SequenceListing_ST25
SEQUENCE LISTING

<110> Agency For Science Technology and Research

<120> Binding Molecules Against Dengue Virus And Uses Thereof

<130> 9869SG1856

<140> PCT/SG2012/000477
<141> 2012-12-17

<150> 201109401-8
<151> 2011-12-16

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ggccaggctc ccagtctcct catctatgaa gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctgcagtct 240

gaagattttg caatttatta ctgtcagcag tataatgact ggctgtggac gttcggccaa 300

gggaccaagg tggaaatcag ac 322

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<400> 33
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cctggacaag ggcttgagtg gctgggaggg atcatccatc cctttggcac agaaaactac 180

gcacagaagt ttcagggcag actcacgatc accgcggacg aatccacgag cacagcctac 240

atggagctga ggagcctgac atctgaggac atggccgtgt atttttgtgc gagacatcac 300

cgccatattt tgactggtga gcgcaccgac tactggggcc agggaaccct ggtcaccgtc 360

tcctcag 367

<210> 34
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<212> DNA
<213> Artificial Sequence

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<223> 10/63 6C-1_091

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atcacttgcc aggcgagtca ggacattcgc aactctttaa attggtatca gcagaaaccg 120

gggaaagccc ctatcctcct gatctacgat gcatccaatt tgaaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat ttcactttca ccatcagcag cctgcagcct 240

gaggatattg caacatattt ctgtcaacat tatgataatc tccccctatt cactttcggc 300

cctgggacca aagtggatat caaac 325

<210> 35
<211> 367
<212> DNA
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<220>
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<400> 35
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tcctgcaagt cttctggagg caccctcaac agctatacta tcagctgggt gcgacaggcc 120

cctggacaag gccttgagtg gatgggaggg atcaatccca tctttggtac aacaaacaac 180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgaa cacagtctac 240

atggagctga gcagcctgag gtctgacgac acggccgtgt attactgtgc gagaggggggc 300

caccatattt tgactgggcg ttacattgac gactggggcc agggaaccct ggtcaccgtc 360

tcctcag 367

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gggaaaggcc ctaagctcct gatctacgat gcatccaatt tggagacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

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caggggacca agctggagat caaac 325

<210> 37
<211> 382
<212> DNA
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<400> 37
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ccaggcaagg ggctggagtg ggtggctgtc gtagcatatg atggaattaa taaatattat 180

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ctgcaaatga acagcctgca gcctgaggac acggctgtgt atttctgtgc gaaatcggca 300

ggatctactt tgaaaacagt tattagtctt ctgcagcctt ttgatatctg gggccaaggg 360

acaatggtca ccgtctcttc ag 382

<210> 38
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<212> DNA
<213> Artificial Sequence

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<223> 10/63 7E-1_087

<400> 38
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ctctcctgca gggccagtca gagtgttagc agcaacttag gctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatgat gcatccacca gggccactgg catcccaccc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaggattttg cagtttatta ctgtcagcag tatcatgact ggcctccgta cacttttggc 300

caggggacca agctggagat caaac 325

<210> 39
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<212> DNA
<213> Artificial Sequence

<220>
<223> 10/63 7G1_055

<400> 39
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tcctgtgcgg cctctggatt cactttcagt aatgcctgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggccgt attaaaaaca aaattgatgg tgagacaaca 180

gactacgctg catccgtgaa aggcagattc atcatctcaa gagatgactc aaaaaacacg 240

gtgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgagtattg gtgcaccata 300

tatttctatg atagaagtgg atacttcttt gaccactggg gccagggaac cctggtcacc 360

gtctcctcag 370

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<223> 10/63 7G-1_081

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ttctcctgca gggccagtca gagtgttagc agctacttag cctggtatca acagaaacct 120

ggccaggctc ccaggctcct catctttgat gcgtcccaca gggccactgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcattctca ccatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtctgcag cgtggcaagt ggccttcctt cggccaaggg 300

acacgactgg agattaaac 319

<210> 41
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<212> DNA
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<223> 10/63 7H-1_060

<400> 41
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tcctgtgcgg cctctggatt cactttcagt aatgcctgga tgagctgggt ccgccaggct 120

ccagggaaag ggctggagtg ggttggccgt attaaaaaca aaattgatgg tgagacaaca 180

gactacgctg catccgtgaa aggcagattc atcatctcaa gagatgactc aaaaaacacg 240

gtgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgagtattg gtgcaccata 300

tatttctatg atagaagtgg atacttcttt gaccactggg gccagggaac cctggtcacc 360

gtctcctcag 370

<210> 42
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<212> DNA
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<220>
<223> 10/63 7H-1_038

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ggccaggctc ccaggctcct catctttgat gcgtcccaca agaccactgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcattctca ccatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtctgcag cgtggcaagt ggccttcctt cggccaaggg 300

acacgactgg agattaaac 319

<210> 43
<211> 382
<212> DNA
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<220>
<223> 10/63 8F1_051

<400> 43
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acctgcactg tctctggtgg ctccatcagc tctagttctt actactgggg ctggatccgc 120

cagcccccag ggaaggggct ggaatggatt gggggtatct attacactgg gaccacctac 180

tacaatccgt ccctgaacag tccagtcacc atatccatag acatgtccaa gaatcatttc 240

tccctggagt tgacctctgt gaccgccgca gacacggctg tttattactg tgcgagacaa 300

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accctggtcg tcgtctcctc ag 382

<210> 44
<211> 322
<212> DNA
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<220>
<223> 10/63 8F-1_036

<400> 44
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atcacttgtc gggcgagtca gagttttaac aactggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatggt gcatccactt tacaaagtgg ggtcccatca 180

agattcagcg gcagtggatc agggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag gctagcagtt tcccgtggac gttcggccag 300

gggaccaagg tggagatcaa ac 322

<210> 45
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> 10/50_1B1

<400> 45
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acgtgcagtg tctctggtga ctccatcact aattactact gggcctggat ccggcagccc 120

ccagggaaga ggctggaatg gattgcgaat ctgtattaca ctgggggtac caattacaac 180

ccctccctca aggctcgact caccacgtca gtagacacat ccaagaacac cttttccctc 240

aaggtgaggt ctgcgaccgc tgcggacacg gccgtatatt attgtgcgag agtgacatca 300

ttgagtggga gcgaggtcta cggtatggac gtctggggcc aagggatcac ggtcaccgtc 360

tcctca 366

<210> 46
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<223> 10/50_1B1

<400> 46
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atcacttgcc aggcgagtca ggacattagt aactctttaa cttggtttca gcagaaacca 120

gggaaagccc ctaggctcct gatgtacgct gcgtccaatt tgcaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagacattg caacatatta ctgtcaacag tatgatagta tcccgatcac cttcggccag 300

gggacacgac tggagcttaa ac 322

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<400> 47
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tcctgtgctg cctctggatt caccttcgct ccctttagcc tgacctgggt ccgccaggct 120

ccagggaagg gactggagtg ggtctcatcc attactccta gtagtaatta catattctat 180

gcagactcag tgaagggccg attcaccatc tccagagacg acggcaggaa gtcagtgtat 240

ctgcagatga acagcctcag agtcgaggac acggctgtgt attactgtgc gagagatcct 300

tccgggactt atgactacaa ctactacgca atggacgtct ggggccccgg gaccacggtc 360

accgtctcct ca 372

<210> 48
<211> 328
<212> DNA
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<223> 10/50_1D1

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ctctcctgca gggccagtca gactgttggt agtagttatt tagcctggta ccagcagaaa 120

cctggccagg cgcccaggct cctcatctat ggtacatcca ccagggccac tggcatcgca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtcta ttactgtcaa cagtatggtg gctcacctcc gatcaccttc 300

ggccaaggga cacgactgga gactaaac 328

<210> 49
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<212> DNA
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<220>
<223> 10/50_2F1

<400> 49
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aaggcttcag gttctggtta ccccttttagt agtcatggtt tcagttgggt gcgacaggcc 120

cctggacagg ggcttgagtg gatgggatgg accaccgctt acaatggtga aacacaatat 180

gcacagaagt tcctgggcag agtcaccatg accacagaca cttccacgaa cacagcctac 240

atggagctga ggagcctgag atctgacgac acggccatct actattgtta tagcagcggt 300

cctcgatggg gtcattttga tatctggggc caagggacag tggtcaccgt ctcttcag 358

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<212> DNA
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<223> 10/50_2F3

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gctcccaggc tcctcatcta tggtacatcc agcagggcca ctggcatccc agaaaggttc 180

agtggcagtg ggtctgggac agacttcact ctcaccatca gcagactgga gcctgaagat 240

tttgcagtgt attactgtca ccaatatgat tcctcaccgt ggacgttcgg ccaagggacc 300

agggtggaat tcaaac 316

<210> 51
<211> 382
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<220>
<223> 10/50_3H1

<400> 51
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tcctgtgcag cctctggatt caatttttggc gactatgtca tggcctgggt ccgccaggct 120

ccaggcaagg gcctggagtg ggtctcagtt atttataatg gtggaagtag tacatattat 180

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ctgcacatga gcagcctgag cgccgaagac acggcccgat attactgtgc gaaagatcga 300

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accctggtca ccgtctcctc ag 382

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gaagattttg caacttacta ctgccaacag gggagcactt tcggcggcgg gaccaaggtg 300

gagttcaaac 310

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acatgcactg tctctggtgg ctccctcagc agtgatggtc actcctgggg ctggctccgc 120

cagcccccag gtaagggact ggagtggatt ggtaacatct attatactgg gaccacctac 180

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tccctgaagc tgaactctgt ggccgccgca gacacggctg tctattactg tgcggcctgg 300

aacgcgggac catcgtacta ttttcactac tggggcctgg gaaccctggt caccgtttcc 360

tc 362

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ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

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accaaggtgg aagtcaaac 319

<210> 55
<211> 373
<212> DNA
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<220>
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<400> 55
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acctgcgctg tttatgatgg gtccttcagt ggtttctcct ggacctggat ccgccagtcc 120

ccagggaagg ggctggagtg gattggggaa atcaatcaca gtggaagcac caactacaac 180

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gggaccaagg tggaaatcaa ac 322

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<400> 57
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tcctgcaagg catctggata caccttcagc agctactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg ggtgggaata atcaacccta ggggtggaag cgcaagcgtc 180

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tggggccaag ggacaatggt caccgtctct tca 393

<210> 58
<211> 322
<212> DNA
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<223> 10/50_5C1

<400> 58
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<210> 59
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tggagcgaca agggggtctt tgactactgg ggccagggaa tcccggtcac cgtctcctca 360

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<223> 10/50_5D2

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gaagactttg caacttactc ttgtcaacag gctttcagtt tcccgtggac gttcggccaa 300

gggaccaagg tggaaatcag ac 322

<210> 61
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<212> DNA
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<220>
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<400> 61
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tcctgcaagg catctggata cactttcgcc aacaactata tacactgggt gcgacaagcc 120

cctggacaag ggcttcagtg gatgggagtc atcaacccta gaggtggtag tgcagcctcg 180

gcacagatgt tccagggcag aatcaccatg accagggaca cgtccacgag cacagtctac 240

ctggacctgc gaagcctgag atctgaggac acggccgtct attactgtgc gagaggggga 300

agggcctatt actatgattc ttatacgacc ccccgagacg gagagtcgtg gtggttcgac 360

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<400> 63
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cctggacaag ggcttgaatg gatggggata atcaaccctc gtggtggaag cacaagcatc 180

gcacagcagt tccagggcag aatcaccatg accagggaca cgtccacgag cacagtctac 240

atggaactga gaagcctgac atctgaggac acggccgttt attactgtgc gagagccggc 300

ccagcccttt attatgatag tagtggttat gacccaacta cttatgattc ttttgaagtc 360

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ggccaggcgc ccaggctcct catctatggt gcgtccacta gggccactgg tatcccagcc 180

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gaagattctg cagtttatta ctgtcagcag tataatcact ggcctcggac gttcggccaa 300

gggaccaagg tggaaatcaa ac 322

<210> 65
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<220>
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ccagggaagg ggctggagtg ggtctcagtt atttataccg gcggaggtag cacctactat 180

gcagactccg tgaggggccg gttcaccatc tccagagata attccaagaa caccctgtat 240

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tcag 364

<210> 66
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<400> 66
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gggaaagccc ctaaactcct gatttatggt gtatccactt tgcacagtgg ggtcccatta 180

aggttcagcg gcggtggctc tgggacagaa ttcattctca cgatcagcgg cctgcagcct 240

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gaaatcaaac 310

<210> 67
<211> 370
<212> DNA
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<220>
<223> 10/50_7A1

<400> 67
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ccagggaagg gcctggagtg gatttcatac attagtcgta gtggtaccgc cacatactac 180

gcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

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gtctcctcag 370

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<400> 68
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gggaaagccc cgaagctcct gatctttgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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<210> 69
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<212> DNA
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<220>
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<400> 69
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cctggacaag ggcttgagtg gatgggagta ataaaccctc gtggtggaag cgcaagtagt 180

gcagagaagt tccagggcag aatcaccatg accagggaca cgtccacgag cacagtttac 240

atggagctga gcagcctgag atcggaggac acggccgtat tttactgtgc gagaggggga 300

tgggcctatt attatgatag ttacacgacc ccccgagacg gacagtcgtg gtggttcgac 360

ccctggggcc agggaaccct ggtcaccgtc tcctca 396

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<212> DNA
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<220>
<223> 10/50_7C1

<400> 70
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atcacttgcc aggcgagtca ggacattaga aacttttaa attggtatca gcacaaacca 120

gggaaagccc caaaggtcct gatatacgat gcctccaaat tgaaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagac tttactttca ccatccgcag cctgcagcct 240

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gggacacgac tggagattaa ac 322

<210> 71
<211> 366
<212> DNA
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<220>
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<400> 71
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acctgcactg tctctggtgg ctccatcaat agttactact ggagctggat ccggcagccc 120

ccagggaagg gactggagtg gattgggtat attcattaca gtgggagcac caactacaac 180

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agtgatacca cctgccgtga atacttccag cactggggcc agggcaccct ggtcaccgtc 360

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<210> 72
<211> 322
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<400> 72
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gggaccaagg tggagatcaa ac 322

<210> 73
<211> 370
<212> DNA
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<220>
<223> 10/50_7H1

<400> 73
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ccaggaaagg ggctggagtg ggtggccaac ataaatcaag gtggaagtga gaggcactac 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaggaa ttcgttctac 240

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atggtcgagg tgaccgcact ctccttcttg gactactggg gcgagggaaa cctggtcgcc 360

gtctcctcag 370

<210> 74
<211> 322
<212> DNA
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<220>
<223> 10/50_7H1

<400> 74
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gggaaagccc ctaaactcct gatcttcgct acatctaact tgcaaggtgg cgtcccatca 180

aggttcagtg gcagtggatc tgggggagat ttcactctca ccatcaccag tctgcaacct 240

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gggaccaggg tggacatcaa ac 322

<210> 75
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<220>
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<400> 75
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cccgggaaag gcctagagtg gatggggatt atctatcctg gtaactctga ccccagatac 180

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cactacttct actacggtat ggacctctgg ggccagggga ccacggtcac cgtctcctca 360

<210> 76
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<223> 10/50_9B1

<400> 76
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cctggccagg ctcccaggct cctcatttat ggtgcatcca acagggccga tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcatcatcag cagactggag 240

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cctgggacca aagtggatat caaac 325

<210> 77
<211> 369
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<220>
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<400> 77
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gcagactccg tgaagggccg cttcaccatc tccagagacg attccaagaa cacgctgtat 240

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tggggtgttt cggtcaagcc gggtactttt gatatctggg gccaagggac agtgatcacc 360

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<210> 78
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<400> 78
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gggaaagccc ctaagctcct gatctttgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggctc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

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gggaccaagg tggaaatcaa ac 322

<210> 79
<211> 361
<212> DNA
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<220>
<223> 10/50_11E1

<400> 79
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tcctgtgcag cctctggatt cactttcagc acctatccca tgagctgggt ccgccaggct 120

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gcagactccg tgaagggccg gttcaccatt tccagagata attccaagaa cacgctgtat 240

ctgcaaatga atagcctgag agccgaggac acggccgtat attactgtgc gaaatttgcg 300

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tcaaac 306

<210> 83
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tgatagcaac gcctggccag attgactact ggggccaggg aatcctggtc accgtctcct 360

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<210> 84
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<212> DNA
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tcctgatcta tgctgcatcc aatttgcaag gtggggtccc atcaagattc agtggctctg 180

gatctgggac agatttcact ctcaccatta gtagtctgca acctgaagat tttgcaacct 240

actactgtca acagacttac agttcccctc cgacgttcgg cctagggacc aaggtggaaa 300

tcaaac 306

<210> 85
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acaaatgaat agcctgagag ccgaggacac ggctgtttat tactgtgcga gatggtcccg 300

tggtaactcc gactctgggg gtatggacgt ctggggccaa gggaccacgg tcaccgtctc 360

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gcaaatgaac agcctgagag ccgaggacac ggctgtttat tactgtgcga gactcctatt 300

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<210> 88
<211> 306
<212> DNA
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<223> 1st_BASE_945551_A3-2M2-G8_Ck516

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tcaaac 306

<210> 89
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<212> DNA
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<210> 90
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<212> DNA
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<220>
<223> 1st_BASE_945644_A3-3M1-B11_Ck516

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<212> DNA
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tcaaac 306

<210> 93
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<212> DNA
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<223> 1st_BASE_892606_A3-3M3-G3_PWCgamma

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<210> 94
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<212> DNA
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<210> 95
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<213> Artificial Sequence

<220>
<223> 1st_BASE_945500_A3-2M1-A5_Ck516

<400> 96
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gccagagtgt tagcagcagg ttcttagcct ggtaccagca gaaaccaggc caggctccca 120

ggctcctcat ctacggtgca tccagcaggg cctctggcat cccagatagg ttcagtggca 180

gtgggtctga gacagacttc actctcagca tcagcagact ggagcctgaa gattttgcag 240

tgtatttctg tctgcagtat ggtttctcac ccccgtacac ttttggccag gggaccaaac 300

tggagatcaa ac 312

<210> 97
<211> 359
<212> DNA
<213> Artificial Sequence

<220>
<223> 1st_BASE_896206_A3-2M2-H5_PWCgamma

<400> 97
ggtgcagctg ttggagtctg ggggaggctt ggttcagcct ggggggtccc tgagactctc 60

ctgtgcagcc tctggattca cctttagcaa ctatgccatg agctgggtcc gccaggctcc 120

agggaagggg ctggagtggg tctcagttat ttataacggt ggcagtagca catactatgc 180

agactccgtg aagggccgct tcaccatctc cagagataac tccaagaaca cactgtatct 240

gcgaatgaac agtctgcgag tcgaagacac ggccgtatat tactgcgcga aattcctcgt 300

gttgccagca gctgctgccg actactgggg ccagggaacc ctggtcaccg tctcctcag 359

<210> 98
<211> 292
<212> DNA
<213> Artificial Sequence

<220>
<223> 1st_BASE_945554_A3-2M2-H5_Ck516

<400> 98
agtctccatc cttcctgtct gcatctgtag gagacagagt caccatcact tgccgggcca 60

gtcagggcat tagcagtcat ttagcctggt atcagcagaa accagggaaa gcccctaaac 120

tcctgatcta tgctgcatcc actctgcaca ctggagtccc atcaaggttc agcggcagtg 180

gatctgggac agagttcact ctcacaatca ccagccttca gcctgaagat tttgcgactt 240

attactgtca gcagccgggt gctttcggcc ctgggaccag actggatatc aa 292

<210> 99
<211> 388
<212> DNA
<213> Artificial Sequence

<220>
<223> 1st_BASE_897923_A3-2M3-C9_PWCgamma

<400> 99
ggtgcagctg ttggagtctg ggggaggctt ggtacagcct ggaaggtccc tgagactctc 60

ctgtgcagcc tctggattcc ccttcagtag ctatgaaatg aactgggtcc gccaagctcc 120

agggaagggg ctggagtgga tttcatatat cagtagtact ggtagtccca tccactacgc 180

agactctgtg aggggccgat tcaccatctc cagagacaac gccaagaact cactctatct 240

gcacatgaac agcctgagag ccgaggacac ggctatttat tactgtgcgg gggatttgct 300

gctctgggtc cccgaagcaa caggtgctac agctggtacc ggcggtttgg acgtctgggg 360

ccaagggacc acggtcaccg tctcctca 388

<210> 100
<211> 306
<212> DNA
<213> Artificial Sequence

<220>
<223> 1st_BASE_949089_A3-2M3-C9_Ck516

<400> 100
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gtcagaccat cagtaaatat ttaaattggt accaccagaa gccagggaaa gcccctaatc 120

tcctgatcta tgctgcatca agtttgcaga gtggagtccc atcgaggttc agcggcagtg 180

gatctgggac agatttcact ctcaccatca gcagtctgca gcctgaagac tttgcaactt 240

actactgtca acagagttac agtatccctc ggacgttcgg ccaagggacc aaggtggaaa 300

tcaaac 306

<210> 101
<211> 382
<212> DNA
<213> Artificial Sequence

<220>
<223> 1st_BASE_992133_A3-2M3-E9-H-1_Resend_1146_Resend

<400> 101
gaggtgcagc tggtacagtc tgaaacagag gtgaaagagc ccgggcagtc tctgaagatc 60

tcctgtaagg gttctggata cacctttacc aactactgga tcggctgggt gtgccaaatg 120

cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga aaccagatac 180

agcccgtcct ttcaaggcca ggtcaccatc tcagtcgaca agtccatcag caccgcctac 240

ctgcagtgga gtagcctgaa ggcctcggac accgccatgt attactgtgc gagactcaaa 300

aattactata cttcggggaa ttatgttccg gtgggaggta tggacgtctg gggccaaggg 360

atcacggtca ccgtctcctc ag 382

<210> 102
<211> 309
<212> DNA
<213> Artificial Sequence

<220>
<223> 1st_BASE_949097_A3-2M3-E9_Ck516

<400> 102
agtctccatc ctccctgtct gcatctgtag gagacagagt caccatcact tgccgggcaa 60

gtcagagcgt tagcaactat ttaaattggt atcagcagaa accagggaaa gcccctaaac 120

tcctgatcta tgctgcttcc actttgcaaa gtggggtccc atcaagattc agtggcagtg 180

gatctgggac agatttcact ctctccatca gcagtctgca acctgaagac tttgcaatat 240

actactgtca acagacttac agtccccctc agaacacttt tggccagggg accaagctgg 300

agatcaaac 309

<210> 103
<211> 379
<212> DNA
<213> Artificial Sequence

<220>
<223> 1st_BASE_988416_A3-2M3-F9-H-2_1146

<400> 103
ggccaggtgg agctggtgga gtcgggccca ggactggtga agccttcggg gtccctgtcc 60

ctcacctgcg ctgtctctgg tggctccatc accagtagta actggtggag ttgggtccgc 120

cagcccccag ggaaggggct ggaatggatt ggagaaatct atcatagtgg gagcgccgac 180

tacaacccgt ccctcaagag tcgagtcacc atatcagtag acacctccaa gaaccagttc 240

tccctgaagc tgaggtctgt gaccgccgcg gacacggccg tgtattactg tgcgagggtt 300

gaggttatga ttaagtttgg gggagttatc cgatactttg actactgggg cctgggaacc 360

ctggtcaccg tctcctcag 379

<210> 104
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> 1st_BASE_949101_A3-2M3-F9_Ck516

<400> 104
agtctccatc ctccctgtct gcatctgtag gagacagagt caccatcact tgccaggcga 60

gtcaggacat tagcaactat ttaaattggt atcagcagaa accagggaaa gcccctaagc 120

tcctgatcta ctatgcatcc aatttggaaa caggggtccc atcaaggttc agtggaagtg 180

gatctgggac agattttact ttcaccatca gcagcctgca gcctgaagat tttgcaacat 240

actactgtca acagtatgat aatctccctc cgcggtacac ttttggccag gggaccaagc 300

tggagatcaa ac 312

<210> 105
<211> 385
<212> DNA
<213> Artificial Sequence

<220>
<223> 1st_BASE_897935_A3-2M3-G3_PWCgamma

<400> 105
ggtgcagctg ttggagtctg ggggagcctt ggtacagcca gggcggtccc tgagactctc 60

ctgtacagct tctggattca cctttgggga ttttgctttg agctgggtcc gccaggctcc 120

agggaagggg ctggagtggg taggtgtcat cagaagcaaa ggctatggtg ggacaacaga 180

gtacgccgcg tctgtgaaag gcagattcag tatctcaaga gatgattcca aattcatcgc 240

ctatctgcaa atgaacagcc tggaaaccga ggacactgcc gtgtacttct gtaccagcac 300

aaccttatat tattttgttt cggggagggc aaaagactac gggatggacg tctggggcca 360

agggaccacg gtcaccgtct cctca 385

<210> 106
<211> 306
<212> DNA
<213> Artificial Sequence

<220>
<223> 1st_BASE_949103_A3-2M3-G3_Ck516

<400> 106
agtctccatc ctccctgtct gcatctgttg gagacagtgt caccatcact tgccgggcaa 60

gtcagggcat tagaaatgat ttaggctggt atcagcagaa agcaggtaaa gcccctaagg 120

ccgtgatcta tgctgtatcc actttacaaa gtggggtccc atcgaggttc agcggcagtg 180

gatctggcac agatttcact ctcaccatca gcagcctgca gcctgaagat tttgcaactt 240

attactgtct gcaagattac agttttccgt ggacgttcgg ccaagggacc aaggtggaaa 300

tcaaac 306

<210> 107
<211> 385
<212> DNA
<213> Artificial Sequence

<220>
<223> 1st_BASE_988406_A3-2M3-C2-H-3_1146

<400> 107
gaggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccatcacc agtagtagtt actactgggc ctggctccgc 120

cagcccccag ggaaggggct ggagtggatt gggaatatct attacagtgg gaacaccgac 180

tacaacccgt ccctcaagag tcgagtcacc atatccgcag acacgtccat ggaccaattc 240

tccctgaggc tgaggtctat ggccgcctca gacacggctg tttattattg tgcgagcggg 300

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ggaaccctgg tcaccgtcgc ctcag 385

<210> 108
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> 1st_BASE_949084_A3-2M3-C2_Ck516

<400> 108
agtctccagg caccctgtct ttgtctccag gggaaagagc caccctctcc tgcagggcca 60

gtcagagtgt tagcagcagt ttcttagcct ggtaccagca caaacctggc caggctccca 120

ggctcctcat ctatggtgca tccatcaggg ccactggcat cccagacagg ttcagtggca 180

gtgggtctgg gacagacttc attctcacca tcagcaggct ggagcctgaa gattttgcag 240

tgtattactg tcagcagttt ggtagaacac ctccaatgta cacttttggc caggggacca 300

agctggagat caaac 315

<210> 109
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 11E-H1L1; Heavy Chain; 10/50_11E1

<400> 109

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

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

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

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

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

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

Ala Lys Phe Ala Ala Pro Pro Ser Gly Trp Cys Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 110
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 11E-H1L1; light chain; 10/50_11E1

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 110

Xaa Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
1 5 10 15

Ser Gln Ser Val Ser Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly
20 25 30

Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Thr Leu Glu Ser Gly
35 40 45

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
50 55 60

Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln
65 70 75 80

Gln Ser Gly Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
85 90

<210> 111
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 1B-H1L1; heavy chain; 10/50_1B1

<400> 111

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

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

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

Ala Asn Leu Tyr Tyr Thr Gly Gly Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

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

Lys Val Arg Ser Ala Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Val Thr Ser Leu Ser Gly Ser Glu Val Tyr Gly Met Asp Val Trp
100 105 110

Gly Gln Gly Ile Thr Val Thr Val Ser Ser
115 120

<210> 112
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 1B-H1L1; light chain; 10/50_1B1

<400> 112

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

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

Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Met
35 40 45

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

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

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

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

<210> 113
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 3H-H1L1; heavy chain; 10/50_3H1

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<400> 113

Gln Val Gln Leu Gln 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 Asn Phe Gly Asp Tyr
20 25 30

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

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

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

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

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

Ala Leu Asp His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 114
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 3H-H1L1; light chain; 10/50_3H1

<400> 114

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

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

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

Phe Ala Ala Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

Gly Thr Lys Val Glu Phe Lys
100

<210> 115
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 5A-H1L1; heavy chain; 10/50_5A1

<400> 115

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

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

Ser Trp Thr Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Leu Thr Ile Ala Leu Asp Thr Ser Thr Asn Gln Phe Ser Leu
65 70 75 80

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

Leu Ser Leu Gln Thr Leu Val Arg Gly Leu Val Tyr Ile Asn Phe Asp
100 105 110

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

<210> 116
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 5A-H1L1; light chain; 10/50_5A1

<400> 116

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Thr Thr Tyr
20 25 30

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

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

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

Gly Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Leu Pro Arg
85 90 95

Thr Phe Gly His Gly Thr Lys Val Glu Ile Lys
100 105

<210> 117
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 5D-H6L2; heavy chain; 10/50_5D6

<400> 117

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

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

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

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

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

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

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

Gly Ile Pro Val Thr Val Ser Ser
115 120

<210> 118
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 5D-H6L2, light chain; 10/50_5D2

<400> 118

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Arg
            100                 105
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<210> 119
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 6E-H1L1; heavy chain; 10/50_6E1

<400> 119

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

Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Phe Ser Phe Ser Thr Tyr
            20                  25                  30

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

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

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

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

Ala Gly Gly Gly Ile Val Ser Thr Met Gly Ala Phe Gly Phe Trp Gly
            100                 105                 110

Gln Gly Thr Met Val Ala Val Ser Ser
        115                 120
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<210> 120
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 6E-H1L1; light chain; 10/50_6E1

<400> 120

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Glu Phe Ser Ser Tyr
20 25 30

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

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

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

Glu Asp Val Gly Thr Tyr Tyr Cys Gln Gln Thr Gly Thr Phe Gly Gln
85 90 95

Gly Thr Lys Val Glu Ile Lys
100

<210> 121
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 7A-H1L1; heavy chain; 10/50_7A1

<400> 121

Gln Val Gln Leu Val Gln 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 Phe Ser Ser Tyr
20 25 30

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

Ser Tyr Ile Ser Arg Ser Gly Thr Ala Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Gly Glu Gly Tyr Phe Gly Ser Ala Ala Ile Asn Tyr Phe Ala Phe
100 105 110

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

<210> 122
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 7A-H1L1; light chain; 10/50_7A1

<400> 122

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

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

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

Phe Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

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

<220>
<223> Ab 10/50 7H-H1L1; heavy chain; 10/50_7H1

<400> 123

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

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

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

Ala Asn Ile Asn Gln Gly Gly Ser Glu Arg His Tyr Val Asp Ser Val
50 55 60

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

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

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

Trp Gly Glu Gly Asn Leu Val Ala Val Ser Ser
115 120

<210> 124
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 7H-H1L1; light chain; 10/50_7H1

<400> 124

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Arg Val Asp Ile Lys
100 105

<210> 125
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 9B-H1L1; heavy chain; 10/50_9B1

<400> 125

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

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

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

Gly Ile Ile Tyr Pro Gly Asn Ser Asp Pro Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 126
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 9B-H1L1; light chain; 10/50_9B1

<400> 126

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Phe Ser Ser Ile
20 25 30

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

Ile Tyr Gly Ala Ser Asn Arg Ala Asp Gly Ile Pro Asp Arg Phe Ser
50 55 60

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Asp Asn Ser Phe
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 127
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 1D-H8L1; heavy chain; 10/50_1D8

<400> 127

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Pro Phe
20 25 30

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

Ser Ser Ile Thr Pro Ser Ser Asn Tyr Ile Phe Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Asp Pro Ser Gly Thr Tyr Asp Tyr Asn Tyr Tyr Ala Met Asp
100 105 110

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

<210> 128
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 1D-H8L1; light chain; 10/50_1D1

<400> 128

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

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

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

Ile Tyr Gly Thr Ser Thr Arg Ala Thr Gly Ile Ala Asp Arg Phe Ser
50 55 60

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

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

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

<210> 129
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 2F-H3L1; heavy chain; 10/50_2F1

<400> 129

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

Lys Val Ser Cys Lys Ala Ser Gly Ser Gly Tyr Pro Phe Ser Ser His
20 25 30

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

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

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

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

Tyr Ser Ser Gly Pro Arg Trp Gly His Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Val Val Thr Val Ser Ser
115

<210> 130
<211> 105
<212> PRT
<213> Artificial Sequence

<220>

<223> Ab 10/50 2F-H3L1; light chain; 10/50_2F3

<400> 130

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asp Leu Ala
20 25 30

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

Thr Ser Ser Arg Ala Thr Gly Ile Pro Glu Arg Phe Ser Gly Ser Gly
50 55 60

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

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

Gly Gln Gly Thr Arg Val Glu Phe Lys
100 105

<210> 131
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 4B-H2L1; heavy chain; 10/50_4B2

<220>
<221> misc_feature
<222> (121)..(121)
<223> Xaa can be any naturally occurring amino acid

<400> 131

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Leu Ser Ser Asp
20 25 30

Gly His Ser Trp Gly Trp Leu Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Asn Ile Tyr Tyr Thr Gly Thr Thr Tyr Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Asn Ser Val Ala Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Ala Trp Asn Ala Gly Pro Ser Tyr Tyr Phe His Tyr Trp Gly
100 105 110

Leu Gly Thr Leu Val Thr Val Ser Xaa
115 120

<210> 132
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 4B-H2L1; light chain; 10/50_4B1

<400> 132

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asn
20 25 30

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

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

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

Phe Gly Gln Gly Thr Lys Val Glu Val Lys
100 105

<210> 133
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 5C-H6L1; heavy chain; 10/50_5C6

<400> 133

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

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

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

Gly Ile Ile Asn Pro Arg Gly Gly Ser Ala Ser Val Ala Gln Lys Phe
50 55 60

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

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

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

Thr Pro Tyr Asp Ala Phe Glu Val Trp Gly Gln Gly Thr Met Val Thr
115 120 125

Val Ser Ser
130

<210> 134
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 5C-H6L1; light chain; 10/50_5C1

<400> 134

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Tyr
20 25 30

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

Phe Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Val Tyr Tyr Cys His Gln Tyr Asn His Trp Pro Arg
85 90 95

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

<210> 135
<211> 132

<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 6B-H1L2, heavy chain; 10/50_6B1

<400> 135

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

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

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Gln Trp Met
35 40 45

Gly Val Ile Asn Pro Arg Gly Gly Ser Ala Ala Ser Ala Gln Met Phe
50 55 60

Gln Gly Arg Ile Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Gly Gly Arg Ala Tyr Tyr Tyr Asp Ser Tyr Thr Thr Pro Arg
100 105 110

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

Thr Val Ser Ser
130

<210> 136
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 6B-H1L2; light chain; 10/50_6B2

<400> 136

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

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

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

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

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

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

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

<210> 137
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 6D-H3L1, heavy chain; 10/50_6D3

<400> 137

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

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

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

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

Gln Gly Arg Ile Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Ala Gly Pro Ala Leu Tyr Tyr Asp Ser Ser Gly Tyr Asp Pro
100 105 110

Thr Thr Tyr Asp Ser Phe Glu Val Trp Gly Gln Gly Thr Met Val Thr
115 120 125

Val Ser Ser
130

<210> 138
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 6D-H3L1; light chain; 10/50_6D1

<400> 138

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Arg Ser Tyr
20 25 30

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

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

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

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

<210> 139
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 7C-H3L1; heavy chain; 10/50_7C3

<400> 139

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

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

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

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

Gln Gly Arg Ile Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

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

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

Thr Val Ser Ser
130

<210> 140
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 7C-H3L1; light chain; 10/50_7C1

<400> 140

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

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Arg Asn Phe
20 25 30

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

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

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

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

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

<210> 141
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 7E-H1L1; heavy chain; 10/50_7E1

<400> 141

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

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

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

Gly Tyr Ile His Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

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

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

Arg His Asp Cys Ser Asp Thr Thr Cys Arg Glu Tyr Phe Gln His Trp
100 105 110

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

<210> 142
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 7E-H1L1; light chain; 10/50_7E1

<400> 142

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr Phe
20 25 30

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

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

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

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

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

<210> 143
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/50 9E-H2L2; heavy chain; 10/50_9E2

<400> 143

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

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

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

Ser Ser Ile Ser Asp Ser Asp Asp Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Thr Thr Asn Trp Gly Val Ser Val Lys Pro Gly Thr Phe Asp Ile
            100                 105                 110

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

<210>  144
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Ab 10/50 9E-H2L2; light chain; 10/50_9E2

<400>  144

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

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

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

Phe Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Trp
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 145
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 1D-H4L1; heavy chain; 10/63 1D4_001.ab1

<400> 145

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

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

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

Trp Leu Ala Leu Leu Tyr Trp Asp Asp Asp Arg Arg Tyr Ser Pro Ser
50 55 60

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Arg Trp Glu Asp Ser Thr Phe Gln His Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 146
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 1D-H4L1; light chain; 10/63 1D-1_055

<400> 146

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Ser Asn
20 25 30

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

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr His Asn Trp Gly Thr
85 90 95

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

<210> 147
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 1E-H3L1; heavy chain; 10/63 1E3_061

<400> 147

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

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

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

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

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

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

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

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

<210> 148
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 1E-H3L1; light chain; 10/63 1E-1_053

<400> 148

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

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

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

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

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

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

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

<210> 149
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 5D-H1L2, heavy chain; 10/63 5D1_037

<400> 149

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Asp
            20                  25                  30

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

Gly Ser Ile Ile Pro Ile Phe Ser Arg Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Asn Ala Asp Glu Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

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

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

Thr Leu Ile Thr Val Ser Ser
        115
```

SequenceListing_ST25

<210> 150
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 10/63 5D-2_070.ab1

<400> 150

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Ser Ile Ser Thr Asn
20 25 30

Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Thr Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Val Ser Ser Leu Leu Pro
65 70 75 80

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

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

<210> 151
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 2A-H5L4; heavy chain; 10/63 2A5_014

<400> 151

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

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

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

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

SequenceListing_ST25

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

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

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

<210> 152
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 2A-H5L4; light chain; 10/63 2A-4_049

<400> 152

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

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

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

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

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

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

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

<210> 153
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 2C-H3L2; heavy chain; 10/63 2C3_006.ab1

<400> 153

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Ala Ser Ile Gly Ser Tyr
20 25 30

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

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

Gln Gly Arg Leu Thr Ile Ser Ala Asp Asp Ser Thr Ser Ser Ala Tyr
65 70 75 80

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

Ala Arg Ser Gln Arg His Ile Leu Thr Gly His Tyr Thr Asp Tyr Trp
100 105 110

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

<210> 154
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 2C-H3L2; light chain; 10/63 2C-2_058

<400> 154

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

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

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

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

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

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

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Arg
100 105

<210> 155
<211> 122
<212> PRT
<213> Artificial Sequence

<220>

SequenceListing_ST25

<223> Ab 10/63 2E-H2L2; heavy chain; 10/63 2E2_004

<400> 155

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

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

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

Ala Val Ile Ser Tyr Asp Ala Lys Lys Gln Tyr Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Gly Asp Asp Ala Ala Val Tyr Phe Cys
85 90 95

Ala Lys Leu Gln Arg Pro Asp Ser Thr Val Trp Pro Phe Asp Gln Trp
100 105 110

Gly Gln Gly Ile Leu Val Ile Val Ser Pro
115 120

<210> 156
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 2E-H2L2; light chain; 10/63 2E-2_050

<220>
<221> misc_feature
<222> (106)..(106)
<223> Xaa can be any naturally occurring amino acid

<400> 156

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

Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Met Trp
20 25 30

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

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

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

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

Phe Gly Gln Gly Thr Lys Val Asp Ile Xaa
100 105

<210> 157
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 2F-H1L1; heavy chain; 10/63 2F1_031

<400> 157

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

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

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

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

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

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

Ala Asn Val Leu Gly Tyr Cys Thr Pro Thr Thr Cys Tyr Glu Asp His
100 105 110

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

<210> 158
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 2F-H1L1; heavy chain; 10/63 2F1_059

<400> 158

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

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

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

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Ala
50 55 60

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

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

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

<210> 159
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 2G-H2L1; heavy chain; 10/63 2G2_027.ab1

<400> 159

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

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

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

Gly Ile Ile Tyr Pro Ser Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Ile Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Pro Asp Asp Ser Ser Gly Leu Glu Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 160
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 2G-H2L1; light chain; 10/63 2G-1_079.ab1

<400> 160

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

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

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

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

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

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

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

<210> 161
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 3E-H1L2; heavy chain; 10/63 3E1_030

<400> 161

Gln Val His Leu Val Gln 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 Phe Ser Thr Tyr
20 25 30

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

Ala Asn Ile Lys Ala Asp Gly Arg Gln Glu Tyr Tyr Leu Gln Ser Val
50 55 60

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

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

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

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Pro
115 120

<210> 162
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 3E-H1L2; light chain; 10/63 3E-2_069

<400> 162

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

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

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

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

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

Glu Asp Leu Ala Thr Tyr Tyr Cys Val His His Asn Asp Tyr Pro Arg
85 90 95

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

<210> 163
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 3F-H1L2; heavy chain; 10/63 3F1_026

<400> 163

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr His
20 25 30

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

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

Gln Asp Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Phe Phe Val Lys Tyr Ser Gly Ser His Tyr Tyr Phe Asp Ser
100 105 110

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

<210> 164
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 3F-H1L2; light chain; 10/63 3F-2_065

<400> 164

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

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

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

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

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

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

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

<210> 165
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 4F-H6L1; heavy chain; 10/63 4F6_020.ab1

<400> 165

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

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

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

Gly Arg Ile Lys Asn Lys Ile Asp Gly Glu Thr Thr Asp Tyr Ala Ala
50 55 60

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

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

Trp Cys Thr Ile Tyr Phe Tyr Asp Arg Ser Gly Tyr Phe Phe Asp His
100 105 110

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

<210> 166
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 4F-H6L1; light chain; 10/63 4F-1_076

<400> 166

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

Gln Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

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

Phe Asp Ala Ser His Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Arg Gly Lys Trp Pro Ser
85 90 95

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

<210> 167
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 5A-H6L1; heavy chain; 10/63 5A6_045.ab1

<400> 167

Gln Val Gln Leu Gln 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 Phe Ser Asp Tyr
20 25 30

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

Ser Gly Leu Ser Glu Ser Gly His Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Cys Trp Arg Gly Tyr Asp Pro Leu Thr Gly Tyr Tyr Thr Gly
100 105 110

Tyr Tyr Phe Asp Tyr Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 168
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 5A-H6L1; light chain; 10/63 5A-1_074

<400> 168

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

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

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

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

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

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Asn Ala Pro Val
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 169
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 5B-H1L1, heavy chain; 10/63 5B1_043

<400> 169

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

Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile Ser Ser Ile
20 25 30

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

Trp Ile Gly Ser Leu Ala Tyr Ser Gly Asp Thr Tyr Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Val Asn Ser Val Thr Ala Ala Asp Thr Ala Leu Tyr Phe
85 90 95

Cys Ala Arg His His Ser Ser Gly Asn Ala Leu Asp Tyr Trp Gly Gln
100 105 110

Gly Ile Leu Val Thr Val Ser Ser
115 120

<210> 170
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 5B-H1L1; light chain; 10/63 5B1_053

<400> 170

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

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105

<210>  171
<211>  125
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Ab 10/63 5C-H2L1, heavy chain; 10/63 5C2_041

<400>  171

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

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

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

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

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

Ala Gly Ala Tyr Cys Ser Ala Thr Ser Cys Ser Ser Gly Gln Trp Leu
            100                 105                 110

Val Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
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<210> 172
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 5C-H2L1; light chain; 10/63 5C1_049.ab1

<400> 172

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Phe His Ser
20 25 30

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

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

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
65 70 75 80

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

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

Asp Val Lys
115

<210> 173
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 5H-H3L1; heavy chain; 10/63 5H3_044

<400> 173

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Asn Asn Ser
20 25 30

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

Trp Ile Gly Gly Ile Tyr Phe Ser Gly Thr Thr Tyr Tyr Asn Pro Ser
50 55 60

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

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

Cys Val Arg Gln Met Asn Tyr Tyr His Leu Gly Ser Ser Val Gly Phe
100 105 110

Asp Pro Trp Gly Gln Gly Ala Leu Ala Thr Val Ser Ser
115 120 125

<210> 174
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 5H-H3L1; light chain; 10/63 5H-1_095

<400> 174

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

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

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

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

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

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

<210> 175
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 6C-H8L1; heavy chain; 10/63 6C8_036

<400> 175

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

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

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

Gly Gly Ile Ile His Pro Phe Gly Thr Glu Asn Tyr Ala Gln Lys Phe
    50                  55                  60

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

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

Ala Arg His His Arg His Ile Leu Thr Gly Glu Arg Thr Asp Tyr Trp
            100                 105                 110

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

<210> 176
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 6C-H8L1, light chain; 10/63 6C-1_091

<400> 176

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

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

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105
```

<210> 177
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 6E-H6L1; heavy chain; 10/63 6E6_034

<400> 177

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

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

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

Gly Gly Ile Asn Pro Ile Phe Gly Thr Thr Asn Asn Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn Thr Val Tyr
65 70 75 80

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

Ala Arg Gly Gly His His Ile Leu Thr Gly Arg Tyr Ile Asp Asp Trp
100 105 110

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

<210> 178
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 6E-H6L1; heavy chain; 10/63 6E1_058

<400> 178

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

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

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

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

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

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

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

<210> 179
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 7E-H1L1; heavy chain; 10/63 7E1_061

<400> 179

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

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

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

Ala Val Val Ala Tyr Asp Gly Ile Asn Lys Tyr Tyr Glu Asp Ser Val
50 55 60

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

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

Ala Lys Ser Ala Gly Ser Thr Leu Lys Thr Val Ile Ser Leu Leu Gln
100 105 110

Pro Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125

<210> 180
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 7E-H1L1; light chain; 10/63 7E-1_087

<400> 180

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

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

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

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

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

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

<210> 181
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 7G-H1L1; heavy chain; 10/63 7G1_055

<400> 181

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

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

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

Gly Arg Ile Lys Asn Lys Ile Asp Gly Glu Thr Thr Asp Tyr Ala Ala
50 55 60

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

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

Trp Cys Thr Ile Tyr Phe Tyr Asp Arg Ser Gly Tyr Phe Phe Asp His
100 105 110

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

<210> 182
<211> 106

<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 7G-H1L1; light chain; 10/63 7G-1_081

<400> 182

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

Gln Arg Ala Thr Phe Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

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

Phe Asp Ala Ser His Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Arg Gly Lys Trp Pro Ser
85 90 95

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

<210> 183
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 7H-H1L1; heavy chain; 10/63 7H-1_060

<400> 183

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

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

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

Gly Arg Ile Lys Asn Lys Ile Asp Gly Glu Thr Thr Asp Tyr Ala Ala
50 55 60

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

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

Trp Cys Thr Ile Tyr Phe Tyr Asp Arg Ser Gly Tyr Phe Phe Asp His
100 105 110

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

<210> 184
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 7H-H1L1; light chain; 10/63 7H-1_038

<400> 184

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

Gln Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Arg Gly Lys Trp Pro Ser
85 90 95

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

<210> 185
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 8F-H1L1; heavy chain; 10/63 8F1_051

<400> 185

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

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

Trp Ile Gly Gly Ile Tyr Tyr Thr Gly Thr Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Asn Ser Pro Val Thr Ile Ser Ile Asp Met Ser Lys Asn His Phe
65 70 75 80

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

Cys Ala Arg Gln Ala Val Phe Ala Glu Ala Thr Gly Thr Thr Ile Gly
100 105 110

Ala Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Val Val Ser Ser
115 120 125

<210> 186
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 8F-H1L1; light chain; 10/63 8F-1_036

<400> 186

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

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

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

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

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

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

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

<210> 187
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 3D-H2L2; heavy chain; 10/63 3D

<400> 187

Gly Thr His Ile Glu Trp Leu Val Leu Arg Leu Ser Cys Ala Ala Ser
1 5 10 15

Gly Phe Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro
20 25 30

Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ala Tyr Asp Gly Ile Asn
35 40 45

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

Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Ile Ser Leu Gly Pro Glu
65 70 75 80

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

Cys Ile Asn Ser Phe Leu Thr Pro Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Ile Val Ser Ser
115

<210> 188
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Ab 10/63 3D-H2L2; light chain; 10/63 3D-2_071.ab1

<400> 188

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

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

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

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

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

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

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

<210> 189
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_945644_A3-3M1-B11_Ck516

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 189

Xaa Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
1 5 10 15

Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ser Leu Ala Trp Tyr Gln
20 25 30

Gln Arg Pro Gly Glu Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr
35 40 45

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
50 55 60

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

Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Leu Phe Gly Gly Gly Thr Lys
85 90 95

Val Glu Ile Lys
100

<210> 190
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_945644_A3-3M1-B11_Ck516

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 190

Xaa Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
1 5 10 15

Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ser Leu Ala Trp Tyr Gln
20 25 30

Gln Arg Pro Gly Glu Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr
35 40 45

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
50 55 60

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

Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Leu Phe Gly Gly Gly Thr Lys
85 90 95

Val Glu Ile Lys
100

<210> 191
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_878760_A3-3M1-D1_PWCgamma

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 191

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

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

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

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

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

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

Tyr Cys Thr Arg Thr Arg Gly Ser Ser Trp Ser His Tyr Tyr Tyr Tyr
100 105 110

SequenceListing_ST25

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 192
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_945652_A3-3M1-D1_Ck516

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 192

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

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
20 25 30

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

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
50 55 60

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

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly
85 90 95

Thr Lys Leu Glu Ile Lys
100

<210> 193
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_973574_A3_3M2_D3_H_2_1146

<400> 193

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

Ser Leu Arg Leu Ser Cys Val Gly Ser Gly Phe Asn Phe Gly Arg His
20 25 30

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

```
Ala Asn Ile Lys Glu Asp Gly Ser Ala Lys Tyr Tyr Val Glu Ser Val
    50                  55                  60

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

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

Ala Arg Glu Ser Cys Thr Gly Val Thr Cys Gln Gly Phe Leu Asp Phe
            100                 105                 110

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

<210> 194
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_945681_A3-3M2-D3_Ck516

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 194

```
Xaa Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile
1               5                   10                  15

Ala Cys Arg Ala Ser Gln Asn Ile Gly Ile Phe Leu Asn Trp Tyr His
            20                  25                  30

His Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr
        35                  40                  45

Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
    50                  55                  60

Glu Phe Thr Leu Thr Ile Ser Ser Leu Glu Arg Glu Asp Phe Ala Thr
65                  70                  75                  80

Tyr Tyr Cys Gln Gln Thr Tyr Ser Met Phe Tyr Ser Phe Gly Gln Gly
                85                  90                  95

Thr Asn Leu Val Ile Lys
            100
```

<210> 195
<211> 121

<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_892549_A3-3M2-F5_PWCgamma

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 195

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

Thr Leu Ser Leu Asn Cys Ala Val Ser Gly Gly Ser Ile Ser Thr Ser
20 25 30

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

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

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

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

Gly Arg Thr Gly Val Ile Ala Thr Pro Gly Gln Ile Asp Tyr Trp Gly
100 105 110

Gln Gly Ile Leu Val Thr Val Ser Ser
115 120

<210> 196
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_945687_A3-3M2-F5_Ck516

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 196

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

Thr Cys Arg Ala Ser Gln Ser Ile Ser Arg Phe Leu Asn Trp Tyr Gln
20 25 30

```
Gln Arg Pro Gly Lys Ala Pro Asn Leu Leu Ile Tyr Ala Ala Ser Asn
        35                  40                  45

Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
    50                  55                  60

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

Tyr Tyr Cys Gln Gln Thr Tyr Ser Ser Pro Pro Thr Phe Gly Leu Gly
                85                  90                  95

Thr Lys Val Glu Ile Lys
            100
```

<210> 197
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_892571_A3-3M3-C4_PWCgamma

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 197

```
Xaa 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 Ile Thr Leu Arg Asn Tyr
            20                  25                  30

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

Ser Tyr Ile Ser Ile Arg Gly Asn Thr Ile Tyr Tyr Ala Asp Ser Ala
    50                  55                  60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Glu Asn Ser Val Phe
65                  70                  75                  80

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

Ala Arg Trp Ser Arg Gly Asn Ser Asp Ser Gly Gly Met Asp Val Trp
            100                 105                 110

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

<210> 198
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_945760_A3-3M3-C4_Ck516

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 198

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

Ser Cys Arg Ala Ser Gln Ser Val Asn Ser Arg Phe Leu Ala Trp Tyr
20 25 30

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

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

Thr Asp Phe Thr Leu Thr Ile Asn Arg Leu Glu Pro Glu Asp Val Ala
65 70 75 80

Val Tyr Phe Cys His Gln Tyr Gly Phe Ser Pro Pro Tyr Val Phe Gly
85 90 95

Gln Gly Thr Arg Leu Glu Ile Lys
100

<210> 199
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_892606_A3-3M3-G3_PWCgamma

<400> 199

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

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

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

SequenceListing_ST25

Gly Trp Ile Val Val Gly Ser Asp Met Thr Asn Tyr Ala Arg Lys Leu
50 55 60

Gln Gly Arg Val Thr Ile Thr Trp Asp Met Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Ala Val Gly Thr Ser Pro Pro Pro Tyr Phe Asp His Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 200
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_945781_A3-3M3-G3_Ck516

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 200

Xaa Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
1 5 10 15

Thr Cys Arg Ala Ser Gln Gly Ile Tyr Ser Tyr Leu Ala Trp Phe Gln
20 25 30

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

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
50 55 60

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

Tyr Tyr Cys Gln Gln Leu Asn Gly Tyr Pro Ser Phe Gly Gln Gly Thr
85 90 95

Arg Leu Glu Ile Arg
100

<210> 201
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_904578_A3-2M1-A5_PWCgamma

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 201

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

Ser Leu Arg Leu Ser Cys Thr Ala Ser Asp Phe Thr Phe Ser Asp Tyr
20 25 30

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

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

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

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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 202
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_945500_A3-2M1-A5_Ck516

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 202

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

Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Arg Phe Leu Ala Trp Tyr
20 25 30

SequenceListing_ST25

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

Ser Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Glu
50 55 60

Thr Asp Phe Thr Leu Ser Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
65 70 75 80

Val Tyr Phe Cys Leu Gln Tyr Gly Phe Ser Pro Pro Tyr Thr Phe Gly
85 90 95

Gln Gly Thr Lys Leu Glu Ile Lys
100

<210> 203
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_896204_A3-2M2-G8_PWCgamma

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 203

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

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

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

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

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

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

Ala Arg Leu Leu Leu Leu Trp Leu Gly Glu Thr Thr Ala Met Asp Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 204
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_945551_A3-2M2-G8_Ck516

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 204

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

Thr Cys Arg Ala Ser Gln Lys Ile Asn Arg Phe Leu Asn Trp Tyr Gln
20 25 30

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

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
50 55 60

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

Tyr Tyr Cys Gln Gln Ser Tyr Thr Ser Pro Leu Thr Phe Gly Gly Gly
85 90 95

Thr Lys Val Glu Ile Lys
100

<210> 205
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_896206_A3-2M2-H5_PWCgamma

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 205

Xaa 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 Phe Ser Asn Tyr
20 25 30

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 206
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_945554_A3-2M2-H5_Ck516

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (98)..(98)
<223> Xaa can be any naturally occurring amino acid

<400> 206

```
Xaa Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
1               5                   10                  15

Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser His Leu Ala Trp Tyr Gln
            20                  25                  30

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

Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
    50                  55                  60

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

Tyr Tyr Cys Gln Gln Pro Gly Ala Phe Gly Pro Gly Thr Arg Leu Asp
                85                  90                  95
```

Ile Xaa

<210> 207
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_897923_A3-2M3-C9_PWCgamma

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 207

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Ser Tyr
20 25 30

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

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

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

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

Ala Gly Asp Leu Leu Leu Trp Val Pro Glu Ala Thr Gly Ala Thr Ala
100 105 110

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

Ser Ser
130

<210> 208
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_949089_A3-2M3-C9_Ck516

<220>
<221> misc_feature

<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 208

Xaa Ser Pro Ser Phe Leu Tyr Ala Ser Val Gly Asp Arg Val Thr Ile
1 5 10 15

Thr Cys Arg Ala Ser Gln Thr Ile Ser Lys Tyr Leu Asn Trp Tyr His
20 25 30

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

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
50 55 60

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

Tyr Tyr Cys Gln Gln Ser Tyr Ser Ile Pro Arg Thr Phe Gly Gln Gly
85 90 95

Thr Lys Val Glu Ile Lys
100

<210> 209
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_992133_A3-2M3-E9-H-1_Resend_1146_Resend

<400> 209

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

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

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

Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg

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

<220>
<223> 1st_BASE_949097_A3-2M3-E9_Ck516

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 210

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

Thr Cys Arg Ala Ser Gln Ser Val Ser Asn Tyr Leu Asn Trp Tyr Gln
20 25 30

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

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
50 55 60

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

Tyr Tyr Cys Gln Gln Thr Tyr Ser Pro Pro Gln Asn Thr Phe Gly Gln
85 90 95

Gly Thr Lys Leu Glu Ile Lys
100

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

<220>
<223> 1st_BASE_988416_A3-2M3-F9-H-2_1146

<400> 211

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

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

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

```
Trp Ile Gly Glu Ile Tyr His Ser Gly Ser Ala Asp Tyr Asn Pro Ser
    50                  55                  60

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

Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Val Glu Val Met Ile Lys Phe Gly Gly Val Ile Arg Tyr
            100                 105                 110

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


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

<220>
<223>  1st_BASE_949101_A3-2M3-F9_Ck516


<220>
<221>  misc_feature
<222>  (1)..(1)
<223>  Xaa can be any naturally occurring amino acid

<400>  212

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

Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
            20                  25                  30

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

Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
    50                  55                  60

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

Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Pro Arg Tyr Thr Phe Gly
                85                  90                  95

Gln Gly Thr Lys Leu Glu Ile Lys
            100


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

<220>
<223> 1st_BASE_897935_A3-2M3-G3_PWCgamma

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 213

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

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

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

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

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

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

Phe Cys Thr Ser Thr Thr Leu Tyr Tyr Phe Val Ser Gly Arg Ala Lys
100 105 110

Asp Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 214
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_949103_A3-2M3-G3_Ck516

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 214

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

Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln
20 25 30

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

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
50 55 60

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

Tyr Tyr Cys Leu Gln Asp Tyr Ser Phe Pro Trp Thr Phe Gly Gln Gly
85 90 95

Thr Lys Val Glu Ile Lys
100

<210> 215
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> 1st_BASE_988406_A3-2M3-C2-H-3_1146

<400> 215

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr Ser Ser
20 25 30

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

Trp Ile Gly Asn Ile Tyr Tyr Ser Gly Asn Thr Asp Tyr Asn Pro Ser
50 55 60

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

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

Cys Ala Ser Gly Leu Gln Thr Trp Asp Val Thr Thr Gly Gly Ala Trp
100 105 110

Ala Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ala Ser
115 120 125

<210> 216

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

<220>
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<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 216

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

Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Phe Leu Ala Trp Tyr
20 25 30

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

Ile Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
50 55 60

Thr Asp Phe Ile Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
65 70 75 80

Val Tyr Tyr Cys Gln Gln Phe Gly Arg Thr Pro Pro Met Tyr Thr Phe
85 90 95

Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 217
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3_3M2_D3_H_2_1146; heavy chain; CDR1-IMGT

<400> 217

Gly Phe Asn Phe Gly Arg His Trp
1 5

<210> 218
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3_3M2_D3_H_2_1146; heavy chain; CDR2-IMGT

<400> 218

Ile Lys Glu Asp Gly Ser Ala Lys

1 5

<210> 219
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> A3_3M2_D3_H_2_1146; heavy chain; CDR3-IMGT

<400> 219

Ala Arg Glu Ser Cys Thr Gly Val Thr Cys Gln Gly Phe Leu Asp Phe
1 5 10 15

<210> 220
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M2-D3_Ck516; light chain; CDR1-IMGT

<400> 220

Gln Asn Ile Gly Ile Phe
1 5

<210> 221
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M2-D3_Ck516; light chain; CDR3-IMGT

<400> 221

Gln Gln Thr Tyr Ser Met Phe Tyr Ser
1 5

<210> 222
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M1-A5_PWCgamma; heavy chain; CDR1-IMGT

<400> 222

Asp Phe Thr Phe Ser Asp Tyr Asp
1 5

<210> 223
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M1-A5_PWCgamma; heavy chain; CDR2-IMGT

<400> 223

Ile Asn Ser Arg Gly Val Thr Lys
1 5

<210> 224
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M1-A5_PWCgamma; heavy chain; CDR3-IMGT

<400> 224

Ala Arg Gly Leu Arg Gly His Asp Tyr Gly Met Asp Val
1 5 10

<210> 225
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M1-A5_Ck516; light chain; CDR1-IMGT

<400> 225

Gln Ser Val Ser Ser Arg Phe
1 5

<210> 226
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M1-A5_Ck516; light chain; CDR3-IMGT

<400> 226

Leu Gln Tyr Gly Phe Ser Pro Pro Tyr Thr
1 5 10

<210> 227
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M2-G8_PWCgamma; heay chain; CDR1-IMGT

<400> 227

Gly Phe Ser Phe Ser Ser Tyr Glu
1 5

<210> 228
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M2-G8_PWCgamma; heavy chain; CDR2-IMGT

<400> 228

Ile Ser Ser Ser Gly Thr Thr Ile
1 5

<210> 229
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M2-G8_PWCgamma; heavy chain; CDR3-IMGT

<400> 229

Ala Arg Leu Leu Leu Leu Trp Leu Gly Glu Thr Thr Ala Met Asp Gly
1 5 10 15

Met Asp Val

<210> 230
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M2-G8_Ck516; light chain; CDR1-IMGT

<400> 230

Gln Lys Ile Asn Arg Phe
1 5

<210> 231
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M2-G8_Ck516; light chain; CDR3-IMGT

<400> 231

Gln Gln Ser Tyr Thr Ser Pro Leu Thr
1 5

<210> 232
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M2-H5_PWCgamma; heavy chain; CDR1-IMGT

<400> 232

Gly Phe Thr Phe Ser Asn Tyr Ala
1 5

<210> 233

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M2-H5_PWCgamma; heavy chain; CDR2-IMGT

<400> 233

Ile Tyr Asn Gly Gly Ser Ser Thr
1 5

<210> 234
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M2-H5_PWCgamma; heavy chain; CDR3-IMGT

<400> 234

Ala Lys Phe Leu Val Leu Pro Ala Ala Ala Ala Asp Tyr
1 5 10

<210> 235
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M2-H5_Ck516; light chain; CDR1-IMGT

<400> 235

Gln Gly Ile Ser Ser His
1 5

<210> 236
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M2-H5_Ck516; light chain; CDR3-IMGT

<400> 236

Gln Gln Pro Gly Ala
1 5

<210> 237
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-C2-H-3_1146; heavy chain; CDR1-IMGT

<400> 237

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

<210> 238
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-C2-H-3_1146; heavy chain; CDR2-IMGT

<400> 238

Ile Tyr Tyr Ser Gly Asn Thr
1 5

<210> 239
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-C2-H-3_1146; heavy chain; CDR3-IMGT

<400> 239

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

Ser Leu Asp Tyr
20

<210> 240
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-C2_Ck516; light chain; CDR1-IMGT

<400> 240

Gln Ser Val Ser Ser Ser Phe
1 5

<210> 241
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-C2_Ck516; light chain; CDR3-IMGT

<400> 241

Gln Gln Phe Gly Arg Thr Pro Pro Met Tyr Thr
1 5 10

<210> 242
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-C9_PWCgamma; heavy chain; CDR1-IMGT

<400> 242

Gly Phe Pro Phe Ser Ser Tyr Glu
1 5

<210> 243
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-C9_PWCgamma, heavy chain; CDR2-IMGT

<400> 243

Ile Ser Ser Thr Gly Ser Pro Ile
1 5

<210> 244
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-C9_PWCgamma; heavy chain; CDR3-IMGT

<400> 244

Ala Gly Asp Leu Leu Leu Trp Val Pro Glu Ala Thr Gly Ala Thr Ala
1 5 10 15

Gly Thr Gly Gly Leu Asp Val
20

<210> 245
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-C9_Ck516; light chain; CDR1-IMGT

<400> 245

Gln Thr Ile Ser Lys Tyr
1 5

<210> 246
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-C9_Ck516; light chain; CDR3-IMGT

<400> 246

Gln Gln Ser Tyr Ser Ile Pro Arg Thr
1 5

<210> 247

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-E9-H-1_Resend_1146_Resend; heavy chain; CDR1-IMGT

<400> 247

Gly Tyr Thr Phe Thr Asn Tyr Trp
1 5

<210> 248
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-E9-H-1_Resend_1146_Resend; heavy chain; CDR2-IMGT

<400> 248

Ile Tyr Pro Gly Asp Ser Glu Thr
1 5

<210> 249
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-E9-H-1_Resend_1146_Resend; heavy chain; CDR3-IMGT

<400> 249

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

Gly Met Asp Val
20

<210> 250
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-E9_Ck516; light chain; CDR1-IMGT

<400> 250

Gln Ser Val Ser Asn Tyr
1 5

<210> 251
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-E9_Ck516; light chain; CDR3-IMGT

<400> 251

Gln Gln Thr Tyr Ser Pro Pro Gln Asn Thr
1 5 10

<210> 252
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-F9-H-2_1146; heavy chain; CDR1-IMGT

<400> 252

Gly Gly Ser Ile Thr Ser Ser Asn Trp
1 5

<210> 253
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-F9-H-2_1146; heavy chain; CDR2-IMGT

<400> 253

Ile Tyr His Ser Gly Ser Ala
1 5

<210> 254
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-F9-H-2_1146; heavy chain; CDR3-IMGT

<400> 254

Ala Arg Val Glu Val Met Ile Lys Phe Gly Gly Val Ile Arg Tyr Phe
1 5 10 15

Asp Tyr

<210> 255
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-F9_Ck516, light chain; CDR1-IMGT

<400> 255

Gln Asp Ile Ser Asn Tyr
1 5

<210> 256
<211> 11
<212> PRT

<213> Artificial Sequence

<220>
<223> A3-2M3-F9_Ck516; light chain; CDR3-IMGT

<400> 256

Gln Gln Tyr Asp Asn Leu Pro Pro Arg Tyr Thr
1 5 10

<210> 257
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-G3_PWCgamma; heavy chain; CDR1-IMGT

<400> 257

Gly Phe Thr Phe Gly Asp Phe Ala
1 5

<210> 258
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-G3_PWCgamma; heavy chain; CDR2-IMGT

<400> 258

Ile Arg Ser Lys Gly Tyr Gly Gly Thr Thr
1 5 10

<210> 259
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-G3_PWCgamma; heavy chain; CDR3-IMGT

<400> 259

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

Gly Met Asp Val
20

<210> 260
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-G3_Ck516; light chain; CDR1-IMGT

<400> 260

Gln Gly Ile Arg Asn Asp

1 5

<210> 261
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-2M3-G3_Ck516; light chain; CDR3-IMGT

<400> 261

Leu Gln Asp Tyr Ser Phe Pro Trp Thr
1 5

<210> 262
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M1-B11_PWCgamma; heavy chain; CDR1-IMGT

<400> 262

Glu Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 263
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M1-B11_PWCgamma; heavy chain; CDR2-IMGT

<400> 263

Thr Ser Tyr Asp Gly Ile Asn Thr
1 5

<210> 264
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M1-B11_PWCgamma; heavy chain; CDR3-IMGT

<400> 264

Ala Arg Ala Pro Gln Glu His Asp Ser Ser Gly Asn Pro Leu Asp Tyr
1 5 10 15

Gly Met Asp Leu
20

<210> 265
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M1-B11_Ck516; light chain; CDR1-IMGT

<400> 265

Gln Gly Ile Ser Ser Ser
1 5

<210> 266
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M1-B11_Ck516; light chain; CDR3-IMGT

<400> 266

Gln Gln Leu Asn Ser Tyr Leu
1 5

<210> 267
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M1-D1_PWCgamma, heavy chain; CDR1-IMGT

<400> 267

Gly Phe Thr Phe Gly Asp Tyr Ala
1 5

<210> 268
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M1-D1_PWCgamma; heavy chain; CDR2-IMGT

<400> 268

Ile Arg Ser Lys Ala Tyr Gly Gly Thr Thr
1 5 10

<210> 269
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M1-D1_PWCgamma; heavy chain; CDR3-IMGT

<400> 269

Thr Arg Thr Arg Gly Ser Ser Trp Ser His Tyr Tyr Tyr Tyr Gly Met
1 5 10 15

Asp Val

<210> 270
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M1-D1_Ck516; light chain; CDR1-IMGT

<400> 270

Gln Ser Ile Ser Ser Tyr
1 5

<210> 271
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M1-D1_Ck516; light chain; CDR3-IMGT

<400> 271

Gln Gln Ser Tyr Ser Thr Pro Tyr Thr
1 5

<210> 272
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M2-F5_PWCgamma; heavy chain; CDR1-IMGT

<400> 272

Gly Gly Ser Ile Ser Thr Ser Asn Trp
1 5

<210> 273
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M2-F5_PWCgamma; heavy chain; CDR2-IMGT

<400> 273

Ile His His Ser Gly Asn Thr
1 5

<210> 274
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M2-F5_PWCgamma; heavy chain; CDR3-IMGT

<400> 274

Gly Arg Thr Gly Val Ile Ala Thr Pro Gly Gln Ile Asp Tyr

1 5 10

<210> 275
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M2-F5_Ck516; light chain; CDR1-IMGT

<400> 275

Gln Ser Ile Ser Arg Phe
1 5

<210> 276
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M2-F5_Ck516; light chain; CDR3-IMGT

<400> 276

Gln Gln Thr Tyr Ser Ser Pro Pro Thr
1 5

<210> 277
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M3-C4_PWCgamma; heavy chain; CDR1-IMGT

<400> 277

Gly Ile Thr Leu Arg Asn Tyr Glu
1 5

<210> 278
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M3-C4_PWCgamma; heavy chain; CDR2-IMGT

<400> 278

Ile Ser Ile Arg Gly Asn Thr Ile
1 5

<210> 279
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M3-C4_PWCgamma; heavy chain; CDR3-IMGT

<400> 279

Ala Arg Trp Ser Arg Gly Asn Ser Asp Ser Gly Gly Met Asp Val
1 5 10 15

<210> 280
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M3-C4_Ck516; light chain; CDR1-IMGT

<400> 280

Gln Ser Val Asn Ser Arg Phe
1 5

<210> 281
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M3-C4_Ck516; light chain; CDR3-IMGT

<400> 281

His Gln Tyr Gly Phe Ser Pro Pro Tyr Val
1 5 10

<210> 282
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M3-G3_PWCgamma; light chain; CDR1-IMGT

<400> 282

Gly Phe Thr Phe Thr Ser Ser Gly
1 5

<210> 283
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M3-G3_PWCgamma; heavy chain; CDR2-IMGT

<400> 283

Ile Val Val Gly Ser Asp Met Thr
1 5

<210> 284
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M3-G3_PWCgamma; heavy chain; CDR3-IMGT

<400> 284

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

<210> 285
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M3-G3_Ck516; light chain; CDR1-IMGT

<400> 285

Gln Gly Ile Tyr Ser Tyr
1 5

<210> 286
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> A3-3M3-G3_Ck516; light chain; CDR3-IMGT

<400> 286

Gln Gln Leu Asn Gly Tyr Pro Ser
1 5

<210> 287
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 1D-H4L1; 10/63_1D4_001.ab1; heavy chain; CDR1-IMGT

<400> 287

Gly Phe Ser Leu Ser Thr Ser Gly Val Asn
1 5 10

<210> 288
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 1D-H4L1; 10/63_1D4_001.ab1; heavy chain; CDR2-IMGT

<400> 288

Leu Tyr Trp Asp Asp Asp Arg
1 5

<210> 289
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 1D-H4L1; 10/63_1D4_001.ab1; heavy chain; CDR3-IMGT

<400> 289

Ala His Arg Arg Trp Glu Asp Ser Thr Phe Gln His
1 5 10

<210> 290
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 1D-H4L1; 10/63_1D-1_055; light chain; CDR1-IMGT

<400> 290

Gln Ser Val Asn Ser Asn
1 5

<210> 291
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 1D-H4L1; 10/63_1D-1_055; light chain; CDR3-IMGT

<400> 291

Gln His Tyr His Asn Trp Gly Thr
1 5

<210> 292
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 1E-H3L1; 10/63_1E3_061; heavy chain; CDR1-IMGT

<400> 292

Gly Tyr Thr Phe Pro Thr Tyr Ala
1 5

<210> 293
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 1E-H3L1; 10/63_1E3_061; heavy chain; CDR2-IMGT

<400> 293

Ile Asn Thr Asn Thr Gly Asn Pro
1 5

<210> 294
<211> 15
<212> PRT

<213> Artificial Sequence

<220>
<223> 1E-H3L1; 10/63_1E3_061; heavy chain; CDR3-IMGT

<400> 294

Ala Arg Gly Arg Gly Gly Phe Ala Ala Thr Ala Gly Thr Asp Tyr
1 5 10 15

<210> 295
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 1E-H3L1; 10/63_1E-1_053; light chain; CDR1-IMGT

<400> 295

Gln Pro Ile Ser Ser Trp
1 5

<210> 296
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 1E-H3L1; 10/63_1E-1_053; light chain; CDR3-IMGT

<400> 296

Gln Gln Ala Asn Ser Phe Pro Tyr Thr
1 5

<210> 297
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2A-H3L1; 10/63_2A5_014; heavy chain; CDR1-IMGT

<400> 297

Gly Gly Ser Phe Asn Asn Tyr Ala
1 5

<210> 298
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2A-H3L1; 10/63_2A5_014; heavy chain; CDR2-IMGT

<400> 298

Ile Ile Thr Val Phe Gly Arg Gly
1 5

<210> 299

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

<220>
<223> 2A-H3L1; 10/63_2A5_014; heavy chain; CDR3-IMGT

<400> 299

Val Arg Asp Tyr Thr Phe Val Arg Gly Val Ala Ser Trp Glu Tyr
1 5 10 15

<210> 300
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 2A-H3L1; 10/63_2A-4_049; light chain; CDR1-IMGT

<400> 300

Gln Pro Ile Ser Ser Trp
1 5

<210> 301
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 2A-H3L1; 10/63_2A-4_049; light chain; CDR3-IMGT

<400> 301

Gln Gln Ala Asn Ser Phe Pro Tyr Thr
1 5

<210> 302
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C-H3L2; 10/63_2C3_006.ab1; heavy chain; CDR1-IMGT

<400> 302

Gly Ala Ser Ile Gly Ser Tyr Thr
1 5

<210> 303
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C-H3L2; 10/63_2C3_006.ab1; heavy chain; CDR2-IMGT

<400> 303

Ile Asn Pro Ile Phe Gly Thr Val
1 5

<210> 304
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C-H3L2; 10/63_2C3_006.ab1; heavy chain; CDR3-IMGT

<400> 304

Ala Arg Ser Gln Arg His Ile Leu Thr Gly His Tyr Thr Asp Tyr
1 5 10 15

<210> 305
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C-H3L2; 10/63_2C-2_058; light chain; CDR1-IMGT

<400> 305

Gln Asp Ile Lys Asn Tyr
1 5

<210> 306
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C-H3L2; 10/63_2C-2_058; light chain; CDR3-IMGT

<400> 306

Gln His Tyr Glu Asn Leu Pro Ala Leu Thr
1 5 10

<210> 307
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2E-H2L2; 10/63_2E2_004; heavy chain; CDR1-IMGT

<400> 307

Gly Phe Thr Phe Ser Asn Tyr Gly
1 5

<210> 308
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2E-H2L2; 10/63_2E2_004; heavy chain; CDR2-IMGT

<400> 308

Ile Ser Tyr Asp Ala Lys Lys Gln

1 5

<210> 309
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 2E-H2L2; 10/63_2E2_004; heavy chain; CDR3-IMGT

<400> 309

Ala Lys Leu Gln Arg Pro Asp Ser Thr Val Trp Pro Phe Asp Gln
1 5 10 15

<210> 310
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 2E-H2L2; 10/63_2E-2_050; light chain; CDR1-IMGT

<400> 310

Gln Ser Ile Ser Met Trp
1 5

<210> 311
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2E-H2L2; 10/63_2E-2_050; light chain; CDR3-IMGT

<400> 311

Gln Gln Tyr Lys Thr Ser Trp Thr
1 5

<210> 312
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2F-H1L1; 10/63_2F1_031; heavy chain; CDR1-IMGT

<400> 312

Gly Phe Thr Phe Asn Asn Phe Glu
1 5

<210> 313
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2F-H1L1; 10/63_2F1_031; heavy chain; CDR2-IMGT

<400> 313

Ile Ser Val Ser Asp Gly Asn Thr
1 5

<210> 314
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 2F-H1L1; 10/63_2F1_031; heavy chain; CDR3-IMGT

<400> 314

Ala Asn Val Leu Gly Tyr Cys Thr Pro Thr Thr Cys Tyr Glu Asp His
1 5 10 15

<210> 315
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 2F-H1L1; 10/63_2F1_059; light chain; CDR1-IMGT

<400> 315

Gln Gly Ile Arg Asn Asp
1 5

<210> 316
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 2F-H1L1; 10/63_2F1_059; light chain; CDR3-IMGT

<400> 316

Leu Gln His Asn Ser Phe Pro Gly Ser
1 5

<210> 317
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2G-H2L1; 10/63_2G2_027.ab1; heavy chain; CDR1-IMGT

<400> 317

Gly Tyr Thr Phe Thr Thr Tyr Trp
1 5

<210> 318
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2G-H2L1; 10/63_2G2_027.ab1; heavy chain; CDR2-IMGT

<400> 318

Ile Tyr Pro Ser Asp Ser Asp Thr
1 5

<210> 319
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 2G-H2L1; 10/63_2G2_027.ab1; heavy chain; CDR3-IMGT

<400> 319

Ala Arg Pro Asp Asp Ser Ser Gly Leu Glu Ala Phe Asp Ile
1 5 10

<210> 320
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 2G-H2L1; 10/63_2G-1_079.ab1; light chain; CDR1-IMGT

<400> 320

Gln Pro Ile Ser Ser Trp
1 5

<210> 321
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 2G-H2L1; 10/63_2G-1_079.ab1; light chain; CDR3-IMGT

<400> 321

Gln Gln Ala Asn Ser Phe Pro Tyr Thr
1 5

<210> 322
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D-H2L2; 10/63_3D; heavy chain; CDR1-IMGT

<400> 322

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 323
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D-H2L2; 10/63_3D; heavy chain; CDR2-IMGT

<400> 323

Ile Ala Tyr Asp Gly Ile Asn Lys
1 5

<210> 324
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D-H2L2; 10/63_3D; heavy chain; CDR3-IMGT

<400> 324

Ala Arg Glu Tyr Cys Ser Ser Thr Thr Cys Ile Asn Ser Phe Leu Thr
1 5 10 15

Pro Asp Tyr

<210> 325
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D-H2L2; 10/63_3D-2_071.ab1; light chain; CDR1-IMGT

<400> 325

Gln Pro Ile Ser Ser Trp
1 5

<210> 326
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D-H2L2; 10/63_3D-2_071.ab1; light chain; CDR3-IMGT

<400> 326

Gln Gln Ala Asn Ser Phe Pro Tyr Thr
1 5

<210> 327
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3E-H1L2; 10/63_3E1_030; heavy chain; CDR1-IMGT

<400> 327

Gly Phe Thr Phe Ser Thr Tyr Trp
1 5

<210> 328
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3E-H1L2; 10/63_3E1_030; heavy chain; CDR2-IMGT

<400> 328

Ile Lys Ala Asp Gly Arg Gln Glu
1 5

<210> 329
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 3E-H1L2; 10/63_3E1_030; heavy chain; CDR3-IMGT

<400> 329

Val Arg Asp Val Ser Ser Tyr Ser Ile Ile Trp Ser Asp Ala Phe Glu
1 5 10 15

Ile

<210> 330
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 3E-H1L2; 10/63_3E-2_069; light chain; CDR1-IMGT

<400> 330

Gln Gly Ile Arg Asn Asp
1 5

<210> 331
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 3E-H1L2; 10/63_3E-2_069; light chain; CDR3-IMGT

<400> 331

Val His His Asn Asp Tyr Pro Arg Thr
1 5

<210> 332
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F-H1L2; 10/63_3F1_026; heavy chain; CDR1-IMGT

<400> 332

Gly Gly Thr Phe Ser Thr His Ser
1 5

<210> 333
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F-H1L2; 10/63_3F1_026; heavy chain; CDR2-IMGT

<400> 333

Asn Ile Pro Ile Phe Gly Lys Ala
1 5

<210> 334
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F-H1L2; 10/63_3F1_026; heavy chain; CDR3-IMGT

<400> 334

Ala Arg Phe Phe Val Lys Tyr Ser Gly Ser His Tyr Tyr Phe Asp Ser
1 5 10 15

<210> 335
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F-H1L2; 10/63_3F-2_065; light chain; CDR1-IMGT

<400> 335

Gln Pro Ile Ser Ser Trp
1 5

<210> 336
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F-H1L2; 10/63_3F-2_065; light chain; CDR3-IMGT

<400> 336

Gln Gln Ala Asn Ser Phe Pro Tyr Thr
1 5

<210> 337
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 4F-H6L1; 10/63_4F6_020.ab1; heavy chain; CDR1-IMGT

<400> 337

Gly Phe Thr Phe Ser Asn Ala Trp
1 5

<210> 338
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4F-H6L1; 10/63_4F6_020.ab1; heavy chain; CDR2-IMGT

<400> 338

Ile Lys Asn Lys Ile Asp Gly Glu Thr Thr
1 5 10

<210> 339
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 4F-H6L1; 10/63_4F6_020.ab1; heavy chain; CDR3-IMGT

<400> 339

Thr Ile Tyr Phe Tyr Asp Arg Ser Gly Tyr Phe Phe Asp His
1 5 10

<210> 340
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 4F-H6L1; 10/63_4F-1_076; light chain; CDR1-IMGT

<400> 340

Gln Ser Val Ser Ser Tyr
1 5

<210> 341
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 4F-H6L1; 10/63_4F-1_076; light chain; CDR3-IMGT

<400> 341

Leu Gln Arg Gly Lys Trp Pro Ser
1 5

<210> 342
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> 5A-H6L1; 10/63_5A6_045.ab1; heavy chain; CDR1-IMGT

<400> 342

Gly Phe Thr Phe Ser Asp Tyr Ala
1 5

<210> 343
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5A-H6L1; 10/63_5A6_045.ab1; heavy chain; CDR2-IMGT

<400> 343

Leu Ser Glu Ser Gly His Asn Thr
1 5

<210> 344
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> 5A-H6L1; 10/63_5A6_045.ab1; heavy chain; CDR3-IMGT

<400> 344

Ala Arg Cys Trp Arg Gly Tyr Asp Pro Leu Thr Gly Tyr Tyr Thr Gly
1 5 10 15

Tyr Tyr Phe Asp Tyr
20

<210> 345
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 5A-H6L1; 10/63_5A-1_074; light chain; CDR1-IMGT

<400> 345

Gln Asp Ile Ser Asn Tyr
1 5

<210> 346
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 5A-H6L1; 10/63_5A-1_074; light chain; CDR3-IMGT

<400> 346

Gln Lys Tyr Asn Asn Ala Pro Val Thr

1 5

<210> 347
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 5B-H1L1; 10/63_5B1_043; heavy chain; CDR1-IMGT

<400> 347

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

<210> 348
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 5B-H1L1; 10/63_5B1_043; heavy chain; CDR2-IMGT

<400> 348

Leu Ala Tyr Ser Gly Asp Thr
1 5

<210> 349
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 5B-H1L1; 10/63_5B1_043; heavy chain; CDR3-IMGT

<400> 349

Ala Arg His His Ser Ser Gly Asn Ala Leu Asp Tyr
1 5 10

<210> 350
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 5B-H1L1; 10/63_5B1_053; light chain; CDR1-IMGT

<400> 350

Gln Gly Ile Ser Ser Tyr
1 5

<210> 351
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 5B-H1L1; 10/63_5B1_053; light chain; CDR3-IMGT

<400> 351

Gln Gln Leu Asn Asn Tyr Val Leu Thr
1 5

<210> 352
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C-H2L1; 10/63_5C2_041; heavy chain; CDR1-IMGT

<400> 352

Gly Gly Thr Phe Asn Asn Tyr Ala
1 5

<210> 353
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C-H2L1; 10/63_5C2_041; heavy chain; CDR2-IMGT

<400> 353

Ile Asn Pro Leu Phe Arg Thr Val
1 5

<210> 354
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C-H2L1; 10/63_5C2_041; heavy chain; CDR3-IMGT

<400> 354

Ala Gly Ala Tyr Cys Ser Ala Thr Ser Cys Ser Ser Gly Gln Trp Leu
1 5 10 15

Val Tyr

<210> 355
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C-H2L1; 10/63_5C1_049.ab1; light chain; CDR1-IMGT

<400> 355

Gln Ser Val Phe His Ser Ser Asn Asn Lys Asn Tyr
1 5 10

<210> 356
<211> 11
<212> PRT

<213> Artificial Sequence

<220>
<223> 5C-H2L1; 10/63_5C1_049.ab1; light chain; CDR3-IMGT

<400> 356

Gln Gln Tyr Tyr Ser Ser Pro Pro Val Phe Thr
1 5 10

<210> 357
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D-H1L2; 10/63_5D1_037; heavy chain; CDR1-IMGT

<400> 357

Gly Gly Thr Phe Ser Ser Asp Ser
1 5

<210> 358
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D-H1L2; 10/63_5D1_037; heavy chain; CDR2-IMGT

<400> 358

Ile Ile Pro Ile Phe Ser Arg Ala
1 5

<210> 359
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D-H1L2; 10/63_5D1_037; heavy chain; CDR3-IMGT

<400> 359

Ala Arg Thr Pro Val Thr Gly Pro Asp Leu Asp Tyr
1 5 10

<210> 360
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D-H1L2; 10/63_5D-2_070.ab1; light chain; CDR1-IMGT

<400> 360

Glu Ser Ile Ser Thr Asn
1 5

<210> 361

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

<220>
<223> 5D-H1L2; 10/63_5D-2_070.ab1; light chain; CDR3-IMGT

<400> 361

Gln Gln Thr Tyr Asn Thr Pro Arg Thr
1 5

<210> 362
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 5H-H3L1; 10/63_5H3_044; heavy chain; CDR1-IMGT

<400> 362

Gly Gly Ser Ile Asn Asn Ser Asn Tyr Tyr
1 5 10

<210> 363
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 5H-H3L1; 10/63_5H3_044; heavy chain; CDR2-IMGT

<400> 363

Ile Tyr Phe Ser Gly Thr Thr
1 5

<210> 364
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 5H-H3L1; 10/63_5H3_044; heavy chain; CDR3-IMGT

<400> 364

Val Arg Gln Met Asn Tyr Tyr His Leu Gly Ser Ser Val Gly Phe Asp
1 5 10 15

Pro

<210> 365
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 5H-H3L1; 10/63_5H-1_095; light chain; CDR1-IMGT

<400> 365

Gln Ser Val Ser Ser Asn
1 5

<210> 366
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 5H-H3L1; 10/63_5H-1_095; light chain; CDR3-IMGT

<400> 366

Gln Gln Tyr Asn Asp Trp Leu Trp Thr
1 5

<210> 367
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 6C-H8L1; 10/63_6C8_036; heavy chain; CDR1-IMGT

<400> 367

Gly Asp Thr Leu Asn Thr Tyr Thr
1 5

<210> 368
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 6C-H8L1; 10/63_6C8_036; heavy chain; CDR2-IMGT

<400> 368

Ile Ile His Pro Phe Gly Thr Glu
1 5

<210> 369
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 6C-H8L1; 10/63_6C8_036; heavy chain; CDR3-IMGT

<400> 369

Ala Arg His His Arg His Ile Leu Thr Gly Glu Arg Thr Asp Tyr
1 5 10 15

<210> 370
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 6C-H8L1; 10/63_6C-1_091; light chain; CDR1-IMGT

<400> 370

Gln Asp Ile Arg Asn Ser
1 5

<210> 371
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 6C-H8L1; 10/63_6C-1_091; light chain; CDR3-IMGT

<400> 371

Gln His Tyr Asp Asn Leu Pro Leu Phe Thr
1 5 10

<210> 372
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 6E-H6L1; 10/63_6E6_034; heavy chain; CDR1-IMGT

<400> 372

Gly Gly Thr Leu Asn Ser Tyr Thr
1 5

<210> 373
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 6E-H6L1; 10/63_6E6_034; heavy chain; CDR2-IMGT

<400> 373

Ile Asn Pro Ile Phe Gly Thr Thr
1 5

<210> 374
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 6E-H6L1; 10/63_6E6_034; heavy chain; CDR3-IMGT

<400> 374

Ala Arg Gly Gly His His Ile Leu Thr Gly Arg Tyr Ile Asp Asp
1 5 10 15

<210> 375
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 6E-H6L1; 10/63_6E1_058; light chain; CDR1-IMGT

<400> 375

Gln Asp Ile Ser Asn Tyr
1 5

<210> 376
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 6E-H6L1; 10/63_6E1_058; light chain; CDR3-IMGT

<400> 376

Gln Gln Tyr Asp Asn Leu Pro Arg His Thr
1 5 10

<210> 377
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 7E-H1L1; 10/63_7E1_061; heavy chain; CDR1-IMGT

<400> 377

Gly Phe Asn Phe Asn Glu Tyr Gly
1 5

<210> 378
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 7E-H1L1; 10/63_7E1_061; heavy chain; CDR2-IMGT

<400> 378

Val Ala Tyr Asp Gly Ile Asn Lys
1 5

<210> 379
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> 7E-H1L1; 10/63_7E1_061; heavy chain; CDR3-IMGT

<400> 379

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

Pro Phe Asp Ile
20

<210> 380
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 7E-H1L1; 10/63_7E-1_087; light chain; CDR1-IMGT

<400> 380

Gln Ser Val Ser Ser Asn
1 5

<210> 381
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 7E-H1L1; 10/63_7E-1_087; light chain; CDR3-IMGT

<400> 381

Gln Gln Tyr His Asp Trp Pro Pro Tyr Thr
1 5 10

<210> 382
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 7G-H1L1; 10/63_7G1_055; heavy chain; CDR1-IMGT

<400> 382

Gly Phe Thr Phe Ser Asn Ala Trp
1 5

<210> 383
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 7G-H1L1; 10/63_7G1_055; heavy chain; CDR2-IMGT

<400> 383

Ile Lys Asn Lys Ile Asp Gly Glu Thr Thr
1 5 10

<210> 384
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 7G-H1L1; 10/63_7G1_055; heavy chain; CDR3-IMGT

<400> 384

Thr Ile Tyr Phe Tyr Asp Arg Ser Gly Tyr Phe Phe Asp His

1 5 10

<210> 385
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 7G-H1L1; 10/63_7G-1_081; light chain; CDR1-IMGT

<400> 385

Gln Ser Val Ser Ser Tyr
1 5

<210> 386
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 7G-H1L1; 10/63_7G-1_081; light chain; CDR3-IMGT

<400> 386

Leu Gln Arg Gly Lys Trp Pro Ser
1 5

<210> 387
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 7H-H1L1; 10/63_7H-1_060; heavy chain; CDR1-IMGT

<400> 387

Gly Phe Thr Phe Ser Asn Ala Trp
1 5

<210> 388
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 7H-H1L1; 10/63_7H-1_060; heavy chain; CDR2-IMGT

<400> 388

Ile Lys Asn Lys Ile Asp Gly Glu Thr Thr
1 5 10

<210> 389
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 7H-H1L1; 10/63_7H-1_060; heavy chain; CDR2-IMGT

<400> 389

Thr Ile Tyr Phe Tyr Asp Arg Ser Gly Tyr Phe Phe Asp His
1 5 10

<210> 390
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 7H-H1L1; 10/63_7H-1_038; light chain; CDR1-IMGT

<400> 390

Gln Ser Val Ser Ser Tyr
1 5

<210> 391
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 7H-H1L1; 10/63_7H-1_038; light chain; CDR3-IMGT

<400> 391

Leu Gln Arg Gly Lys Trp Pro Ser
1 5

<210> 392
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 8F-H1L1; 10/63_8F-1_036; light chain; CDR1-IMGT

<400> 392

Gly Gly Ser Ile Ser Ser Ser Ser Tyr Tyr
1 5 10

<210> 393
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 8F-H1L1; 10/63_8F-1_036; light chain; CDR2-IMGT

<400> 393

Ile Tyr Tyr Thr Gly Thr Thr
1 5

<210> 394
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> 8F-H1L1; 10/63_8F-1_036; light chain; CDR3-IMGT

<400> 394

Ala Arg Gln Ala Val Phe Ala Glu Ala Thr Gly Thr Thr Ile Gly Ala
1 5 10 15

Ile Asp Tyr

<210> 395
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 8F-H1L1; 10/63_8F-1_036; light chain; CDR1-IMGT

<400> 395

Gln Ser Phe Asn Asn Trp
1 5

<210> 396
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 8F-H1L1; 10/63_8F-1_036; light chain; CDR3-IMGT

<400> 396

Gln Gln Ala Ser Ser Phe Pro Trp Thr
1 5

<210> 397
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 11E-H1L1; 10/50_11E1; heavy chain; CDR1-IMGT

<400> 397

Gly Phe Thr Phe Ser Thr Tyr Pro
1 5

<210> 398
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 11E-H1L1; 10/50_11E1; heavy chain; CDR2-IMGT

<400> 398

Ile Phe Asn Gly Gly Ser Ser Thr
1 5

<210> 399

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

<220>
<223> 11E-H1L1; 10/50_11E1; heavy chain; CDR3-IMGT

<400> 399

Ala Lys Phe Ala Ala Pro Pro Ser Gly Trp Cys Asp Tyr
1 5 10

<210> 400
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 11E-H1L1; 10/50_11E1; light chain; CDR1-IMGT

<400> 400

Gln Ser Val Ser Asn Trp
1 5

<210> 401
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 11E-H1L1; 10/50_11E1; light chain; CDR3-IMGT

<400> 401

Gln Gln Ser Gly Thr
1 5

<210> 402
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 1B-H1L1; 10/50_1B; heavy chain; CDR1-IMGT

<400> 402

Gly Asp Ser Ile Thr Asn Tyr Tyr
1 5

<210> 403
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 1B-H1L1; 10/50_1B; heavy chain; CDR2-IMGT

<400> 403

Leu Tyr Tyr Thr Gly Gly Thr
1 5

<210> 404
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 1B-H1L1; 10/50_1B; heavy chain; CDR3-IMGT

<400> 404

Ala Arg Val Thr Ser Leu Ser Gly Ser Glu Val Tyr Gly Met Asp Val
1 5 10 15

<210> 405
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 1B-H1L1; 10/50_1B1; light chain; CDR1-IMGT

<400> 405

Gln Asp Ile Ser Asn Ser
1 5

<210> 406
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 1B-H1L1; 10/50_1B1; light chain; CDR3-IMGT

<400> 406

Gln Gln Tyr Asp Ser Ile Pro Ile Thr
1 5

<210> 407
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 1D-H8L1; 10/50_1D8; Heavy Chain; CDR1-IMGT

<400> 407

Gly Phe Thr Phe Ala Pro Phe Ser
1 5

<210> 408
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 1D-H8L1; 10/50_1D8; Heavy Chain; CDR2-IMGT

<400> 408

Ile Thr Pro Ser Ser Asn Tyr Ile

1 5

<210> 409
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 1D-H8L1; 10/50_1D8; Heavy Chain; CDR3-IMGT

<400> 409

Ala Arg Asp Pro Ser Gly Thr Tyr Asp Tyr Asn Tyr Tyr Ala Met Asp
1 5 10 15

Val

<210> 410
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 1D-H8L1; 10/50_1D1; light chain; CDR1-IMGT

<400> 410

Gln Thr Val Gly Ser Ser Tyr
1 5

<210> 411
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 1D-H8L1; 10/50_1D1; light chain; CDR3-IMGT

<400> 411

Gln Gln Tyr Gly Gly Ser Pro Pro Ile Thr
1 5 10

<210> 412
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2F-H1L3; 10/50_2F1; heavy chain; CDR1-IMGT

<400> 412

Gly Tyr Pro Phe Ser Ser His Gly
1 5

<210> 413
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2F-H1L3; 10/50_2F1; heavy chain; CDR2-IMGT

<400> 413

Thr Thr Ala Tyr Asn Gly Glu Thr
1 5

<210> 414
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 2F-H1L3; 10/50_2F1; heavy chain; CDR3-IMGT

<400> 414

Tyr Ser Ser Gly Pro Arg Trp Gly His Phe Asp Ile
1 5 10

<210> 415
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 2F-H1L3; 10/50_2F3; light chain; CDR1-IMGT

<400> 415

Ala Ser Gln Ser Val Asp
1 5

<210> 416
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 2F-H1L3; 10/50_2F3; light chain; CDR3-IMGT

<400> 416

His Gln Tyr Asp Ser Ser Pro Trp Thr
1 5

<210> 417
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3H-H1L1; 10/50_3H1; heavy chain; CDR1-IMGT

<400> 417

Gly Phe Asn Phe Gly Asp Tyr Val
1 5

<210> 418
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> 3H-H1L1; 10/50_3H1; heavy chain; CDR2-IMGT

<400> 418

Ile Tyr Asn Gly Gly Ser Ser Thr
1 5

<210> 419
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> 3H-H1L1; 10/50_3H1; heavy chain; CDR3-IMGT

<400> 419

Ala Lys Asp Arg Gln Ser Leu His Asp Pro Gly Ser Gly Ser Tyr Val
1 5 10 15

Ala Leu Asp His
20

<210> 420
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 3H-H1L1; 10/50_3H1; light chain; CDR1-IMGT

<400> 420

Gln Ser Ile Ser Gly Ser
1 5

<210> 421
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 3H-H1L1; 10/50_3H1; light chain; CDR3-IMGT

<400> 421

Gln Gln Gly Ser Thr
1 5

<210> 422
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B-H2L1; 10/50_4B2; heavy chain; CDR1-IMGT

<400> 422

Gly Gly Ser Leu Ser Ser Asp Gly His Ser

1 5 10

<210> 423
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B-H2L1; 10/50_4B2; heavy chain; CDR2-IMGT

<400> 423

Ile Tyr Tyr Thr Gly Thr Thr
1 5

<210> 424
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B-H2L1; 10/50_4B2; heavy chain; CDR3-IMGT

<400> 424

Ala Ala Trp Asn Ala Gly Pro Ser Tyr Tyr Phe His Tyr
1 5 10

<210> 425
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B-H2L1; 10/50_4B1; light chain; CDR1-IMGT

<400> 425

Gln Ser Val Ser Asn Asn
1 5

<210> 426
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B-H2L1; 10/50_4B1; light chain; CDR3-IMGT

<400> 426

Gln Gln Tyr Glu Ser Trp Trp Thr
1 5

<210> 427
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5A-H1L1; 10/50_5A1: heavy chain; CDR1-IMGT

<400> 427

Asp Gly Ser Phe Ser Gly Phe Ser
1 5

<210> 428
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 5A-H1L1; 10/50_5A1: heavy chain; CDR2-IMGT

<400> 428

Ile Asn His Ser Gly Ser Thr
1 5

<210> 429
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> 5A-H1L1; 10/50_5A1: heavy chain; CDR3-IMGT

<400> 429

Ala Leu Ser Leu Gln Thr Leu Val Arg Gly Leu Val Tyr Ile Asn Phe
1 5 10 15

Asp Tyr

<210> 430
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 5A-H1L1; 10/50_5A1; light chain; CDR1-IMGT

<400> 430

Gln Ala Ile Thr Thr Tyr
1 5

<210> 431
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 5A-H1L1; 10/50_5A1; light chain; CDR3-IMGT

<400> 431

Gln Gln Ser Tyr Asn Leu Pro Arg Thr
1 5

<210> 432
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> 5C-H6L1; 10/50_5C6; heavy chain; CDR1-IMGT

<400> 432

Gly Tyr Thr Phe Ser Ser Tyr Tyr
1 5

<210> 433
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C-H6L1; 10/50_5C6; heavy chain; CDR2-IMGT

<400> 433

Ile Asn Pro Arg Gly Gly Ser Ala
1 5

<210> 434
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C-H6L1; 10/50_5C6; heavy chain; CDR3-IMGT

<400> 434

Ala Arg Ala Gly Val Ala Leu Phe Tyr Asp Ser Ser Gly Tyr Asp Pro
1 5 10 15

Thr Pro Tyr Asp Ala Phe Glu Val
20

<210> 435
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C-H6L1; 10/50_5C1; light chain; CDR1-IMGT

<400> 435

Gln Ser Val Arg Ser Tyr
1 5

<210> 436
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C-H6L1; 10/50_5C1; light chain; CDR3-IMGT

<400> 436

His Gln Tyr Asn His Trp Pro Arg Thr

1 5

<210> 437
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D-H6L2; 10/50_5D6; heavy chain; CDR1-IMGT

<400> 437

Gly Phe Thr Phe Thr Thr His Ala
1 5

<210> 438
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D-H6L2; 10/50_5D6; heavy chain; CDR2-IMGT

<400> 438

Ile Ser Ala Ser Gly Asp Gly Thr
1 5

<210> 439
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D-H6L2; 10/50_5D6; heavy chain; CDR3-IMGT

<400> 439

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

<210> 440
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D-H6L2; 10/50_5D2; light chain; CDR1-IMGT

<400> 440

Gln Ala Val Gly Ser Leu
1 5

<210> 441
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D-H6L2; 10/50_5D2; light chain; CDR3-IMGT

<400> 441

Gln Gln Ala Phe Ser Phe Pro Trp Thr
1 5

<210> 442
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<212> PRT
<213> Artificial Sequence

<220>
<223> 6B-H1L2; 10/50_6B1; heavy chain; CDR1-IMGT

<400> 442

Gly Tyr Thr Phe Ala Asn Asn Tyr
1 5

<210> 443
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 6B-H1L2; 10/50_6B1; heavy chain; CDR2-IMGT

<400> 443

Ile Asn Pro Arg Gly Gly Ser Ala
1 5

<210> 444
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 6B-H1L2; 10/50_6B1; heavy chain; CDR3-IMGT

<400> 444

Ala Arg Gly Gly Arg Ala Tyr Tyr Tyr Asp Ser Tyr Thr Thr Pro Arg
1 5 10 15

Asp Gly Glu Ser Trp Trp Phe Asp Pro
20 25

<210> 445
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 6B-H1L2; 10/50_6B2; light chain; CDR1-IMGT

<400> 445

Gln Asp Ile Arg Lys Tyr
1 5

<210> 446
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> 6B-H1L2; 10/50_6B2; light chain; CDR3-IMGT

<400> 446

Gln His Ser Asp Tyr Leu Pro Ile Thr
1 5

<210> 447
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 6D-H3L1; 10/50_6D3; heavy chain; CDR1-IMGT

<400> 447

Gly Tyr Ser Phe Thr Ser Asn Tyr
1 5

<210> 448
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 6D-H3L1; 10/50_6D3; heavy chain; CDR2-IMGT

<400> 448

Ile Asn Pro Arg Gly Gly Ser Thr
1 5

<210> 449
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> 6D-H3L1; 10/50_6D3; heavy chain; CDR3-IMGT

<400> 449

Ala Arg Ala Gly Pro Ala Leu Tyr Tyr Asp Ser Ser Gly Tyr Asp Pro
1 5 10 15

Thr Thr Tyr Asp Ser Phe Glu Val
20

<210> 450
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 6D-H3L1; 10/50_6D1; light chain; CDR1-IMGT

<400> 450

Gln Gly Val Arg Ser Tyr

1 5

<210> 451
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 6D-H3L1; 10/50_6D1; light chain; CDR3-IMGT

<400> 451

Gln Gln Tyr Asn His Trp Pro Arg Thr
1 5

<210> 452
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 6E-H1L1; 10/50_6E1; heavy chain; CDR1-IMGT

<400> 452

Glu Phe Ser Phe Ser Thr Tyr Ala
1 5

<210> 453
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 6E-H1L1; 10/50_6E1; heavy chain; CDR2-IMGT

<400> 453

Ile Tyr Thr Gly Gly Gly Ser Thr
1 5

<210> 454
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 6E-H1L1; 10/50_6E1; heavy chain; CDR3-IMGT

<400> 454

Ala Gly Gly Gly Ile Val Ser Thr Met Gly Ala Phe Gly Phe
1 5 10

<210> 455
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 6E-H1L1; 10/50_6E1; light chain; CDR1-IMGT

<400> 455

Gln Glu Phe Ser Ser Tyr
1 5

<210> 456
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 6E-H1L1; 10/50_6E1; light chain; CDR3-IMGT

<400> 456

Gln Gln Thr Gly Thr
1 5

<210> 457
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 7A-H1L1; 10/50_7A1; heavy chain; CDR1-IMGT

<400> 457

Gly Phe Thr Phe Ser Ser Tyr Glu
1 5

<210> 458
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 7A-H1L1; 10/50_7A1; heavy chain; CDR2-IMGT

<400> 458

Ile Ser Arg Ser Gly Thr Ala Thr
1 5

<210> 459
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 7A-H1L1; 10/50_7A1; heavy chain; CDR3-IMGT

<400> 459

Ala Gly Glu Gly Tyr Phe Gly Ser Ala Ala Ile Asn Tyr Phe Ala Phe
1 5 10 15

<210> 460
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 7A-H1L1; 10/50_7A1; light chain; CDR1-IMGT

<400> 460

Gln Thr Ile Gly Thr Tyr
1 5

<210> 461
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 7A-H1L1; 10/50_7A1; light chain; CDR3-IMGT

<400> 461

Leu Gln Thr Tyr Ser Ser Leu Tyr Thr
1 5

<210> 462
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 7C-H3L1; 10/50_7C3; heavy chain; CDR1-IMGT

<400> 462

Gly Tyr Thr Phe Ser Asn Tyr Tyr
1 5

<210> 463
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 7C-H3L1; 10/50_7C3; heavy chain; CDR2-IMGT

<400> 463

Ile Asn Pro Arg Gly Gly Ser Ala
1 5

<210> 464
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 7C-H3L1; 10/50_7C3; heavy chain; CDR3-IMGT

<400> 464

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

Asp Gly Gln Ser Trp Trp Phe Asp Pro
20 25

<210> 465

<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 7C-H3L1; 10/50_7C1; light chain; CDR1-IMGT

<400> 465

Gln Asp Ile Arg Asn Phe
1 5

<210> 466
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 7C-H3L1; 10/50_7C1; light chain; CDR3-IMGT

<400> 466

Gln Gln Ser Asp Asn Leu Pro Ile Thr
1 5

<210> 467
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 7E-H1L1; 10/50_7E1; heavy chain; CDR1-IMGT

<400> 467

Gly Gly Ser Ile Asn Ser Tyr Tyr
1 5

<210> 468
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 7E-H1L1; 10/50_7E1; heavy chain; CDR2-IMGT

<400> 468

Ile His Tyr Ser Gly Ser Thr
1 5

<210> 469
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 7E-H1L1; 10/50_7E1; heavy chain; CDR3-IMGT

<400> 469

Ala Arg His Asp Cys Ser Asp Thr Thr Cys Arg Glu Tyr Phe Gln His
1 5 10 15

<210> 470
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 7E-H1L1; 10/50_7E1; light chain; CDR1-IMGT

<400> 470

Gln Ser Ile Ser Thr Phe
1 5

<210> 471
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 7E-H1L1; 10/50_7E1; light chain; CDR3-IMGT

<400> 471

Gln Glu Ser Tyr Ser Met Met Tyr Thr
1 5

<210> 472
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 7H-H1L1; 10/50_7H1; heavy chain; CDR1-IMGT

<400> 472

Gly Phe Thr Phe Ser Arg Tyr Trp
1 5

<210> 473
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 7H-H1L1; 10/50_7H1; heavy chain; CDR2-IMGT

<400> 473

Ile Asn Gln Gly Gly Ser Glu Arg
1 5

<210> 474
<211> 16
<212> PRT
<213> 7H-H1L1; 10/50_7H1; heavy chain; CDR3-IMGT

<400> 474

Ala Arg Glu Gly Met Val Glu Val Thr Ala Leu Ser Phe Leu Asp Tyr
1 5 10 15

<210> 475
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 7H-H1L1; 10/50_7H1; light chain; CDR1-IMGT

<400> 475

Gln Thr Ile Gly Thr Phe
1 5

<210> 476
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 7H-H1L1; 10/50_7H1; light chain; CDR3-IMGT

<400> 476

Gln Gln Thr Tyr Ser Met Ile Tyr Thr
1 5

<210> 477
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 9B-H1L1; 10/50_9B1; heavy chain; CDR1-IMGT

<400> 477

Gly Tyr Ile Phe Thr Ser Tyr Trp
1 5

<210> 478
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 9B-H1L1; 10/50_9B1; heavy chain; CDR2-IMGT

<400> 478

Ile Tyr Pro Gly Asn Ser Asp Pro
1 5

<210> 479
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 9B-H1L1; 10/50_9B1; heavy chain; CDR3-IMGT

<400> 479

Ser Arg Leu Asp His Tyr Phe Tyr Tyr Gly Met Asp Leu
1 5 10

<210> 480
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 9B-H1L1; 10/50_9B1; light chain; CDR1-IMGT

<400> 480

Gln Thr Phe Ser Ser Ile Tyr
1 5

<210> 481
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 9B-H1L1; 10/50_9B1; light chain; CDR3-IMGT

<400> 481

Gln His Tyr Asp Asn Ser Phe Phe Thr
1 5

<210> 482
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 9E-H2L2; 10/50_9E2; heavy chain; CDR1-IMGT

<400> 482

Gly Phe Thr Leu Arg Ser Tyr Ala
1 5

<210> 483
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 9E-H2L2; 10/50_9E2; heavy chain; CDR2-IMGT

<400> 483

Ile Ser Asp Ser Asp Asp Ser Thr
1 5

<210> 484
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 9E-H2L2; 10/50_9E2; heavy chain; CDR3-IMGT

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SequenceListing_ST25

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Gln Gly Ile Ser Ser Tyr
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<400> 486

Gln Gln Ala Asn Ser Phe Pro Trp Thr
1 5