SEQUENCE LISTING

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HAZENBOS, Wouter L.W.
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XIA, Yi

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<130> 146392008240

<150> PCT/NL2010/050456
<151> 2010-07-15

<150> US 61/225,878
<151> 2009-07-15

<150> EP 091655589
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<400> 1
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Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser
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<223> Xaa = M or I

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Gln His Tyr Xaa Arg Phe Pro Tyr Thr
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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe
            20   25   30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35   40   45
Ala Ser Ile Asn Asn Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50   55   60
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65   70   75   80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85   90   95
Lys Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser Trp Gly Pro
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

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<220>
<221> VARIANT
<222> 92
<223> Xaa = M or I

<400> 8
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Glu Asn Val Gly Asp Trp
            20   25   30
Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35   40   45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Xaa Arg Phe Pro Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
            100   105   110

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<220>
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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe
            20   25   30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35   40   45
Ala Ser Ile Asn Asn Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50   55   60
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65   70   75   80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85   90   95
Lys Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser Trp Gly Pro
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

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 1   5   10   15
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            20   25   30
Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35   40   45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Xaa Arg Phe Pro Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala
            100   105

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Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Glu Asn Val Gly Asp Trp
            20   25   30
Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35   40   45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Xaa Arg Phe Pro Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val
            100   105   110

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cgctttgcca tgagc 15

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<400> 13
tcgatcaata atgggaataa cccatactac gcacggtcgg tacaatac 48

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<220>
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gatcacccta gtagtggctg gcccaccttt gactcc 36

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<220>
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<400> 15
cgggccagtg aaaacgttgg tgactggttg gcc 33

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<400> 16
aagacatcta ttctagaaag t 21

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<400> 17
caacactata tacgtttccc gtacact 27

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<400> 18
atggctgagg tgcagctggt ggagtctg 28

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g 61

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<400> 20
cggctcgacc gatatccagc tgacccagag 30

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<400> 21
gatttccagc ttggtaccct ggccg 25

<210> 22
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<400> 23
cgtagtaggg gttgttgccg ctgttgatgc tggccacc 38

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<400> 24

Asn Asn Gly Asn Asn
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<210> 25
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<400> 25
aac 3

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agc 3

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<400> 28
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<210> 29
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<210> 30
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<400> 30
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<400> 31
Leu Pro Xaa Thr Gly
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Ser Asp Ser Asp
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<220>
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Ser Asp Ser Asp Ser
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<220>
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<400> 34
Ser Asp Ser Asp Ser Asp
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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ctt agc cgc ttt 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe
20 25 30

gcc atg agc tgg gtc cgc cag gct cca gga agg gga ctg gaa tgg gtc 144
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
35 40 45

gca tcg atc aat aat ggg aat aac cca tac tac gca cgg tcg gta caa 192
Ala Ser Ile Asn Asn Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
50 55 60

tac cgc ttc acc gtc tcc cgg gac gtc tcc cag aac act gtg tct ctg 240
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65 70 75 80

cag atg aac aac ctg aga gcc gaa gac tcg gcc aca tat ttc tgt gct 288
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
85 90 95

aaa gat cac cct agt agt ggc tgg ccc acc ttt gac tcc tgg ggc ccg 336
Lys Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser Trp Gly Pro
100 105 110

gga acc ctg gtc acc gtc tcc tcg 360
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 36
<211> 120
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<220>
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<400> 36
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe
            20   25   30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35   40   45
Ala Ser Ile Asn Asn Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50   55   60
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65   70   75   80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85   90   95
Lys Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser Trp Gly Pro
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

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<220>
<221> CDS
<222> (1)..(90)

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gag gtg caa ctg ttg gag tcg ggg ggg ggc ttg gtg cag ccg ggg ggg 48
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ctt agc   90
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser
            20   25   30

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<220>
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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser
            20   25   30

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<222> (1)..(42)

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tgg gtc cgc cag gct cca gga agg gga ctg gaa tgg gtc gca 42
Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val Ala
1 5 10

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<212> PRT
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<400> 40
Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val Ala
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<220>
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cgc ttc acc gtc tcc cgg gac gtc tcc cag aac act gtg tct ctg cag 48
Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu Gln
1 5 10 15

atg aac aac ctg aga gcc gaa gac tcg gcc aca tat ttc tgt gct aaa 96
Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala Lys
20 25 30

<210> 42
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<212> PRT
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<220>
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<400> 42
Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu Gln
 1   5   10   15
Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala Lys
            20   25   30

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<220>
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<220>
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<222> (1)..(33)

<400> 43
tgg ggc ccg gga acc ctg gtc acc gtc tcc tcg   33
Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser
1   5   10

<210> 44
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<400> 44
Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser
 1   5   10

<210> 45
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<220>
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<220>
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<400> 45
gac atc cag ttg acc cag tct cct tcc gcc ctg cct gca tct gtg gga   48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
1   5   10   15

gac aga gtc agc atc act tgt cgg gcc agt gaa aac gtt ggt gac tgg   96
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Glu Asn Val Gly Asp Trp
            20   25   30

ttg gcc tgg tat cgg cag aaa ccg ggg aaa gcc cct aat ctt ctc atc   144
Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35   40   45

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tat aag aca tct att cta gaa agt ggg gtc cca tca agg ttc agc ggc      192
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

agt ggg tct ggg aca gaa ttc act ctc acc atc agc agc ctg cag cct      240
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

gat gat ttt gca act tat tac tgt caa cac tat ata cgt ttc ccg tac      288
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Ile Arg Phe Pro Tyr
                85                  90                  95

act ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg              330
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
            100                 105                 110


<210> 46
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<212> PRT
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<220>
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<400> 46
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
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Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Glu Asn Val Gly Asp Trp
            20                  25                  30
Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35                  40                  45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Ile Arg Phe Pro Tyr
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
            100                 105                 110


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<212> DNA
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<220>
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<220>
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<222> (1)..(69)

<400>  47
gac atc cag ttg acc cag tct cct tcc gcc ctg cct gca tct gtg gga       48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
1               5                   10                  15

gac aga gtc agc atc act tgt                                          69
Asp Arg Val Ser Ile Thr Cys
            20


<210> 48
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<211> 23
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<220>
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<400> 48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Ser Ile Thr Cys
            20

<210> 49
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<220>
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<220>
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<222> (1)..(45)

<400> 49
tgg tat cgg cag aaa ccg ggg aaa gcc cct aat ctt ctc atc tat   45
Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile Tyr
1   5   10   15

<210> 50
<211> 15
<212> PRT
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<220>
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<400> 50
Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile Tyr
 1   5   10   15

<210> 51
<211> 96
<212> DNA
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<220>
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<220>
<223> F1 Light Chain FW3

<220>
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<222> (1)..(96)

<400> 51
ggg gtc cca tca agg ttc agc ggc agt ggg tct ggg aca gaa ttc act   48
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1   5   10   15

ctc acc atc agc agc ctg cag cct gat gat ttt gca act tat tac tgt 96
Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

<210> 52
<211> 32
<212> PRT
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<220>
<223> Synthetic construct

<400> 52
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15
Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

<210> 53
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ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg 39
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
1 5 10

<210> 54
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<212> PRT
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<220>
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<400> 54
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
1 5 10

<210> 55
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<220>
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1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe

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            20                  25                  30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35                  40                  45
Ala Ser Ile Asn Asn Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50                  55                  60
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65                  70                  75                  80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85                  90                  95
Lys Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser Trp Gly Pro
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
Lys Thr His Thr Cys Pro
225                 230
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<210> 56
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 A114C

<400> 56

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe
            20                  25                  30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35                  40                  45
Ala Ser Ile Asn Ser Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50                  55                  60
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65                  70                  75                  80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85                  90                  95
Lys Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser Trp Gly Pro
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ser Cys Ser Thr Lys Gly Pro Ser Val
        115                 120                 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
```

```
    210                 215                 220
Lys Thr His Thr Cys Pro
225                 230


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

<220>
<223> Synthetic construct

<220>
<223> rF1 Light Chain

<400> 57
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Glu Asn Val Gly Asp Trp
            20                  25                  30
Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35                  40                  45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Met Arg Phe Pro Tyr
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Pro
            100                 105                 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
    210


<210> 58
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 V205C

<400> 58
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Glu Asn Val Gly Asp Trp
            20                  25                  30
Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35                  40                  45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
```

65 70 75 80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Met Arg Phe Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Cys Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> 59
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 59

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val
1 5 10

<210> 60
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 A114C

<400> 60

Ser Ile Asn Ser Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln Tyr
1 5 10 15

<210> 61
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 Heavy Chain

<400> 61
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser
20 25 30

<210> 62
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 A114C

<400> 62
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe
            20   25   30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35   40   45
Ala Ser Ile Asn Ser Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50   55   60
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65   70   75   80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85   90   95
Lys Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser Trp Gly Pro
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 63
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 Heavy Chain

<400> 63
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1   5   10   15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20   25   30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35   40   45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50   55   60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65   70   75   80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85   90   95
Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
            100   105   110

<210> 64
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 Light Chain

<400> 64
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
1 5 10 15
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
20 25 30
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
35 40 45
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
50 55 60
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
65 70 75 80
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
85 90 95
Lys Ser Phe Asn Arg Gly Glu Cys
100

<210> 65
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 V205C light chain constant region

<400> 65

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
1 5 10 15
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
20 25 30
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
35 40 45
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
50 55 60
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
65 70 75 80
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Cys Thr
85 90 95
Lys Ser Phe Asn Arg Gly Glu Cys
100

<210> 66
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 Heavy Chain

<400> 66

Cys Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys

```
                85                  90                  95
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
            100                 105                 110
```