr Lys Val Val Val Lys
100 105 110

<210> 92
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4120 VL region

<400> 92
gcattcgaat tgagccagac tccagcctcc gtggaggcag ctgtgggagg cacagtcacc 60

atcaagtgcc aggccagtca gagcattagc actgcattag cctggtatca gcagaaacca 120

gggcagcgtc ccaagctcct gatctatggt gcatccactc tggcatctgg ggtctcatcg 180

cggttcaaag gcagtggatc tgggacagag ttcactctca ccatcagcga cctggagtgt 240

gccgatgctg ccacttacta ctgtcaaagc tattatggta cgagtagtgg tggttcttgg 300

gctttcggcg gagggaccaa ggtggtcgtc aaa 333

<210> 93
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4120 VH region

<400> 93

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

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

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

Ala Cys Ile Tyr Thr Gly Ser Ser Gly Asp Thr Tyr Tyr Ala Ser Trp
50 55 60

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

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

Ala Arg Gly Pro Tyr Val Gly Tyr Gly Tyr Asp Leu Gln Tyr Leu Tyr
100 105 110

Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 94
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4120 VH region

<400> 94
cagtcattgg aggagtccgg gggagacctg gtcaagcctg gggcatccct gacactcacc 60

tgcacagcct ctggattctc cttcagtagt agctactaca tgtgctgggt ccgccagtct 120

ccagggaagg ggctggagtg gatcgcatgc atttatactg gtagtagtgg tgacacttac 180

tacgcgagct gggcgaaagg ccgattcacc atctccaaaa cctcgtcgac cacggtgtct 240

ctgcaaatga ccagtctgac agccgcggac acggccactt atttctgtgc gagagggcct 300

tatgttggtt atggttatga tcttcaatac ttgtacttgt ggggcccggg gaccctcgtc 360

accgtctcga gt 372

<210> 95
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1

<400> 95

Gln Ala Ser Gln Ser Ile Ser Thr Ala Leu Ala
1 5 10

<210> 96
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2

<400> 96

Gly Ala Ser Thr Leu Ala Ser
1 5

<210> 97
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL3

<400> 97

Gln Ser Tyr Tyr Gly Thr Ser Ser Gly Gly Ser Trp Ala
1 5 10

<210> 98
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH1

<400> 98

Gly Phe Ser Phe Ser Ser Ser Tyr Tyr Met Cys
1 5 10

<210> 99
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH2

<400> 99

Cys Ile Tyr Thr Gly Ser Ser Gly Asp Thr Tyr Tyr Ala Ser Trp Ala
1 5 10 15

Lys Gly

<210> 100
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3

<400> 100

Gly Pro Tyr Val Gly Tyr Gly Tyr Asp Leu Gln Tyr Leu Tyr Leu
1 5 10 15

<210> 101
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4126 VL region

<400> 101

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

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

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

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

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

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

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

<210> 102
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4126 VL region

<400> 102
gacattgtga tgacccagac tccagcctcc gtggaggcag ctgtgggagg cacagtcacc 60

atcaagtgcc aggccagtca gaacattggt agtggtttag cctggtatca gcagaaacca 120

gggcagcctc ccaagctcct gatctattat gcatccactc tggcatctgg ggtcccatca 180

aggttcaaag gcagtggatc tgggacacag ttcactctca ccatcagcga cctggagtgt 240

gccgacgctg ccacttacta ctgtcaaagt catgattata gtagtgttcg gagttacggt 300

aatgctttcg gcggagggac cgaggtggtg gtcaaa 336

<210> 103
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4126 VH region

<400> 103

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

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

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

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

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

Thr Leu Gln Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Ala Tyr Gly Ser Gly Gly Ser Gly Tyr Ile Gly Cys Tyr

100 105 110

Phe Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 104
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4126 VH region

<400> 104
cagcagcacc tggaggagtc cgggggaggc ctggtcaagc ctggaggaac cctgacactc 60

acctgcaaag cctctggaat cgacttcagt agctactact acatgtgctg ggtccgccag 120

gctccaggga aggggctgga gtgggtcgcg tgcattgatc ctgctagtag tggtactact 180

tactacgcga cctgggcgaa aggccgattc accatctcca aaacctcgtc gaccacggtg 240

actctgcaaa tgaccagtct gacagccgcg gacacggcca cctatttctg tgcgagggca 300

tatggtagtg ggggtagtgg ttatataggg tgctactttg acttgtgggg ccaaggcacc 360

ctcgtcaccg tctcgagt 378

<210> 105
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1

<400> 105

Gln Ala Ser Gln Asn Ile Gly Ser Gly Leu Ala
1 5 10

<210> 106
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2

<400> 106

Tyr Ala Ser Thr Leu Ala Ser
1 5

<210> 107
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL3

<400> 107

Gln Ser His Asp Tyr Ser Ser Val Arg Ser Tyr Gly Asn Ala
1 5 10

<210> 108
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH1

<400> 108

Gly Ile Asp Phe Ser Ser Tyr Tyr Tyr Met Cys
1 5 10

<210> 109
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH2

<400> 109

Cys Ile Asp Pro Ala Ser Ser Gly Thr Thr Tyr Tyr Ala Thr Trp Ala
1 5 10 15

Lys Gly

<210> 110
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3

<400> 110

Ala Tyr Gly Ser Gly Gly Ser Gly Tyr Ile Gly Cys Tyr Phe Asp Leu
1 5 10 15

<210> 111
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4127 VL region

<400> 111

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

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

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

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

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

Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Ala Gly Tyr Lys Ser Asp
85 90 95

Ser Asp Asp Gly Thr Thr Phe Gly Gly Gly Thr Lys Val Val Val Glu
100 105 110

<210> 112
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4127 VL region

<400> 112
gccatcgtga tgacccagac tccatcttcc aagtctgtcc ctatgggagg cacagtcacc 60

atcaactgcc aggccagtca gagtgtttat ggtaataacg aattatcctg gtatcagcag 120

aaaccagggc agcctcccaa gctcctgatc tatttggcat ccaggctggc atcgggggtc 180

ccatcgcggt ttagcggcag tggatctggg acacagttca ctctcaccat cagcggcgtg 240

cagtgtgacg atgctgccac ttactactgt gcaggctata aaagtgatag tgatgatggc 300

actactttcg gcggagggac caaggtggtg gtcgaa 336

<210> 113
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4127 VH region

<400> 113

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

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

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

Gly Cys Ile Asp Ile Ser Ser Ser Gly Ser Thr Tyr Tyr Ala Ser Trp
50 55 60

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

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


Ala Arg Asp Tyr Tyr Ser Ser Asp Trp Gly Val Arg Phe Asn Leu Trp
            100                 105                 110


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


<210>  114
<211>  366
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Rabbit Ab 4127 VH region

<400>  114
cagcagctgg aggagtccgg gggagacctg gtcaagcctg gggcatccct gacactcacc       60

tgcacagcct ctggattctc cttcagtaat ctctattaca tgtgttgggt ccgccaggct      120

ccagggaagg ggctggagtt gatcggatgc attgatatta gcagtagtgg tagcacttac      180

tacgcgagct gggcgaaagg ccgattcacc atctccaaaa cctcgtcgac cacggtgact      240

ctgcagatga ccagtctgac agccgcggac acggccacct atttctgtgc gagagattac      300

tattctagtg actggggtgt tagatttaac ttgtggggcc agggcaccct cgtcaccgtc      360

tcgagt                                                                 366


<210>  115
<211>  13
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CDRL1

<400>  115

Gln Ala Ser Gln Ser Val Tyr Gly Asn Asn Glu Leu Ser
1               5                   10


<210>  116
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<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2

<400> 116

Leu Ala Ser Arg Leu Ala Ser
1 5

<210> 117
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL3

<400> 117

Ala Gly Tyr Lys Ser Asp Ser Asp Asp Gly Thr Thr
1 5 10

<210> 118
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH1

<400> 118

Gly Phe Ser Phe Ser Asn Leu Tyr Tyr Met Cys
1 5 10

<210> 119
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH2

<400> 119

Cys Ile Asp Ile Ser Ser Ser Gly Ser Thr Tyr Tyr Ala Ser Trp Ala

1 5 10 15

Lys Gly

<210> 120
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3

<400> 120

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

<210> 121
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4128 VL region

<400> 121

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

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

Leu Ser Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
35 40 45

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

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

Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Ile Tyr Tyr Ser Ala Ser Gly

85 90 95

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

<210> 122
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4128 VL region

<400> 122
gacattgtga tgacccagac tccagcctcc gtggaggcag ctgtgggagg cacagtcacc 60

atcaagtgcc aggccagtga aagcattagc aactacttat cctggtttca gcagaaacca 120

gggcagcctc ccaagctcct gatctatgct tcatccaaac tgtcatctgg ggtcccatcg 180

cggttcaaag gcgatagatc tgggacagag tacactctca ccatcagcga cctggagtgt 240

gccgatgctg ccacttacta ctgtcaaatc tattattcgg ctagtggcag tcgtgattgg 300

actttcggcg gagggaccaa ggtggtcgtc gaa 333

<210> 123
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4128 VH region

<400> 123

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

Leu Thr Leu Thr Cys Lys Gly Ser Gly Leu Asp Phe Ser Ser Tyr Trp
20 25 30

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

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

50 55 60

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

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

Arg Gly Gly Gly Ala Gly Tyr Ser Gly Ala Phe Asp Leu Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 124
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4128 VH region

<400> 124
cagtcgttgg aggagtccgg gggagacctg gtccagcctg agggatccct gacactcacc 60

tgcaaaggct ccgggttaga cttcagtagc tactggatat gctgggtccg ccaggctcca 120

gggaaggggc tggagtggat cgcatgcatt gttactggta gtagtgataa cacttactac 180

gcgagctggg cgaaaggccg attcaccatc tccaaaacct cgtcgaccac ggtgactctg 240

caaatgacca gtctgacagc cgcggacacg gccacctatt tctgtgcgag aggtggtggt 300

gctggttata gtggtgcctt tgacttgtgg ggccaaggga ccctcgtcac cgtctcgagt 360

<210> 125
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1

<400> 125

Gln Ala Ser Glu Ser Ile Ser Asn Tyr Leu Ser

1 5 10

<210> 126
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2

<400> 126

Ala Ser Ser Lys Leu Ser Ser
1 5

<210> 127
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL3

<400> 127

Gln Ile Tyr Tyr Ser Ala Ser Gly Ser Arg Asp Trp Thr
1 5 10

<210> 128
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH1

<400> 128

Gly Leu Asp Phe Ser Ser Tyr Trp Ile Cys
1 5 10

<210> 129
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH2

<400> 129

Cys Ile Val Thr Gly Ser Ser Asp Asn Thr Tyr Tyr Ala Ser Trp Ala
1 5 10 15

Lys Gly

<210> 130
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3

<400> 130

Gly Gly Gly Ala Gly Tyr Ser Gly Ala Phe Asp Leu
1 5 10

<210> 131
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4130 VL region

<400> 131

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

Gly Thr Val Ser Ile Ser Cys Gln Ser Ser Gln Ser Val Tyr Asn Thr
20 25 30

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

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

Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Asp Leu

65 70 75 80

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

Ser Asp Leu Asn Val Phe Gly Gly Gly Thr Lys Val Val Val Lys
100 105 110

<210> 132
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4130 VL region

<400> 132
gccgccgtgc tgacccagac tccatctccc gtgtctgcag ctgtgggagg cacagtcagc 60

atcagttgcc agtccagtca gagtgtttat aatacaaagg acttagcctg gtatcagcag 120

aaaccagggc agcctcccaa gctcctgatc tatggtacat ccactctggc atctggggtc 180

tcatcacggt tcagcggcag tggatctggg acagagttca ctctcaccat cagcgacctg 240

gagtgtgacg atgctgccac ttattactgt caaggcggtt ttagtagtag tgatttgaat 300

gttttcggcg gagggaccaa ggtggtggtc aaa 333

<210> 133
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4130 VH region

<400> 133

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

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

Tyr Asp Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp

35 40 45

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

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

Thr Leu Gln Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr Phe
85 90 95

Cys Ala Arg Asp Val Ser Asn Ser Asp His Tyr Thr Arg Leu Asp Leu
100 105 110

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

<210> 134
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4130 VH region

<400> 134
cagcagcagc tggaggagtc cgggggagac ctggtcaggc ctgagggatc cctgacactc 60

acctgcacag cctctggatt cgacttcagt ggcggctacg acatttcctg ggtccgccag 120

gctccaggga aggggctgga gtggatcgga tgcatttatg gtggtatcaa tagtgtcact 180

gactacgcga gctgggcgaa aggccgagtc accatctcca aaacctcgtc gaccacggtg 240

actctgcaga tgaccagtct gacagccgcg gacacggcca cctatttctg tgcgagagat 300

gttagtaata gcgatcatta tactcggttg gatctctggg gccaaggcac cctggtcacc 360

gtctcgagt 369

<210> 135
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1

<400> 135

Gln Ser Ser Gln Ser Val Tyr Asn Thr Lys Asp Leu Ala
1 5 10

<210> 136
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2

<400> 136

Gly Thr Ser Thr Leu Ala Ser
1 5

<210> 137
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL3

<400> 137

Gln Gly Gly Phe Ser Ser Ser Asp Leu Asn Val
1 5 10

<210> 138
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH1

<400> 138

Gly Phe Asp Phe Ser Gly Gly Tyr Asp Ile Ser
1 5 10

<210> 139

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

<220>
<223> CDRH2

<400> 139

Cys Ile Tyr Gly Gly Ile Asn Ser Val Thr Asp Tyr Ala Ser Trp Ala
1 5 10 15

Lys Gly

<210> 140
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3

<400> 140

Asp Val Ser Asn Ser Asp His Tyr Thr Arg Leu Asp Leu
1 5 10

<210> 141
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4132 VL region

<400> 141

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

Gly Thr Val Thr Ile Lys Cys Gln Ala Ser Glu Thr Ile Ser Ser Arg
20 25 30

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

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

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

Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Gly Tyr Tyr Tyr Ser Ser Gly
85 90 95

Ser Asp Tyr Gly Phe Gly Gly Gly Thr Lys Val Val Val Lys
100 105 110

<210> 142
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4132 VL region

<400> 142
gacattgtga tgacccagac tccagcctcc gtggaggcag ctgtgggagg cacagtcacc 60

atcaagtgcc aggccagtga gaccattagt agtagattag cctggtatca gcagaagcta 120

gggcagcctc ccaaactcct gatctattct gcatccactc tggcgtctgg ggtcccatcg 180

cggttcaaag gcagtggatc tgggacagag tacactctca ccatcagcgg cgtgcagtgt 240

gccgatgctg ccacttatta ctgtcaaggc tattattata gtagtggtag tgattatggt 300

ttcggcggag ggaccaaggt ggtcgtcaaa 330

<210> 143
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4132 VH region

<400> 143

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

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

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

Gly Cys Ile Asn Ser Gly Thr Gly Gly Thr Ala Tyr Ala Ser Trp Ala
    50                  55                  60

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  144
<211>  363
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Rabbit Ab 4132 VH region

<400>  144
cagtcgttgg aggagtccgg gggagacctg gtcaagcctg gggcatccct gacactcacc       60

tgcacagcct ctggattctc cttcagtagc agctactgga tatgctgggt ccgccaggct      120

ccagggaagg ggctggagtg gagcggatgc attaatagtg gtactggtgg cactgcctac      180

gcgagctggg cgaaaggccg attcaccatc tccaattcct cgtcgaccac ggtgactctt      240

caaatgacca gtctgacagc cgcggacacg gccacctatt tctgtgcgag agaatgggtt      300

agtggttatt ataaagatgc ttttgatctc tggggccagg gcaccctggt caccgtctcg      360

agt                                                                    363
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<210> 145
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1

<400> 145

Gln Ala Ser Glu Thr Ile Ser Ser Arg Leu Ala
1 5 10

<210> 146
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2

<400> 146

Ser Ala Ser Thr Leu Ala Ser
1 5

<210> 147
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL3

<400> 147

Gln Gly Tyr Tyr Tyr Ser Ser Gly Ser Asp Tyr Gly
1 5 10

<210> 148
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH1

<400> 148

Gly Phe Ser Phe Ser Ser Ser Tyr Trp Ile Cys
1 5 10

<210> 149
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH2

<400> 149

Cys Ile Asn Ser Gly Thr Gly Gly Thr Ala Tyr Ala Ser Trp Ala Lys
1 5 10 15

Gly

<210> 150
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3

<400> 150

Glu Trp Val Ser Gly Tyr Tyr Lys Asp Ala Phe Asp Leu
1 5 10

<210> 151
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH1 dAbH1

<400> 151

Gly Ile Asp Leu Ser Asn Tyr Ala Ile Asn
1 5 10

<210> 152

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

<220>
<223> CDRH2 dAbH1

<400> 152

Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys Gly
1 5 10 15

<210> 153
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3 dAbH1

<400> 153

Thr Val Pro Gly Tyr Ser Thr Ala Pro Tyr Phe Asp Leu
1 5 10

<210> 154
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1 dAbL1

<400> 154

Gln Ser Ser Pro Ser Val Trp Ser Asn Phe Leu Ser
1 5 10

<210> 155
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2 dAbL1

<400> 155

Glu Ala Ser Lys Leu Thr Ser

1 5

<210> 156
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL3 dAbL1

<400> 156

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

<210> 157
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain variable domain of anti-albumin antibody (no ds)

<400> 157

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

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

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

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

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

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

Arg Thr Val Pro Gly Tyr Ser Thr Ala Pro Tyr Phe Asp Leu Trp Gly

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 158
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain variable domain of anti-albumin antibody (ds)

<400> 158

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

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

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

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

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

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

Arg Thr Val Pro Gly Tyr Ser Thr Ala Pro Tyr Phe Asp Leu Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 159
<211> 112
<212> PRT

<213> Artificial Sequence

<220>
<223> Light chain variable domain of anti-albumin antibody (no ds)

<400> 159

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1               5                  10                  15


Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn
            20                  25                  30


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


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


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


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


Ser Asp Thr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr
            100                 105                 110
```

<210> 160
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain variable domain of anti-albumin antibody (ds)

<400> 160

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Gly Lys Pro Thr His
1               5                  10                  15


Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
            20                  25                  30
```

```
Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn
        35                  40                  45

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

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

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
                85                  90                  95

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile
            100                 105                 110

Ser Asp Thr Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Arg Thr
        115                 120                 125
```

<210> 161
<211> 847
<212> PRT
<213> Artificial Sequence

<220>
<223> Human CD22

<400> 161

```
Met His Leu Leu Gly Pro Trp Leu Leu Leu Leu Val Leu Glu Tyr Leu
1               5                   10                  15

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

Tyr Ala Trp Glu Gly Ala Cys Val Trp Ile Pro Cys Thr Tyr Arg Ala
        35                  40                  45

Leu Asp Gly Asp Leu Glu Ser Phe Ile Leu Phe His Asn Pro Glu Tyr
    50                  55                  60

Asn Lys Asn Thr Ser Lys Phe Asp Gly Thr Arg Leu Tyr Glu Ser Thr
```

65 70 75 80

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

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

Asp Ser Gly Gln Leu Gly Leu Arg Met Glu Ser Lys Thr Glu Lys Trp
115 120 125

Met Glu Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His
130 135 140

Ile Gln Leu Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr
145 150 155 160

Cys Leu Leu Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp
165 170 175

Leu Leu Glu Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser
180 185 190

Leu Thr Ile Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro
195 200 205

Gln Trp Ser His His Gly Lys Ile Val Thr Cys Gln Leu Gln Asp Ala
210 215 220

Asp Gly Lys Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His
225 230 235 240

Thr Pro Lys Leu Glu Ile Lys Val Thr Pro Ser Asp Ala Ile Val Arg
245 250 255

Glu Gly Asp Ser Val Thr Met Thr Cys Glu Val Ser Ser Ser Asn Pro
260 265 270

Glu Tyr Thr Thr Val Ser Trp Leu Lys Asp Gly Thr Ser Leu Lys Lys

275 280 285

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

Gly Lys Tyr Cys Cys Gln Val Ser Asn Asp Val Gly Pro Gly Arg Ser
305 310 315 320

Glu Glu Val Phe Leu Gln Val Gln Tyr Ala Pro Glu Pro Ser Thr Val
325 330 335

Gln Ile Leu His Ser Pro Ala Val Glu Gly Ser Gln Val Glu Phe Leu
340 345 350

Cys Met Ser Leu Ala Asn Pro Leu Pro Thr Asn Tyr Thr Trp Tyr His
355 360 365

Asn Gly Lys Glu Met Gln Gly Arg Thr Glu Glu Lys Val His Ile Pro
370 375 380

Lys Ile Leu Pro Trp His Ala Gly Thr Tyr Ser Cys Val Ala Glu Asn
385 390 395 400

Ile Leu Gly Thr Gly Gln Arg Gly Pro Gly Ala Glu Leu Asp Val Gln
405 410 415

Tyr Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile
420 425 430

Arg Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn
435 440 445

Pro Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu
450 455 460

Pro Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr
465 470 475 480

Thr Ile Ala Cys Ala Ala Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro

485 490 495

Val Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys
500 505 510

Ile Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln
515 520 525

Cys Asp Phe Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu
530 535 540

Lys Asn Gly Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser
545 550 555 560

Ile Ser Pro Glu Asp Ala Gly Ser Tyr Ser Cys Trp Val Asn Asn Ser
565 570 575

Ile Gly Gln Thr Ala Ser Lys Ala Trp Thr Leu Glu Val Leu Tyr Ala
580 585 590

Pro Arg Arg Leu Arg Val Ser Met Ser Pro Gly Asp Gln Val Met Glu
595 600 605

Gly Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val
610 615 620

Ser His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro Tyr His
625 630 635 640

Ser Gln Lys Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala
645 650 655

Tyr Trp Cys Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu
660 665 670

Ser Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg Val
675 680 685

Ala Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys

```
    690                 695                 700

Gly Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly
705                 710                 715                 720

Leu Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys
                725                 730                 735

Val Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr
            740                 745                 750

Asn Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro
        755                 760                 765

Glu Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln
    770                 775                 780

Arg Pro Pro Pro Asp Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His
785                 790                 795                 800

Lys Arg Gln Val Gly Asp Tyr Glu Asn Val Ile Pro Asp Phe Pro Glu
                805                 810                 815

Asp Glu Gly Ile His Tyr Ser Glu Leu Ile Gln Phe Gly Val Gly Glu
            820                 825                 830

Arg Pro Gln Ala Gln Glu Asn Val Asp Tyr Val Ile Leu Lys His
        835                 840                 845


<210>  162
<211>  226
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Human CD79a

<400>  162

Met Pro Gly Gly Pro Gly Val Leu Gln Ala Leu Pro Ala Thr Ile Phe
1               5                   10                  15
```

```
Leu Leu Phe Leu Leu Ser Ala Val Tyr Leu Gly Pro Gly Cys Gln Ala
            20                  25                  30

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

Asp Ala His Phe Gln Cys Pro His Asn Ser Ser Asn Asn Ala Asn Val
    50                  55                  60

Thr Trp Trp Arg Val Leu His Gly Asn Tyr Thr Trp Pro Pro Glu Phe
65                  70                  75                  80

Leu Gly Pro Gly Glu Asp Pro Asn Gly Thr Leu Ile Ile Gln Asn Val
                85                  90                  95

Asn Lys Ser His Gly Gly Ile Tyr Val Cys Arg Val Gln Glu Gly Asn
            100                 105                 110

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

Pro Pro Arg Pro Phe Leu Asp Met Gly Glu Gly Thr Lys Asn Arg Ile
    130                 135                 140

Ile Thr Ala Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly
145                 150                 155                 160

Thr Leu Leu Leu Phe Arg Lys Arg Trp Gln Asn Glu Lys Leu Gly Leu
                165                 170                 175

Asp Ala Gly Asp Glu Tyr Glu Asp Glu Asn Leu Tyr Glu Gly Leu Asn
            180                 185                 190

Leu Asp Asp Cys Ser Met Tyr Glu Asp Ile Ser Arg Gly Leu Gln Gly
        195                 200                 205

Thr Tyr Gln Asp Val Gly Ser Leu Asn Ile Gly Asp Val Gln Leu Glu
    210                 215                 220
```

Lys Pro
225

<210> 163
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Human CD79b

<400> 163

Met Ala Arg Leu Ala Leu Ser Pro Val Pro Ser His Trp Met Val Ala
1 5 10 15

Leu Leu Leu Leu Leu Ser Ala Glu Pro Val Pro Ala Ala Arg Ser Glu
20 25 30

Asp Arg Tyr Arg Asn Pro Lys Gly Ser Ala Cys Ser Arg Ile Trp Gln
35 40 45

Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr Val Lys Met His
50 55 60

Cys Tyr Met Asn Ser Ala Ser Gly Asn Val Ser Trp Leu Trp Lys Gln
65 70 75 80

Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu Glu Lys Gly Arg Met
85 90 95

Glu Glu Ser Gln Asn Glu Ser Leu Ala Thr Leu Thr Ile Gln Gly Ile
100 105 110

Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln Gln Lys Cys Asn Asn
115 120 125

Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu Leu Arg Val Met Gly
130 135 140

Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly

145 150 155 160

Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile Ile Val Pro
165 170 175

Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser Lys Ala Gly Met Glu Glu
180 185 190

Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu
195 200 205

Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val Gly Glu
210 215 220

His Pro Gly Gln Glu
225