eolf-seql

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<151> 2014-07-16

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

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Ser Leu

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Leu Arg

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Arg Ser Glu Gln
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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
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Ser Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr Ile Ser Gly Val
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20 25 30

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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
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Thr Ser Pro Ser Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg Glu
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<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
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<210> 84
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4450 VH region

<400> 84

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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
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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 4122 VL region

<400> 91

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

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

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

Tyr Gln Ala Ser Lys 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 Asp Leu Glu Cys
65                  70                  75                  80

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

Asn Val Phe Phe Ala Phe Gly Gly Gly Thr Lys Val Val Val Glu
            100                 105                 110
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<210> 92
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4122 VL region

<400> 92

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gacattgtga tgacccagac tccagcctcc gtgtctgaac ctgtgggagg cacagtcacc       60

atcatgtgcc aggccagtca gagcattagc aattggttag cctggtatca acagaaacca      120

gggcagcctc ccaagctcct gatctaccag gcatccaaac tggcatctgg ggtcccatcg      180

cggttcaaag gcagtggatc tgggacagag tacactctca ccatcagcga cctggagtgt      240

gccgatgctg ccacttacta ctgtcaaagc tattatgata gtggtagtaa tgtttttttt      300
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gctttcggcg gagggaccaa ggtggtggtc gaa 333

<210> 93
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4122 VH region

<400> 93

Leu 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 Ala Gly Tyr
20 25 30

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

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

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

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

Ala Arg Gly Asn Ala Gly Val Ala Val Gly Ala Leu Trp Gly Pro Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 94
<211> 357
<212> DNA

<213> Artificial Sequence

<220>
<223> Rabbit Ab 4122 VH region

<400> 94
ctgtcgttgg aggagtccgg gggagacctg gtcaagcctg gggcatccct gacactcacc 60

tgcacagcct ctggattctc cttcagtgcc ggctattgga tatgttgggt ccgccaggct 120

ccagggaagg ggctggagtg gatcgcatgc acttatgctg gtcgtagtgg tagcacttac 180

tacgcgaact gggtgaatgg ccgattcacc atccccaaaa cctcgtcgac cacggtgact 240

ctgcaaatga ccagtctgtc aggcgcggac acggccagct atttctgtgc gagaggtaat 300

gctggtgttg ctgttggtgc cttgtggggc ccaggcaccc tggtcaccgt ctcgagt 357

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

<220>
<223> CDRL1

<400> 95

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

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

<220>
<223> CDRL2

<400> 96

Gln Ala Ser Lys Leu Ala Ser
1 5

<210> 97

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

<220>
<223> CDRL3

<400> 97

Gln Ser Tyr Tyr Asp Ser Gly Ser Asn Val Phe Phe Ala
1 5 10

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

<220>
<223> CDRH1

<400> 98

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

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

<220>
<223> CDRH2

<400> 99

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

Asn Gly

<210> 100
<211> 10
<212> PRT

<213> Artificial Sequence

<220>
<223> CDRH3

<400> 100

Gly Asn Ala Gly Val Ala Val Gly Ala Leu
1 5 10

<210> 101
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4129 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 Asn Cys Gln Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

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

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

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

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

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

<210> 102
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4129 VL region

<400> 102
gacattgtga tgacccagac tccagcctcc gtggaggcag ctgtgggagg cacagtcacc 60

atcaattgcc aagccagtca gagcattagc agttggttat cctggtatca gcagaaacca 120

gggcagcctc ccaagctcct gatctatggt gcatccaatc tggcatctgg ggtcccatca 180

cggttcagcg gcagtggatc tgggacacag ttcagtctca ccatcagcga cctggagtgt 240

gccgatgctg ccacttacta ctgtcaaagc tattatgata gtggtagtag tgttttttt 300

aatttcggcg gagggaccaa ggtggtcgtc aaa 333

<210> 103
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4129 VH region

<400> 103

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 Ala Gly Tyr
20 25 30

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

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

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

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

Ala Arg Gly Asn Ala Gly Val Ala Val Gly Ala Leu Trp Gly Pro Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 104
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4129 VH region

<400> 104
cagtcgttgg aggagtccgg gggagacctg gttaagcctg gggcatccct gacactcacc 60

tgcacagcct ctggattctc cttcagtgcc ggctattgga tatgttgggt ccgccaggct 120

ccagggaagg ggctggagtg gatcgcatgc atttatgctg gtagtagtgg tagcacttac 180

tacgcgagct gggcgaaagg ccgattcacc atccccaaaa cctcgtcgac cacggtgact 240

ctgcaaatga ccagtctgac aggcgcggac acggccacct atttctgtgc gagaggtaat 300

gctggtgttg ctgttggtgc cttgtggggc ccaggcaccc tcgtcaccgt ctcgagt 357

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

<220>
<223> CDRL1

<400> 105

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

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

<220>
<223> CDRL2

<400> 106

Gly Ala Ser Asn Leu Ala Ser
1 5

<210> 107
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL3

<400> 107

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

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

<220>
<223> CDRH1

<400> 108

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

<210> 109

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

<220>
<223> CDRH2

<400> 109

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

Lys Gly

<210> 110
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3

<400> 110

Gly Asn Ala Gly Val Ala Val Gly Ala Leu
1 5 10

<210> 111
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4131 VL region

<400> 111

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

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

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

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

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

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

Ala Phe Gly Gly Gly Thr Glu Val Val Val Lys
            100                 105
```

<210> 112
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4131 VL region

<400> 112

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gacattgtga tgacccagac tccagcctcc gtgtctgaac ctgtgggagg ctcagtcacc       60

atcaagtgcc aggccagtca gagcttttac aacctcttag cctggtatca gcagaaacca      120

gggcagcctc ccaaactcct gatctatgat gcatccgatc tggcatctgg ggtcccatcg      180

cggttcaaag gcagtggatc tgggactgat ttcactctca ccatcagcga cctggagtgt      240

gccgatgctg ccgcttacta ctgtcaaagt gctgatggta gtagttacgc tttcggcgga      300

gggaccgagg tggtcgtcaa a                                                321
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<210> 113
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4131 VH region

<400> 113

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 114
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4131 VH region

<400> 114
caggagcaat tggaggagtc cgggggaggc ctggtcaagc ctgagggatc cctgacactc 60

acctgcacag cctctggagt ctccttcagt agcagctatt ggatatactg ggtccgccag 120

gctccaggga aggggctgga gtggatcgca tgcatttata ctggtagtag tggtagcact 180

tactacgcga gctgggcgaa aggccgattc accgtctccg aaacctcgtc gaccacggtg 240

actctgcaaa tgaccagtct gacagccgcg gacacggcca cctatttctg tgcgagagca 300

agcgcttgga cctacggcat ggacctctgg ggcccgggca ccctcgtcac cgtctcgagt 360

<210> 115
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1

<400> 115

Gln Ala Ser Gln Ser Phe Tyr Asn Leu Leu Ala
1 5 10

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

<220>
<223> CDRL2

<400> 116

Asp Ala Ser Asp Leu Ala Ser
1 5

<210> 117
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL3

<400> 117

Gln Ser Ala Asp Gly Ser Ser Tyr Ala
1 5

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

<220>
<223> CDRH1

<400> 118

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

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

<220>
<223> CDRH2

<400> 119

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

Lys Gly

<210> 120
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3

<400> 120

Ala Ser Ala Trp Thr Tyr Gly Met Asp Leu

eolf-seql
1 5 10

<210> 121
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4133 VL region

<400> 121

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

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

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

Leu Ile Tyr Asp 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 Leu Gly Gly Tyr Tyr Ser
85 90 95

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

<210> 122
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4133 VL region

<400> 122
gcgcaagtgc tgacccagac tccatctccc gtgtctgcag ttgtgggagg cacagtcagc 60

atcagttgcc aggccagtca gagtgtttat aataacaaca acttatcctg gtatcagcag 120

aaaccagggc agcctcccaa gctcttgatc tacgatgcat ccaaattggc atctggggtc 180

ccatcccggt tcaaaggcag tggatctggg acacagttca ctctcaccat cagcggcgtg 240

cagtgtgacg atgctgccac ttactactgt ctaggcggtt attatagtag tggttggtat 300

tttgctttcg gcggagggac caaggtggtg gtcaaa 336

<210> 123
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4133 VH region

<400> 123

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

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

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

Ile Gly Cys Leu Tyr Thr Gly Ser Ser Gly Ser Thr Tyr Tyr Ala Ser
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 Asp Leu Gly Tyr Glu Ile Asp Gly Tyr Gly Gly Leu Trp
100 105 110

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

<210> 124
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Rabbit Ab 4133 VH region

<400> 124
caggagcagc tggtggagtc cgggggaggc ctggtccagc ctgagggatc cctgacacta 60

acctgcacag cttctggatt ctccttcagt ggcaactact acatgtgctg ggtccgccag 120

gctccaggga aggggctgga gtggatcgga tgcctttata ctggtagtag tggtagcaca 180

tattacgcga gctgggcgaa aggccgattc accatctcca aaacctcgtc gaccacggtg 240

actctgcaaa tgaccagtct gacagccgcg gacacggcca cctatttctg tgcgagagat 300

ctaggttatg aaattgatgg ttatgggggc ttgtggggcc agggcaccct cgtcaccgtc 360

tcgagt 366

<210> 125
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1

<400> 125

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

<210> 126

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

<220>
<223> CDRL2

<400> 126

Asp Ala Ser Lys Leu Ala Ser
1 5

<210> 127
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL3

<400> 127

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

<210> 128
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH1

<400> 128

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

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

<220>
<223> CDRH2

<400> 129

Cys Leu Tyr Thr Gly Ser Ser Gly Ser 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

Asp Leu Gly Tyr Glu Ile Asp Gly Tyr Gly Gly Leu
1 5 10

<210> 131
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH1 dAbH1

<400> 131

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

<210> 132
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH2 dAbH1

<400> 132

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

<210> 133
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3 dAbH1

<400> 133

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

<210> 134
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1 dAbL1

<400> 134

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

<210> 135
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2 dAbL1

<400> 135

Glu Ala Ser Lys Leu Thr Ser
1 5

<210> 136

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

<220>
<223> CDRL3 dAbL1

<400> 136

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

<210> 137
<211> 121
<212> PRT
<213> Artificial Sequence

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

<400> 137

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> 138
<211> 121
<212> PRT
<213> Artificial Sequence

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

<400> 138

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> 139
<211> 112
<212> PRT
<213> Artificial Sequence

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

<400> 139

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> 140
<211> 128
<212> PRT
<213> Artificial Sequence

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

<400> 140

```
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> 141
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> Human CD79a

<400> 141

```
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

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210 215 220

Lys Pro
225

<210> 142
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Human CD79b

<400> 142

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
```

<210> 143
<211> 1304
<212> PRT
<213> Artificial Sequence

<220>
<223> Human CD45

<400> 143

```
Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe Leu Asp
1               5                   10                  15

Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser Pro Thr Gly
            20                  25                  30

Leu Thr Thr Ala Lys Met Pro Ser Val Pro Leu Ser Ser Asp Pro Leu
```

```
        35                  40                  45

Pro Thr His Thr Thr Ala Phe Ser Pro Ala Ser Thr Phe Glu Arg Glu
    50                  55                  60

Asn Asp Phe Ser Glu Thr Thr Thr Ser Leu Ser Pro Asp Asn Thr Ser
65                  70                  75                  80

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

Thr Gly Val Ser Ser Val Gln Thr Pro His Leu Pro Thr His Ala Asp
            100                 105                 110

Ser Gln Thr Pro Ser Ala Gly Thr Asp Thr Gln Thr Phe Ser Gly Ser
        115                 120                 125

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

Asp Val Pro Gly Glu Arg Ser Thr Ala Ser Thr Phe Pro Thr Asp Pro
145                 150                 155                 160

Val Ser Pro Leu Thr Thr Thr Leu Ser Leu Ala His His Ser Ser Ala
                165                 170                 175

Ala Leu Pro Ala Arg Thr Ser Asn Thr Thr Ile Thr Ala Asn Thr Ser
            180                 185                 190

Asp Ala Tyr Leu Asn Ala Ser Glu Thr Thr Thr Leu Ser Pro Ser Gly
        195                 200                 205

Ser Ala Val Ile Ser Thr Thr Thr Ile Ala Thr Thr Pro Ser Lys Pro
    210                 215                 220

Thr Cys Asp Glu Lys Tyr Ala Asn Ile Thr Val Asp Tyr Leu Tyr Asn
```

225 230 235 240

Lys Glu Thr Lys Leu Phe Thr Ala Lys Leu Asn Val Asn Glu Asn Val
245 250 255

Glu Cys Gly Asn Asn Thr Cys Thr Asn Asn Glu Val His Asn Leu Thr
260 265 270

Glu Cys Lys Asn Ala Ser Val Ser Ile Ser His Asn Ser Cys Thr Ala
275 280 285

Pro Asp Lys Thr Leu Ile Leu Asp Val Pro Pro Gly Val Glu Lys Phe
290 295 300

Gln Leu His Asp Cys Thr Gln Val Glu Lys Ala Asp Thr Thr Ile Cys
305 310 315 320

Leu Lys Trp Lys Asn Ile Glu Thr Phe Thr Cys Asp Thr Gln Asn Ile
325 330 335

Thr Tyr Arg Phe Gln Cys Gly Asn Met Ile Phe Asp Asn Lys Glu Ile
340 345 350

Lys Leu Glu Asn Leu Glu Pro Glu His Glu Tyr Lys Cys Asp Ser Glu
355 360 365

Ile Leu Tyr Asn Asn His Lys Phe Thr Asn Ala Ser Lys Ile Ile Lys
370 375 380

Thr Asp Phe Gly Ser Pro Gly Glu Pro Gln Ile Ile Phe Cys Arg Ser
385 390 395 400

Glu Ala Ala His Gln Gly Val Ile Thr Trp Asn Pro Pro Gln Arg Ser
405 410 415

Phe His Asn Phe Thr Leu Cys Tyr Ile Lys Glu Thr Glu Lys Asp Cys

420 425 430

Leu Asn Leu Asp Lys Asn Leu Ile Lys Tyr Asp Leu Gln Asn Leu Lys
435 440 445

Pro Tyr Thr Lys Tyr Val Leu Ser Leu His Ala Tyr Ile Ile Ala Lys
450 455 460

Val Gln Arg Asn Gly Ser Ala Ala Met Cys His Phe Thr Thr Lys Ser
465 470 475 480

Ala Pro Pro Ser Gln Val Trp Asn Met Thr Val Ser Met Thr Ser Asp
485 490 495

Asn Ser Met His Val Lys Cys Arg Pro Pro Arg Asp Arg Asn Gly Pro
500 505 510

His Glu Arg Tyr His Leu Glu Val Glu Ala Gly Asn Thr Leu Val Arg
515 520 525

Asn Glu Ser His Lys Asn Cys Asp Phe Arg Val Lys Asp Leu Gln Tyr
530 535 540

Ser Thr Asp Tyr Thr Phe Lys Ala Tyr Phe His Asn Gly Asp Tyr Pro
545 550 555 560

Gly Glu Pro Phe Ile Leu His His Ser Thr Ser Tyr Asn Ser Lys Ala
565 570 575

Leu Ile Ala Phe Leu Ala Phe Leu Ile Ile Val Thr Ser Ile Ala Leu
580 585 590

Leu Val Val Leu Tyr Lys Ile Tyr Asp Leu His Lys Lys Arg Ser Cys
595 600 605

Asn Leu Asp Glu Gln Gln Glu Leu Val Glu Arg Asp Asp Glu Lys Gln

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610 615 620

Leu Met Asn Val Glu Pro Ile His Ala Asp Ile Leu Leu Glu Thr Tyr
625 630 635 640

Lys Arg Lys Ile Ala Asp Glu Gly Arg Leu Phe Leu Ala Glu Phe Gln
645 650 655

Ser Ile Pro Arg Val Phe Ser Lys Phe Pro Ile Lys Glu Ala Arg Lys
660 665 670

Pro Phe Asn Gln Asn Lys Asn Arg Tyr Val Asp Ile Leu Pro Tyr Asp
675 680 685

Tyr Asn Arg Val Glu Leu Ser Glu Ile Asn Gly Asp Ala Gly Ser Asn
690 695 700

Tyr Ile Asn Ala Ser Tyr Ile Asp Gly Phe Lys Glu Pro Arg Lys Tyr
705 710 715 720

Ile Ala Ala Gln Gly Pro Arg Asp Glu Thr Val Asp Asp Phe Trp Arg
725 730 735

Met Ile Trp Glu Gln Lys Ala Thr Val Ile Val Met Val Thr Arg Cys
740 745 750

Glu Glu Gly Asn Arg Asn Lys Cys Ala Glu Tyr Trp Pro Ser Met Glu
755 760 765

Glu Gly Thr Arg Ala Phe Gly Asp Val Val Val Lys Ile Asn Gln His
770 775 780

Lys Arg Cys Pro Asp Tyr Ile Ile Gln Lys Leu Asn Ile Val Asn Lys
785 790 795 800

Lys Glu Lys Ala Thr Gly Arg Glu Val Thr His Ile Gln Phe Thr Ser

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```
                805                 810                 815

Trp Pro Asp His Gly Val Pro Glu Asp Pro His Leu Leu Leu Lys Leu
            820                 825                 830

Arg Arg Arg Val Asn Ala Phe Ser Asn Phe Phe Ser Gly Pro Ile Val
        835                 840                 845

Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr Ile Gly Ile
    850                 855                 860

Asp Ala Met Leu Glu Gly Leu Glu Ala Glu Asn Lys Val Asp Val Tyr
865                 870                 875                 880

Gly Tyr Val Val Lys Leu Arg Arg Gln Arg Cys Leu Met Val Gln Val
                885                 890                 895

Glu Ala Gln Tyr Ile Leu Ile His Gln Ala Leu Val Glu Tyr Asn Gln
            900                 905                 910

Phe Gly Glu Thr Glu Val Asn Leu Ser Glu Leu His Pro Tyr Leu His
        915                 920                 925

Asn Met Lys Lys Arg Asp Pro Pro Ser Glu Pro Ser Pro Leu Glu Ala
    930                 935                 940

Glu Phe Gln Arg Leu Pro Ser Tyr Arg Ser Trp Arg Thr Gln His Ile
945                 950                 955                 960

Gly Asn Gln Glu Glu Asn Lys Ser Lys Asn Arg Asn Ser Asn Val Ile
                965                 970                 975

Pro Tyr Asp Tyr Asn Arg Val Pro Leu Lys His Glu Leu Glu Met Ser
            980                 985                 990

Lys Glu Ser Glu His Asp Ser Asp  Glu Ser Ser Asp Asp  Asp Ser Asp
```

995 1000 1005

Ser Glu Glu Pro Ser Lys Tyr Ile Asn Ala Ser Phe Ile Met Ser
1010 1015 1020

Tyr Trp Lys Pro Glu Val Met Ile Ala Ala Gln Gly Pro Leu Lys
1025 1030 1035

Glu Thr Ile Gly Asp Phe Trp Gln Met Ile Phe Gln Arg Lys Val
1040 1045 1050

Lys Val Ile Val Met Leu Thr Glu Leu Lys His Gly Asp Gln Glu
1055 1060 1065

Ile Cys Ala Gln Tyr Trp Gly Glu Gly Lys Gln Thr Tyr Gly Asp
1070 1075 1080

Ile Glu Val Asp Leu Lys Asp Thr Asp Lys Ser Ser Thr Tyr Thr
1085 1090 1095

Leu Arg Val Phe Glu Leu Arg His Ser Lys Arg Lys Asp Ser Arg
1100 1105 1110

Thr Val Tyr Gln Tyr Gln Tyr Thr Asn Trp Ser Val Glu Gln Leu
1115 1120 1125

Pro Ala Glu Pro Lys Glu Leu Ile Ser Met Ile Gln Val Val Lys
1130 1135 1140

Gln Lys Leu Pro Gln Lys Asn Ser Ser Glu Gly Asn Lys His His
1145 1150 1155

Lys Ser Thr Pro Leu Leu Ile His Cys Arg Asp Gly Ser Gln Gln
1160 1165 1170

Thr Gly Ile Phe Cys Ala Leu Leu Asn Leu Leu Glu Ser Ala Glu

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```
    1175                1180                1185

Thr Glu  Glu Val Val Asp Ile  Phe Gln Val Val Lys  Ala Leu Arg
    1190                1195                1200

Lys Ala  Arg Pro Gly Met Val  Ser Thr Phe Glu Gln  Tyr Gln Phe
    1205                1210                1215

Leu Tyr  Asp Val Ile Ala Ser  Thr Tyr Pro Ala Gln  Asn Gly Gln
    1220                1225                1230

Val Lys  Lys Asn Asn His Gln  Glu Asp Lys Ile Glu  Phe Asp Asn
    1235                1240                1245

Glu Val  Asp Lys Val Lys Gln  Asp Ala Asn Cys Val  Asn Pro Leu
    1250                1255                1260

Gly Ala  Pro Glu Lys Leu Pro  Glu Ala Lys Glu Gln  Ala Glu Gly
    1265                1270                1275
```