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SEQUENCE LISTING

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<120> ANTIBODIES TO HPD-1

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<150> 60/944583
<151> 2007-06-18

<160> 38

<170> PatentIn version 3.5

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gagaagttca agagcaaggc cacactgact gtagacaaat cctccagcac agcctacatg 300

caactcagca gcctgacatc tgaggactct gcggtctatt actgtacaag aagggattct 360

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cctgtggagg aggaggacgc tgcaacctat tattgtcagc acagttggga gcttccgctc 360

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cctgtggagg aggaggatgc tgcaacctat tactgtcagc acagtaggga ccttccgctc 360

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1 5 10 15

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

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

Gly Gly Val Asn Pro Ser Asn Gly Gly Thr Asn Phe Ser Glu Lys Phe
50 55 60

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

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

Thr Arg Arg Asp Ser Asn Tyr Asp Gly Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Leu Thr Val Ser Ser Ala Lys
115 120

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<212> PRT

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

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

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

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

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

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

Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

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1 5 10 15

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

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

Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe
50 55 60

Lys Asn Lys Ala Thr Leu Thr Val Asp Ser Ser Ser Ser Thr Thr Tyr
65 70 75 80

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

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

Gly Thr Thr Leu Thr Val Ser Ser Ala Lys
115 120

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1 5 10 15

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

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

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

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

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

Asp Leu Pro Leu Thr Phe Gly Thr Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 9
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Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Phe Ser Tyr Leu His

1 5 10 15

<210> 10
<211> 7
<212> PRT
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<223> hPD-1.08A light chain CDR2

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Leu Ala Ser Asn Leu Glu Ser
1 5

<210> 11
<211> 9
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<220>
<223> hPD-1-08A light chain CDR3

<400> 11

Gln His Ser Trp Glu Leu Pro Leu Thr
1 5

<210> 12
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<212> PRT
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<220>
<223> hPD-1.08A heavy chain CDR1

<400> 12

Ser Tyr Tyr Leu Tyr

1 5

<210> 13
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<213> Artificial Sequence

<220>
<223> hPD-1.08A heavy chain CDR2

<400> 13

Gly Val Asn Pro Ser Asn Gly Gly Thr Asn Phe Ser Glu Lys Phe Lys
1 5 10 15

Ser

<210> 14
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<212> PRT
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<220>
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<400> 14

Arg Asp Ser Asn Tyr Asp Gly Gly Phe Asp Tyr
1 5 10

<210> 15
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<212> PRT
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<220>
<223> hPD-1.09A light chain CDR1

<400> 15

Arg Ala Ser Lys Gly Val Ser Thr Ser Gly Tyr Ser Tyr Leu His
1 5 10 15

<210> 16
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<400> 16

Leu Ala Ser Tyr Leu Glu Ser
1 5

<210> 17
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<400> 17

Gln His Ser Arg Asp Leu Pro Leu Thr
1 5

<210> 18
<211> 5
<212> PRT
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<220>
<223> hPD-1.09A heavy chain CDR1

<400> 18

Asn Tyr Tyr Met Tyr
1 5

<210> 19
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> hPD-1.09A heavy chain CDR2

<400> 19

Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe Lys
1 5 10 15

Asn

<210> 20
<211> 11
<212> PRT
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<400> 20

Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr
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<210> 21
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tgcaaggctt ctggctacac ctttaccaac tactatatgt actgggtgcg acaggccccct 180

ggacaagggc ttgagtggat gggagggatt aatcctagca atggtggtac taacttcaat 240

gagaagttca agaacagagt caccttgacc acagactcat ccacgaccac agcctacatg 300

gaactgaaga gcctgcaatt tgacgacacg gccgtttatt actgtgcgag aagggattat 360

aggttcgaca tgggctttga ctactggggc caagggacca cggtcaccgt ctcgagc 417

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tgcaaggcct ccggctacac cttcaccaac tactacatgt actgggtgcg gcaggctccc 180

ggccagggac tggagtggat gggcggcatc aacccttcca acggcggcac caacttcaac 240

gagaagttca agaaccgggt gaccctgacc accgactcct ccaccaccac cgcctacatg 300

gagctgaagt ccctgcagtt cgacgacacc gccgtgtact actgcgccag gcgggactac 360

cggttcgaca tgggcttcga ctactggggc cagggcacca ccgtgaccgt gtcctcc 417

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<220>
<221> sig_peptide
<222> (1)..(57)

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tgtaaggcct ccggctacac cttcaccaac tactacatgt actgggtgcg gcaggcccca 180

ggccagggac tggagtggat gggcggcatc aacccttcca acggcggcac caacttcaac 240

gagaagttca agaaccgggt gaccctgacc accgactcct ccaccacaac cgcctacatg 300

gaactgaagt ccctgcagtt cgacgacacc gccgtgtact actgcgccag gcgggactac 360

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agcaccaagg gcccttccgt gttccctctg gccccttgct cccggtccac ctccgagtcc 480

accgccgctc tgggctgtct ggtgaaggac tacttccctg agcctgtgac cgtgagctgg 540

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ctctcctgca gggccagcaa aggtgtcagt acatctggct atagttattt gcactggtat 180

caacagaaac ctggccaggc tcccaggctc ctcatctatc ttgcatccta cctagaatct 240

ggcgtcccag ccaggttcag tggtagtggg tctgggacag acttcactct caccatcagc 300

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acgttcggcg gagggaccaa agtggagatc aaa 393

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gaaattgtgc tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 120

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ctccagaagc cagggcagtc tccacagctc ctgatctatc ttgcatccta cctagaatct 240

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acgtttggcc aggggaccaa gctggagatc aaa 393

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<211> 393
<212> DNA
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<220>
<223> K09A-L-17 light chain variable region

<220>
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<222> (1)..(60)

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atctcctgca gggccagcaa aggtgtcagt acatctggct atagttattt gcattggtat 180

ctgcagaagc cagggcagtc tccacagctc ctgatctatc ttgcatccta cctagaatct 240

ggagtcccag acaggttcag tggcagtggg tcaggcactg ctttcacact gaaaatcagc 300

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acgtttggcc aggggaccaa gctggagatc aaa 393

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<212> DNA
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tttggcggcg gaacaaaggt ggagatcaag 390

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<212> DNA
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<223> Codon optimized K09A-L-16 light chain variable region

<220>

<221> sig_peptide
<222> (1)..(57)

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atcgtgctga cccagtcccc tctgtccctg cctgtgaccc ctggcgagcc tgcctccatc 120

tcctgccggg cctccaaggg cgtgtccacc tccggctact cctacctgca ctggtatctg 180

cagaagcctg gccagtcccc ccagctgctg atctacctgg cctcctacct ggagtccggc 240

gtgcctgacc ggttctccgg ctccggcagc ggcaccgact tcaccctgaa gatctcccgg 300

gtggaggccg aggacgtggg cgtgtactac tgccagcact cccgggacct gcctctgacc 360

ttcggccagg gcaccaagct ggagatcaag 390

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atcgtgatga cccagacccc tctgtccctg cctgtgaccc ctggcgagcc tgcctccatc 120

tcctgccggg cctccaaggg cgtgtccacc tccggctact cctacctgca ctggtatctg 180

cagaagcctg gccagtcccc tcagctgctg atctacctgg cctcctacct ggagtccggc 240

gtgcctgacc ggttctccgg ctccggaagc ggcaccgctt ttaccctgaa gatctccaga 300

gtggaggccg aggacgtggg cctgtactac tgccagcact cccgggacct gcctctgacc 360

ttcggccagg gcaccaagct ggagatcaag 390

<210> 30
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<223> 109A-H heavy chain variable region

<220>
<221> sig_peptide
<222> (1)..(19)

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

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

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

Glu Trp Met Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn
65 70 75 80

Glu Lys Phe Lys Asn Arg Val Thr Leu Thr Thr Asp Ser Ser Thr Thr

85 90 95

Thr Ala Tyr Met Glu Leu Lys Ser Leu Gln Phe Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
130 135

<210> 31
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> 409A-H heavy chain full length

<220>
<221> sig_peptide
<222> (1)..(19)

<400> 31

Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

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

Glu Trp Met Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn
65 70 75 80

Glu Lys Phe Lys Asn Arg Val Thr Leu Thr Thr Asp Ser Ser Thr Thr
85 90 95

Thr Ala Tyr Met Glu Leu Lys Ser Leu Gln Phe Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
180 185 190

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

Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val
210 215 220

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
225 230 235 240

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
275 280 285

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
305 310 315 320

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
325 330 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
340 345 350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
370 375 380

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

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
405 410 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
420 425 430

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
450 455 460

Gly Lys
465

<210> 32
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<221> sig_peptide
<222> (1)..(19)

<400> 32

Met Ala Pro Val Gln Leu Leu Gly Leu Leu Val Leu Phe Leu Pro Ala
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Met Arg Cys Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu
20 25 30

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Gly Val
35 40 45

Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Gln Ala Pro Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly
65 70 75 80

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
85 90 95

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
100 105 110

His Ser Arg Asp Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
115 120 125

Ile Lys
130

<210> 33
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> K09A-L-16 light chain variable region

<220>
<221> sig_peptide
<222> (1)..(19)

<400> 33

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

Met Arg Cys Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val
20 25 30

Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ala Ser Lys Gly Val
35 40 45

Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
50 55 60

Gln Ser Pro Gln Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly
65 70 75 80

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
85 90 95

Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln
100 105 110

His Ser Arg Asp Leu Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu
115 120 125

Ile Lys
130

<210> 34
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> K09A-L-17 light chain variable region

<220>
<221> sig_peptide
<222> (1)..(19)

<400> 34

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

Met Arg Cys Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
20 25 30

Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ala Ser Lys Gly Val
35 40 45

Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
50 55 60

Gln Ser Pro Gln Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly
65 70 75 80

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu
85 90 95

Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Gln
100 105 110

His Ser Arg Asp Leu Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu
115 120 125

Ile Lys
130

<210> 35
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> 109A-H heavy chain full length

<220>
<221> sig_peptide
<222> (1)..(19)

<400> 35

Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

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

Glu Trp Met Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn
65 70 75 80

Glu Lys Phe Lys Asn Arg Val Thr Leu Thr Thr Asp Ser Ser Thr Thr
85 90 95

Thr Ala Tyr Met Glu Leu Lys Ser Leu Gln Phe Asp Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
180 185 190

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

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
210 215 220

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
225 230 235 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
245 250 255

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
260 265 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
275 280 285

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
290 295 300

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
305 310 315 320

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
325 330 335

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
340 345 350

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
355 360 365

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
370 375 380

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385 390 395 400

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
405 410 415

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
420 425 430

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
435 440 445

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
450 455 460

Leu Ser Pro Gly Lys
465

<210> 36
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> K09A-L-11 light chain full length

<220>
<221> sig_peptide
<222> (1)..(19)

<400> 36

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

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

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Gly Val

35 40 45

Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Gln Ala Pro Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly
65 70 75 80

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
85 90 95

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
100 105 110

His Ser Arg Asp Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
115 120 125

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
165 170 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
180 185 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
195 200 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
210 215 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 37
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> K09A-L-16 light chain full length

<220>
<221> sig_peptide
<222> (1)..(19)

<400> 37

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

Met Arg Cys Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val
20 25 30

Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ala Ser Lys Gly Val
35 40 45

Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
50 55 60

Gln Ser Pro Gln Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly
65 70 75 80

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
85 90 95

Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln
100 105 110

His Ser Arg Asp Leu Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu
115 120 125

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
165 170 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
180 185 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
195 200 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
210 215 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 38
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> K09A-L-17 light chain full length

<220>
<221> sig_peptide
<222> (1)..(19)

<400> 38

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

Met Arg Cys Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
20 25 30

Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ala Ser Lys Gly Val
35 40 45

Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
50 55 60

Gln Ser Pro Gln Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly
65 70 75 80

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu
85 90 95

Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Gln
100 105 110

His Ser Arg Asp Leu Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu
115 120 125

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
165 170 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
180 185 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
195 200 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
210 215 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235