SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Anti-human CD19 antibodies with high affinity

<130> P33118-WO

<150> EP15188262.8
<151> 2015-10-02

<150> EP16167893.3
<151> 2016-05-02

<160> 115

<170> PatentIn version 3.5

<210> 1
<211> 273
<212> PRT
<213> Homo sapiens

<400> 1

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


Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln Gln Leu Thr
            20                  25                  30


Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu Ser Leu Gly
        35                  40                  45


Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile Trp Leu Phe
    50                  55                  60


Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu Cys Gln Pro
65                  70                  75                  80


Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Asn Val
                85                  90                  95


Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp Leu Gly Gly
            100                 105                 110
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Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro Ser Ser Pro
        115                 120                 125


Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala Lys Asp Arg
    130                 135                 140


Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro Arg Asp Ser
145                 150                 155                 160


Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro Gly Ser Thr
                165                 170                 175


Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser Arg Gly Pro
            180                 185                 190


Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser Leu Leu Ser
        195                 200                 205


Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp Val Met Glu
    210                 215                 220


Thr Gly Leu Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala Gly Lys Tyr
225                 230                 235                 240


Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu Glu Ile Thr
                245                 250                 255


Ala Arg Pro Val Leu Trp His Trp Leu Leu Arg Thr Gly Gly Trp Lys
            260                 265                 270


Val
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<210> 2
<211> 274
<212> PRT
<213> Cynomolgus

<400> 2

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

Leu Gln Cys Leu Glu Gly Thr Ser Asp Gly Pro Thr Gln Gln Leu Val
            20                  25                  30

Trp Cys Arg Asp Ser Pro Phe Glu Pro Phe Leu Asn Leu Ser Leu Gly
        35                  40                  45

Leu Pro Gly Met Gly Ile Arg Met Gly Pro Leu Gly Ile Trp Leu Leu
    50                  55                  60

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

Gly Leu Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Ser Val
                85                  90                  95

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

Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro Ser Ser Pro
        115                 120                 125

Ser Gly Lys Leu Asn Ser Ser Gln Leu Tyr Val Trp Ala Lys Asp Arg
    130                 135                 140

Pro Glu Met Trp Glu Gly Glu Pro Val Cys Gly Pro Pro Arg Asp Ser
145                 150                 155                 160

Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro Gly Ser Thr
                165                 170                 175

Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser Arg Gly Pro
            180                 185                 190

Leu Ser Trp Thr His Val Arg Pro Lys Gly Pro Lys Ser Ser Leu Leu
        195                 200                 205
```

```
Ser Leu Glu Leu Lys Asp Asp Arg Pro Asp Arg Asp Met Trp Val Val
    210                 215                 220


Asp Thr Gly Leu Leu Leu Thr Arg Ala Thr Ala Gln Asp Ala Gly Lys
225                 230                 235                 240


Tyr Tyr Cys His Arg Gly Asn Trp Thr Lys Ser Phe Tyr Leu Glu Ile
                245                 250                 255


Thr Ala Arg Pro Ala Leu Trp His Trp Leu Leu Arg Ile Gly Gly Trp
            260                 265                 270


Lys Val
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<210> 3
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of Fc hole chain

<400> 3

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ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca      120

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac      180

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac      240

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag      300

tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa      360

gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag      420

aaccaggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag      480

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc      540

gacggctcct tcttcctcgt gagcaagctc accgtggaca agagcaggtg gcagcagggg      600

aacgtcttct catgctccgt gatgcatgag gctctgcaca accgcttcac gcagaagagc      660

ctctccctgt ctccgggtaa a                                                681
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<210> 4
<211> 1602
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of human CD19 antigen Fc knob chain avi tag

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aagggcacct ccgatggccc tacccagcag ctgacctggt ccagagagag ccccctgaag 120

cccttcctga agctgtctct gggcctgcct ggcctgggca tccatatgag gcctctggcc 180

atctggctgt tcatcttcaa cgtgtcccag cagatgggcg gcttctacct gtgtcagcct 240

ggcccccat ctgagaaggc ttggcagcct ggctggaccg tgaacgtgga aggatccggc 300

gagctgttcc ggtggaacgt gtccgatctg ggcggcctgg gatgcggcct gaagaacaga 360

tctagcgagg gccccagcag ccccagcggc aaactgatga gccccaagct gtacgtgtgg 420

gccaaggaca gacccgagat ctgggagggc gagcctcctt gcctgccccc tagagacagc 480

ctgaaccaga gcctgagcca ggacctgaca atggcccctg gcagcacact gtggctgagc 540

tgtggcgtgc cacccgactc tgtgtctaga ggccctctga gctggaccca cgtgcaccct 600

aagggcccta agagcctgct gagcctggaa ctgaaggacg acaggcccgc cagagatatg 660

tgggtcatgg aaaccggcct gctgctgcct agagccacag cccaggatgc cggcaagtac 720

tactgccaca gaggcaacct gaccatgagc ttccacctgg aaatcaccgc cagacccgtg 780

ctgtggcact ggctgctgag aacaggcggc tggaaggtcg acgctagcgg tggtagtccg 840

acacctccga cacccggggg tggttctgca gacaaaactc acacatgccc accgtgccca 900

gcacctgaag ccgcaggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 960

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 1020

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1080

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1140

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcggagcc 1200

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1260

ctgcccccat gccgggatga gctgaccaag aaccaggtca gcctgtggtg cctggtcaaa 1320

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1380

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1440

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1500

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atccggaggc 1560

ctgaacgaca tcttcgaggc ccagaagatt gaatggcacg ag 1602

<210> 5
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc hole chain

<400> 5

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

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115   120   125

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130   135   140

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145   150   155   160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165   170   175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
            180   185   190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195   200   205

His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser
    210   215   220

Pro Gly Lys
225

<210> 6
<211> 534
<212> PRT
<213> Artificial Sequence

<220>
<223> human CD19 antigen Fc knob chain avi tag

<400> 6

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

Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln Gln Leu Thr
            20   25   30

Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu Ser Leu Gly
        35   40   45

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Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile Trp Leu Phe
    50                  55                  60

Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu Cys Gln Pro
65                  70                  75                  80

Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Asn Val
                85                  90                  95

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

Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro Ser Ser Pro
        115                 120                 125

Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala Lys Asp Arg
    130                 135                 140

Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro Arg Asp Ser
145                 150                 155                 160

Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro Gly Ser Thr
                165                 170                 175

Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser Arg Gly Pro
            180                 185                 190

Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser Leu Leu Ser
        195                 200                 205

Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp Val Met Glu
    210                 215                 220

Thr Gly Leu Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala Gly Lys Tyr
225                 230                 235                 240

Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu Glu Ile Thr
                245                 250                 255
```

```
Ala Arg Pro Val Leu Trp His Trp Leu Leu Arg Thr Gly Gly Trp Lys
            260                 265                 270

Val Asp Ala Ser Gly Gly Ser Pro Thr Pro Pro Thr Pro Gly Gly Gly
        275                 280                 285

Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
    290                 295                 300

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
305                 310                 315                 320

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
                325                 330                 335

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            340                 345                 350

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
        355                 360                 365

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
    370                 375                 380

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala
385                 390                 395                 400

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
                405                 410                 415

Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln
            420                 425                 430

Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
        435                 440                 445

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    450                 455                 460
```

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
465 470 475 480

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
485 490 495

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
500 505 510

Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln
515 520 525

Lys Ile Glu Trp His Glu
530

<210> 7
<211> 1605
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of cynomolgus CD19 antigen Fc knob chain avi tag

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gaaggcacct ccgatggccc tacacagcag ctcgtgtggt gcagagacag ccccttcgag 120

cccttcctga acctgtctct gggcctgcct ggcatgggca tcagaatggg ccctctgggc 180

atctggctgc tgatcttcaa cgtgtccaac cagaccggcg gcttctacct gtgtcagcct 240

ggcctgccaa gcgagaaggc ttggcagcct ggatggaccg tgtccgtgga aggatctggc 300

gagctgttcc ggtggaacgt gtccgatctg ggcggcctgg gatgcggcct gaagaacaga 360

agcagcgagg gccctagcag ccccagcggc aagctgaata gcagccagct gtacgtgtgg 420

gccaaggaca gacccgagat gtgggagggc gagcctgtgt gtggcccccc tagagatagc 480

ctgaaccaga gcctgagcca ggacctgaca atggcccctg gcagcacact gtggctgagc 540

tgtggcgtgc cacccgactc tgtgtccaga ggccctctga gctggacaca cgtgcggcca 600

aagggcccta agagcagcct gctgagcctg gaactgaagg acgaccggcc cgaccgggat 660

atgtgggtgg tggatacagg cctgctgctg accagagcca cagcccagga tgccggcaag 720

tactactgcc acagaggcaa ctggaccaag agcttttacc tggaaatcac cgccagaccc 780

gccctgtggc actggctgct gagaatcgga ggctggaagg tcgacgctag cggtggtagt 840

ccgacacctc cgacacccgg gggtggttct gcagacaaaa ctcacacatg cccaccgtgc 900

ccagcacctg aagccgcagg gggaccgtca gtcttcctct tcccccccaaa acccaaggac 960

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 1020

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1080

aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 1140

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctcgga 1200

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1260

accctgcccc catgccggga tgagctgacc aagaaccagg tcagcctgtg gtgcctggtc 1320

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1380

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1440

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1500

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaatccgga 1560

ggcctgaacg acatcttcga ggcccagaag attgaatggc acgag 1605

<210> 8
<211> 535
<212> PRT
<213> Artificial Sequence

<220>
<223> cynomolgus CD19 antigen Fc knob chain avi tag

<400> 8

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

Leu Gln Cys Leu Glu Gly Thr Ser Asp Gly Pro Thr Gln Gln Leu Val
20 25 30

```
Trp Cys Arg Asp Ser Pro Phe Glu Pro Phe Leu Asn Leu Ser Leu Gly
        35                  40                  45

Leu Pro Gly Met Gly Ile Arg Met Gly Pro Leu Gly Ile Trp Leu Leu
    50                  55                  60

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

Gly Leu Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Ser Val
                85                  90                  95

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

Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro Ser Ser Pro
        115                 120                 125

Ser Gly Lys Leu Asn Ser Ser Gln Leu Tyr Val Trp Ala Lys Asp Arg
    130                 135                 140

Pro Glu Met Trp Glu Gly Glu Pro Val Cys Gly Pro Pro Arg Asp Ser
145                 150                 155                 160

Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro Gly Ser Thr
                165                 170                 175

Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser Arg Gly Pro
            180                 185                 190

Leu Ser Trp Thr His Val Arg Pro Lys Gly Pro Lys Ser Ser Leu Leu
        195                 200                 205

Ser Leu Glu Leu Lys Asp Asp Arg Pro Asp Arg Asp Met Trp Val Val
    210                 215                 220

Asp Thr Gly Leu Leu Leu Thr Arg Ala Thr Ala Gln Asp Ala Gly Lys
225                 230                 235                 240
```

```
Tyr Tyr Cys His Arg Gly Asn Trp Thr Lys Ser Phe Tyr Leu Glu Ile
                245                 250                 255

Thr Ala Arg Pro Ala Leu Trp His Trp Leu Leu Arg Ile Gly Gly Trp
            260                 265                 270

Lys Val Asp Ala Ser Gly Gly Ser Pro Thr Pro Pro Thr Pro Gly Gly
        275                 280                 285

Gly Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
    290                 295                 300

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
305                 310                 315                 320

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
                325                 330                 335

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
            340                 345                 350

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
        355                 360                 365

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
    370                 375                 380

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly
385                 390                 395                 400

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
                405                 410                 415

Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn
            420                 425                 430

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
        435                 440                 445
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Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
450 455 460

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
465 470 475 480

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
485 490 495

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
500 505 510

Ser Leu Ser Pro Gly Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala
515 520 525

Gln Lys Ile Glu Trp His Glu
530 535

<210> 9
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence CD19 (8B8) VH Parental clone DNA

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agctgcaaag catctggtta caccttcact gactatatca tgcactgggt tcgtcaggcc 120

ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat 180

accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac 240

atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtact 300

tactactacg gttccgccct ctttgattac tggggccaag gtaccacggt gaccgtaagc 360

tct 363

<210> 10
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Nucleotide sequence CD19 (8B8) VL Parental clone DNA

<400> 10
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atttcttgca aatccagcca atctctggaa aactccaacg gcaacacgta cctgaactgg 120

tatctccaga aaccgggtca gagcccgcag ctgctgatct accgtgtatc taagcgcttc 180

tccggcgttc ctgatcgttt cagcggttct ggatccggca ccgactttac tctgaaaatc 240

agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcagttgac ccacgttccg 300

tacaccttcg gtcaaggaac taaactggaa attaaa 336

<210> 11
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> 43-45: 40% Y, 6% A/S/T/G/P/D/N/E/Q/V, 49-51: 40% N, 6% A/S/T/Y/G/P/D/E/Q/V, 55-57: 25% S/T/Q/E, 61-63: 25% S/T/Q/E

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<221> misc_feature
<222> (43)..(45)
<223> n is a, c, g or t

<220>
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<222> (49)..(51)
<223> n is a, c, g or t

<220>
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<222> (55)..(57)
<223> n is a, c, g or t

<220>
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<222> (61)..(63)
<223> n is a, c, g or t

<400> 11
cagctgcggg ctctgacccg gtttctggag ataccagttc agnnncgtnn ngccnnngga 60

nnnttccaga gattggctgg atttgcaaga aatg 94

<210> 12
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> 40-42: 30% R, 20% E, 5% A/S/T/Y/G/P/D/N/Q/V. 49-51: 30% K, 20% S, 5% A/N/T/Y/G/P/D/E/Q/V, 55-57: 40% F, 5% A/S/T/Y/G/P/D/E/Q/V/I/L, 58-60: 40% S, 6.6% A/T/Y/G/P/D/E/Q/V, 67-69: 50% P, 50% L

<220>
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<222> (40)..(42)
<223> n is a, c, g or t

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<222> (49)..(51)
<223> n is a, c, g or t

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<222> (55)..(57)
<223> n is a, c, g or t

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<222> (58)..(60)
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<222> (67)..(69)
<223> n is a, c, g or t

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ggcgttnnng atcgtttcag cggttctgga tccggcacc 99

<210> 13
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> 40-42: 52% H, 4% G/A/S/P/T/N/Y/D/E/Q/V/I, 46-48: 30% I, 15% Y, 5%

G/A/S/T/P/N/H/D/E/Q/V, 49-51: 52% Y, 4% G/A/S/P/T/N/H/D/E/Q/V/I, 52-54: 30% D, 15% G, 5% A/S/P/Y/N/H/D/E/Q/V/I, 55-57: 52% T, 4% G/A/S/P/Y/N/H/D/E/Q/V/I, 61-63: 52% T, 4% G/A/S/P/Y/N/H/D/E/Q/V/I

<220>
<221> misc_feature
<222> (40)..(42)
<223> n is a, c, g or t

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<222> (46)..(48)
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<223> n is a, c, g or t

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<222> (52)..(54)
<223> n is a, c, g or t

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<221> misc_feature
<222> (61)..(63)
<223> n is a, c, g or t

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nnngtaacca gatgctttgc agctcacttt aacggaagc 99

<210> 14
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> 34-36: 45% Y, 5% others, 40-42: 52% N, 4% others, 46-48: 40% Y, 5% others, 49-51: 30% N, 15% S, 5% others, 52-54: 30% D, 15% G, 5% others, 55-57: 52% G, 4% others, 61-63: 30% K, 15% N, 4% others, 70-72: 30% E, 15% Q, 5% others

<220>
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<222> (34)..(36)
<223> n is a, c, g or t

<220>
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<222> (40)..(42)
<223> n is a, c, g or t

<220>
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<222> (46)..(48)
<223> n is a, c, g or t

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<222> (49)..(51)
<223> n is a, c, g or t

<220>
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<222> (52)..(54)
<223> n is a, c, g or t

<220>
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<222> (55)..(57)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (61)..(63)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (70)..(72)
<223> n is a, c, g or t

<400> 14
caggccccgg gccagggtct ggagtggatg ggcnnnattn nnccannnnn nnnnnnntcc 60

nnntataccn nnaaattcca gggccgcgtc acgatgacc 99

<210> 15
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 H3 reverse constant

<400> 15
cgtcaccggt tcggggaagt agtccttgac cag 33

<210> 16
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> LMB3

<400> 16
caggaaacag ctatgaccat gattac 26

<210> 17
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 L1 forward constant

<400> 17
tggtatctcc agaaaccggg tcagagcccg cag 33

<210> 18
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> 34-36: 52% Y, 4% others, 37-39: 52% P, 4% others, 40-42: 42% V, 10% L, 4% others, 43-45: 52% H, 4% others, 46-48: 42% T, 10% I, 4% others, 49-51: 45% L, 11% G, 4% others

<220>
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<223> n is a, c, g or t

<220>
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<222> (37)..(39)
<223> n is a, c, g or t

<220>
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<222> (40)..(42)
<223> n is a, c, g or t

<220>
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<222> (43)..(45)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (46)..(48)
<223> n is a, c, g or t

<220>
<221> misc_feature
<222> (49)..(51)
<223> n is a, c, g or t

<400> 18
tttaatttcc agtttagttc cttgaccgaa ggtnnnnnnn nnnnnnnnnn nctgcagaca 60

atagtagacg ccaacgtctt cagc 84

<210> 19
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 L3 forward constant

<400> 19
accttcggtc aaggaactaa actggaaatt aaacg 35

<210> 20
<211> 107
<212> DNA
<213> Artificial Sequence

<220>
<223> pos. 59-61: 50% L, 3.8% others, 62-64: 50% A, 4.2% others, 65-67: 50% S, 4.2% others, 68-70: 50% G, 4.2% others, 71-73: 50% Y, 4.2% others, 74-76: 50% Y, 4.2% others, 77-79: 50% Y, 4.2% others, 80-82: 50% T, 4.2% others, 83-85: 50% G, 4.2% others.

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<222> (54)..(58)
<223> n is a, c, g, or t

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<223> n is a, c, g or t

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<223> n is a, c, g or t

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<223> n is a, c, g or t

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<222> (80)..(82)
<223> n is a, c, g or t

<220>
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<222> (83)..(85)
<223> n is a, c, g or t

<400> 20
ttggtgctag cagagcttac ggtcaccgtg gtaccttggc cccagtaatc aaannnnnnn 60

nnnnnnnnnn nnnnnnnnnn gcgtgcacaa tagtaaacag cggtgtc 107

<210> 21
<211> 1615
<212> DNA
<213> Artificial Sequence

<220>
<223> SNAP tag human CD19 ECD- PDGFR DNA

<400> 21
ggccgccgct agcggcatcg actacaagga cgacgatgac aaggccggca tcgatgccat 60

catggacaaa gactgcgaaa tgaagcgcac caccctggat agccctctgg gcaagctgga 120

actgtctggg tgcgaacagg gcctgcacga gatcaagctg ctgggcaaag gaacatctgc 180

cgccgacgcc gtggaagtgc ctgccccagc cgccgtgctg ggcggaccag agccactgat 240

gcaggccacc gcctggctca acgcctactt tcaccagcct gaggccatcg aggagttccc 300

tgtgccagcc ctgcaccacc cagtgttcca gcaggagagc tttacccgcc aggtgctgtg 360

gaaactgctg aaagtggtga agttcggaga ggtcatcagc taccagcagc tggccgccct 420

ggccggcaat cccgccgcca ccgccgccgt gaaaaccgcc ctgagcggaa atcccgtgcc 480

cattctgatc ccctgccacc gggtggtgtc tagctctggc gccgtggggg gctacgaggg 540

cgggctcgcc gtgaaagagt ggctgctggc ccacgagggc cacagactgg gcaagcctgg 600

gctgggtgat atccccgagg aacccctggt cgtgaaggtg gaagagggcg acaatgccgt 660

gctgcagtgc ctgaagggca cctccgatgg ccctacccag cagctgacct ggtccagaga 720

gagccccctg aagcccttcc tgaagctgtc tctgggcctg cctggcctgg gcatccatat 780

gaggcctctg gccatctggc tgttcatctt caacgtgtcc cagcagatgg gcggcttcta 840

cctgtgtcag cctggccccc catctgagaa ggcttggcag cctggctgga ccgtgaacgt 900

ggaaggatcc ggcgagctgt tccggtggaa cgtgtccgat ctgggcggcc tgggatgcgg 960

cctgaagaac agatctagcg agggccccag cagccccagc ggcaaactga tgagccccaa 1020

gctgtacgtg tgggccaagg acagacccga gatctgggag ggcgagcctc cttgcctgcc 1080

ccctagagac agcctgaacc agagcctgag ccaggacctg acaatggccc ctggcagcac 1140

actgtggctg agctgtggcg tgccacccga ctctgtgtct agaggccctc tgagctggac 1200

ccacgtgcac cctaagggcc ctaagagcct gctgagcctg gaactgaagg acgacaggcc 1260

cgccagagat atgtgggtca tggaaaccgg cctgctgctg cctagagcca cagcccagga 1320

tgccggcaag tactactgcc acagaggcaa cctgaccatg agcttccacc tggaaatcac 1380

cgccagaccc gtgctgtggc actggctgct gagaacaggc ggctggaagg tcgacgaaca 1440

aaaactcatc tcagaagagg atctgaatgc tgtgggccag gacacgcagg aggtcatcgt 1500

ggtgccacac tccttgccct ttaaggtggt ggtgatctca gccatcctgg ccctggtggt 1560

gctcaccatc atctccctta tcatcctcat catgctttgg cagaagaagc cacgt 1615

<210> 22
<211> 1620
<212> DNA
<213> Artificial Sequence

<220>
<223> SNAP tag cynomolgus CD19 ECD- PDGFR DNA

<400> 22
ccggccgccg ctagcggcat cgactacaag gacgacgatg acaaggccgg catcgatgcc 60

atcatggaca aagactgcga aatgaagcgc accaccctgg atagccctct gggcaagctg 120

gaactgtctg ggtgcgaaca gggcctgcac gagatcaagc tgctgggcaa aggaacatct 180

gccgccgacg ccgtggaagt gcctgcccca gccgccgtgc tgggcggacc agagccactg 240

atgcaggcca ccgcctggct caacgcctac tttcaccagc ctgaggccat cgaggagttc 300

cctgtgccag ccctgcacca cccagtgttc cagcaggaga gctttacccg ccaggtgctg 360

tggaaactgc tgaaagtggt gaagttcgga gaggtcatca gctaccagca gctggccgcc 420

ctggccggca atcccgccgc caccgccgcc gtgaaaaccg ccctgagcgg aaatcccgtg 480

cccattctga tcccctgcca ccgggtggtg tctagctctg gcgccgtggg gggctacgag 540

ggcgggctcg ccgtgaaaga gtggctgctg gcccacgagg gccacagact gggcaagcct 600

gggctgggtg atatccccca ggaacccctg gtcgtgaagg tggaagaggg cgacaatgcc 660

gtgctccagt gtctcgaggg cacctccgat ggccctacac agcagctcgt gtggtgcaga 720

gacagcccct tcgagccctt cctgaacctg tctctgggcc tgcctggcat gggcatcaga 780

atgggccctc tgggcatctg gctgctgatc ttcaacgtgt ccaaccagac cggcggcttc 840

tacctgtgtc agcctggcct gccaagcgag aaggcttggc agcctggatg gaccgtgtcc 900

gtggaaggat ctggcgagct gttccggtgg aacgtgtccg atctgggcgg cctgggatgc 960

ggcctgaaga acagaagcag cgagggccct agcagcccca gcggcaagct gaatagcagc 1020

cagctgtacg tgtgggccaa ggacagaccc gagatgtggg agggcgagcc tgtgtgtggc 1080

ccccctagag atagcctgaa ccagagcctg agccaggacc tgacaatggc ccctggcagc 1140

acactgtggc tgagctgtgg cgtgccaccc gactctgtgt ccagaggccc tctgagctgg 1200

acacacgtgc ggcctaaggg ccctaagagc agcctgctga gcctggaact gaaggacgac 1260

cggcccgacc gggatatgtg ggtggtggat acaggcctgc tgctgaccag agccacagcc 1320

caggatgccg gcaagtacta ctgccacaga ggcaactgga ccaagagctt ttacctggaa 1380

atcaccgcca gacccgccct gtggcactgg ctgctgagaa tcggaggctg gaaggtcgac 1440

gagcagaagc tgatctccga agaggacctg aacgccgtgg gccaggatac ccaggaagtg 1500

atcgtggtgc cccacagcct gcccttcaag gtggtcgtga tcagcgccat tctggccctg 1560

gtggtgctga ccatcatcag cctgatcatc ctgattatgc tgtggcagaa aaagccccgc 1620

<210> 23
<211> 539
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP tag human CD19 ECD- PDGFR

<400> 23

Pro Ala Ala Ala Ser Gly Ile Asp Tyr Lys Asp Asp Asp Asp Lys Ala
1 5 10 15

Gly Ile Asp Ala Ile Met Asp Lys Asp Cys Glu Met Lys Arg Thr Thr
20 25 30

Leu Asp Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly
35 40 45

Leu His Glu Ile Lys Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala
50 55 60

```
Val Glu Val Pro Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu
65                  70                  75                  80

Met Gln Ala Thr Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala
                85                  90                  95

Ile Glu Glu Phe Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln
            100                 105                 110

Glu Ser Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys
        115                 120                 125

Phe Gly Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn
    130                 135                 140

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

Pro Ile Leu Ile Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val
                165                 170                 175

Gly Gly Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His
            180                 185                 190

Glu Gly His Arg Leu Gly Lys Pro Gly Leu Gly Asp Ile Pro Glu Glu
        195                 200                 205

Pro Leu Val Val Lys Val Glu Glu Gly Asp Asn Ala Val Leu Gln Cys
    210                 215                 220

Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln Gln Leu Thr Trp Ser Arg
225                 230                 235                 240

Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu Ser Leu Gly Leu Pro Gly
                245                 250                 255

Leu Gly Ile His Met Arg Pro Leu Ala Ile Trp Leu Phe Ile Phe Asn
            260                 265                 270
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```
Val Ser Gln Gln Met Gly Gly Phe Tyr Leu Cys Gln Pro Gly Pro Pro
        275                 280                 285

Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Asn Val Glu Gly Ser
    290                 295                 300

Gly Glu Leu Phe Arg Trp Asn Val Ser Asp Leu Gly Gly Leu Gly Cys
305                 310                 315                 320

Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro Ser Ser Pro Ser Gly Lys
                325                 330                 335

Leu Met Ser Pro Lys Leu Tyr Val Trp Ala Lys Asp Arg Pro Glu Ile
            340                 345                 350

Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro Arg Asp Ser Leu Asn Gln
        355                 360                 365

Ser Leu Ser Gln Asp Leu Thr Met Ala Pro Gly Ser Thr Leu Trp Leu
    370                 375                 380

Ser Cys Gly Val Pro Pro Asp Ser Val Ser Arg Gly Pro Leu Ser Trp
385                 390                 395                 400

Thr His Val His Pro Lys Gly Pro Lys Ser Leu Leu Ser Leu Glu Leu
                405                 410                 415

Lys Asp Asp Arg Pro Ala Arg Asp Met Trp Val Met Glu Thr Gly Leu
            420                 425                 430

Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala Gly Lys Tyr Tyr Cys His
        435                 440                 445

Arg Gly Asn Leu Thr Met Ser Phe His Leu Glu Ile Thr Ala Arg Pro
    450                 455                 460

Val Leu Trp His Trp Leu Leu Arg Thr Gly Gly Trp Lys Val Asp Glu
465                 470                 475                 480
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Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly Gln Asp Thr
485 490 495

Gln Glu Val Ile Val Val Pro His Ser Leu Pro Phe Lys Val Val Val
500 505 510

Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr Ile Ile Ser Leu Ile
515 520 525

Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg
530 535

<210> 24
<211> 540
<212> PRT
<213> Artificial Sequence

<220>
<223> SNAP tag cynomolgus CD19 ECD- PDGFR

<400> 24

Pro Ala Ala Ala Ser Gly Ile Asp Tyr Lys Asp Asp Asp Asp Lys Ala
1 5 10 15

Gly Ile Asp Ala Ile Met Asp Lys Asp Cys Glu Met Lys Arg Thr Thr
20 25 30

Leu Asp Ser Pro Leu Gly Lys Leu Glu Leu Ser Gly Cys Glu Gln Gly
35 40 45

Leu His Glu Ile Lys Leu Leu Gly Lys Gly Thr Ser Ala Ala Asp Ala
50 55 60

Val Glu Val Pro Ala Pro Ala Ala Val Leu Gly Gly Pro Glu Pro Leu
65 70 75 80

Met Gln Ala Thr Ala Trp Leu Asn Ala Tyr Phe His Gln Pro Glu Ala
85 90 95

Ile Glu Glu Phe Pro Val Pro Ala Leu His His Pro Val Phe Gln Gln
100 105 110

```
Glu Ser Phe Thr Arg Gln Val Leu Trp Lys Leu Leu Lys Val Val Lys
        115                 120                 125

Phe Gly Glu Val Ile Ser Tyr Gln Gln Leu Ala Ala Leu Ala Gly Asn
    130                 135                 140

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

Pro Ile Leu Ile Pro Cys His Arg Val Val Ser Ser Ser Gly Ala Val
                165                 170                 175

Gly Gly Tyr Glu Gly Gly Leu Ala Val Lys Glu Trp Leu Leu Ala His
            180                 185                 190

Glu Gly His Arg Leu Gly Lys Pro Gly Leu Gly Asp Ile Pro Gln Glu
        195                 200                 205

Pro Leu Val Val Lys Val Glu Glu Gly Asp Asn Ala Val Leu Gln Cys
    210                 215                 220

Leu Glu Gly Thr Ser Asp Gly Pro Thr Gln Gln Leu Val Trp Cys Arg
225                 230                 235                 240

Asp Ser Pro Phe Glu Pro Phe Leu Asn Leu Ser Leu Gly Leu Pro Gly
                245                 250                 255

Met Gly Ile Arg Met Gly Pro Leu Gly Ile Trp Leu Leu Ile Phe Asn
            260                 265                 270

Val Ser Asn Gln Thr Gly Gly Phe Tyr Leu Cys Gln Pro Gly Leu Pro
        275                 280                 285

Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Ser Val Glu Gly Ser
    290                 295                 300

Gly Glu Leu Phe Arg Trp Asn Val Ser Asp Leu Gly Gly Leu Gly Cys
305                 310                 315                 320
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```
Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro Ser Ser Pro Ser Gly Lys
                325                 330                 335

Leu Asn Ser Ser Gln Leu Tyr Val Trp Ala Lys Asp Arg Pro Glu Met
            340                 345                 350

Trp Glu Gly Glu Pro Val Cys Gly Pro Pro Arg Asp Ser Leu Asn Gln
        355                 360                 365

Ser Leu Ser Gln Asp Leu Thr Met Ala Pro Gly Ser Thr Leu Trp Leu
    370                 375                 380

Ser Cys Gly Val Pro Pro Asp Ser Val Ser Arg Gly Pro Leu Ser Trp
385                 390                 395                 400

Thr His Val Arg Pro Lys Gly Pro Lys Ser Ser Leu Leu Ser Leu Glu
                405                 410                 415

Leu Lys Asp Asp Arg Pro Asp Arg Asp Met Trp Val Val Asp Thr Gly
            420                 425                 430

Leu Leu Leu Thr Arg Ala Thr Ala Gln Asp Ala Gly Lys Tyr Tyr Cys
        435                 440                 445

His Arg Gly Asn Trp Thr Lys Ser Phe Tyr Leu Glu Ile Thr Ala Arg
    450                 455                 460

Pro Ala Leu Trp His Trp Leu Leu Arg Ile Gly Gly Trp Lys Val Asp
465                 470                 475                 480

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly Gln Asp
                485                 490                 495

Thr Gln Glu Val Ile Val Val Pro His Ser Leu Pro Phe Lys Val Val
            500                 505                 510

Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr Ile Ile Ser Leu
        515                 520                 525
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Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg
530 535 540

<210> 25
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5H09) CDR-L1

<400> 25

Lys Ser Ser Gln Ser Leu Glu Ser Ser Thr Gly Asn Thr Tyr Leu Asn
1 5 10 15

<210> 26
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19(8B8-5H09) CDR-L2

<400> 26

Arg Val Ser Lys Arg Phe Ser
1 5

<210> 27
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19(8B8-5H09) CDR-L3

<400> 27

Leu Gln Leu Ile Asp Tyr Pro Val Thr
1 5

<210> 28
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19(8B8-5H09) CDR-H1

<400> 28

Asp Tyr Ile Met His
1   5

<210> 29
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19(8B8-5H09) CDR-H2

<400> 29

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

Gly

<210> 30
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR(8B8-5H09) CDR-H3

<400> 30

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

<210> 31
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19(8B8-7H07) CDR-L1

<400> 31

Lys Ser Ser Gln Ser Leu Glu Thr Ser Thr Gly Asn Thr Tyr Leu Asn
1 5 10 15

<210> 32
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-7H07) CDR-L2

<400> 32

Arg Val Ser Lys Arg Phe Ser
1 5

<210> 33
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-7H07) CDR-L3

<400> 33

Leu Gln Ala Thr His Ile Pro Tyr Thr
1 5

<210> 34
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-7H07) CDR-H1

<400> 34

Asp Tyr Ile Met His
1 5

<210> 35
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> CD19 (8B8-7H07) CDR-H2

<400> 35

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

Gly

<210> 36
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-7H07) CDR-H3

<400> 36

Gly Thr Tyr Tyr Tyr Gly Ser Glu Leu Phe Asp Tyr
1   5   10

<210> 37
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B03) CDR-L1

<400> 37

Lys Ser Ser Gln Ser Leu Glu Thr Ser Thr Gly Asn Thr Tyr Leu Asn
1   5   10   15

<210> 38
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B03) CDR-L2

<400> 38

Arg Val Ser Lys Arg Phe Ser
1   5

<210> 39
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B03) CDR-L3

<400> 39

Leu Gln Leu Thr His Val Pro Tyr Thr
1   5

<210> 40
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B03) CDR-H1

<400> 40

Asp Tyr Ile Thr His
1   5

<210> 41
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B03) CDR-H2

<400> 41

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

Gly

<210> 42
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B03) CDR-H3

<400> 42

Gly Thr Tyr Tyr Tyr Gly Pro Asp Leu Phe Asp Tyr
1   5   10

<210> 43
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) CDR-L1

<400> 43

Lys Ser Ser Gln Ser Leu Glu Thr Ser Thr Gly Thr Thr Tyr Leu Asn
1   5   10   15

<210> 44
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) CDR-L2

<400> 44

Arg Val Ser Lys Arg Phe Ser
1   5

<210> 45
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) CDR-L3

<400> 45

Leu Gln Leu Leu Glu Asp Pro Tyr Thr
1   5

<210> 46
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) CDR-H1

<400> 46

Asp Tyr Ile Met His
1 5

<210> 47
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) CDR-H2

<400> 47

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

Gly

<210> 48
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) CDR-H3

<400> 48

Gly Thr Tyr Tyr Tyr Gly Pro Gln Leu Phe Asp Tyr
1 5 10

<210> 49
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> CD19 (8B8-5A07) CDR-L1

<400> 49

Lys Ser Ser Gln Ser Leu Glu Thr Ser Thr Gly Asn Thr Tyr Leu Asn
1 5 10 15

<210> 50
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5A07) CDR-L2

<400> 50

Arg Val Ser Lys Arg Phe Ser
1 5

<210> 51
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5A07) CDR-L3

<400> 51

Leu Gln Pro Gly His Tyr Pro Gly Thr
1 5

<210> 52
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5A07) CDR-H1

<400> 52

Asp Tyr Ile Met His
1 5

<210> 53
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5A07) CDR-H2

<400> 53

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

Gly

<210> 54
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5A07) CDR-H3

<400> 54

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

<210> 55
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5B08) CDR-L1

<400> 55

Lys Ser Ser Gln Ser Leu Glu Thr Ser Thr Gly Asn Thr Tyr Leu Asn
1   5   10   15

<210> 56
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5B08) CDR-L2

<400> 56

Arg Val Ser Lys Arg Phe Ser
1 5

<210> 57
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5B08) CDR-L3

<400> 57

Leu Gln Leu Asp Ser Tyr Pro Asn Thr
1 5

<210> 58
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5B08) CDR-H1

<400> 58

Asp Tyr Ile Met His
1 5

<210> 59
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5B08) CDR-H2

<400> 59

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

Gly

<210> 60
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5B08) CDR-H3

<400> 60

Gly Thr Tyr Tyr Tyr Gly Pro Gln Leu Phe Asp Tyr
1 5 10

<210> 61
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5D08) CDR-L1

<400> 61

Lys Ser Ser Gln Ser Leu Glu Thr Ser Thr Gly Asn Thr Tyr Leu Asn
1 5 10 15

<210> 62
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5D08) CDR-L2

<400> 62

Arg Val Ser Lys Arg Phe Ser
1 5

<210> 63
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5D08) CDR-L3

<400> 63

Leu Gln Leu Thr His Glu Pro Tyr Thr
1 5

<210> 64
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5D08) CDR-H1

<400> 64

Asp Tyr Ile Met His
1 5

<210> 65
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5D08) CDR-H2

<400> 65

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

Gly

<210> 66
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5D08) CDR-H3

<400> 66

Gly Thr Tyr Tyr Tyr Gly Ser Glu Leu Phe Asp Tyr
1 5 10

<210> 67
<211> 657

<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8) parental light chain DNA

<400> 67
gatgctgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca ggtctagtca gagccttgaa aacagtaatg gaaacaccta tttgaactgg 120

tacctccaga aaccaggcca gtctccacaa ctcctgatct acagggtttc caaacgattt 180

tctggggtcc tagacaggtt cagtggtagt ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgagga tttgggagtt tatttctgcc tacaacttac acatgtcccg 300

tacacgttcg gaggggggac caagctggaa ataaaacgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 68
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8) parental heavy chain DNA

<400> 68
gaggtccagc tgcagcagtc tggacctgag ctggtaaagc ctggggcttc agtgaagatg 60

gcctgcaagg cttctggata cacattcact gactatatta tgcactgggt gaagcagaag 120

actgggcagg gccttgagtg gattggatat attaatcctt acaatgatgg ttctaagtac 180

actgagaagt tcaacggcaa ggccacactg acttcagaca aatcttccat cacagcctac 240

atggagctca gcagcctgac ctctgaggac tctgcggtct attactgtgc aagagggacc 300

tattattatg gtagcgccct ctttgactac tggggccaag gcaccactct cacagtctcc 360

tcggctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 69
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8) parental light chain

<400> 69

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Asn Ser
20 25 30

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

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

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

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

Thr His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 70
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8) parental heavy chain

<400> 70

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Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
            20                  25                  30


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


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


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


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


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


Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125


Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140


Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160


Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175


Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190
```

```
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400
```

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 71
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) light chain DNA

<400> 71
gatattgtca tgactcaaac tccactgtct ctgtccgtga ccccgggtca gccagcgagc 60

atttcttgca aatccagcca atctctggaa acctccaccg gcaccacgta cctgaactgg 120

tatctccaga aaccgggtca gagcccgcag ctgctgatct accgtgtatc taagcgcttc 180

tccggcgttc ctgatcgttt cagcggttct ggatccggca ccgactttac tctgaaaatc 240

agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcagctgct ggaagatcca 300

tacaccttcg gtcaaggaac gaaactggaa attaaacgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 72
<211> 1353

<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) heavy chain DNA

<400> 72
caggtgcaat tggttcaatc tggtgctgaa gtaaaaaaac cgggcgcttc cgttaaagtg 60

agctgcaaag catctggtta caccttcact gactatatca tgcactgggt tcgtcaggcc 120

ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat 180

accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac 240

atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtacc 300

tactactacg gtccacagct gtttgattac tggggccaag gtaccacggt gaccgtaagc 360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

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cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 73
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) light chain

<400> 73

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


Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
            20                  25                  30


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


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


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


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


Leu Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125


Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140


Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160
```

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 74
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) heavy chain

<400> 74

Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
20 25 30

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

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

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

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

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

```
Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320
```

```
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys
    450
```

<210> 75
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-7H07) light chain DNA

<400> 75

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gatattgtta tgactcaaac tccactgtct ctgtccgtga ccccgggtca gccagcgagc       60

atttcttgca aatccagcca atctctggaa acctccaccg gcaacacgta cctgaactgg      120

tatctccaga aaccgggtca gagcccgcag ctgctgatct accgtgtatc taagcgcttc      180
```

tccggcgttc ctgatcgttt cagcggttct ggatccggca ccgactttac tctgaaaatc 240

agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcaggcaac ccatatccca 300

tacaccttcg gtcaaggaac taaactggaa attaaacgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 76
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-7H07) heavy chain DNA

<400> 76
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agctgcaaag catctggtta caccttcact gactatatca tgcactgggt tcgtcaggcc 120

ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat 180

accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac 240

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tactactacg gttctgaact gtttgattac tggggccaag gtaccacggt gaccgtaagc 360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

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aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 77
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-7H07) light chain

<400> 77

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
20 25 30

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

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

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

```
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Ala
                85                  90                  95


Thr His Ile Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125


Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140


Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160


Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175


Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190


Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205


Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210>  78
<211>  451
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD19 (8B8-7H07) heavy chain

<400>  78

Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
            20                  25                  30
```

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225                 230                 235                 240
```

```
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445
```

Pro Gly Lys
    450

<210> 79
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B03) light chain DNA

<220>
<221> misc_feature
<222> (320)..(321)
<223> n is a, c, g, or t

<400> 79
gatattgtta tgactcaaac tccactgtct ctgtccgtga ccccgggtca gccagcgagc 60

atttcttgca aatccagcca atctctggaa acctccaccg gcaacacgta cctgaactgg 120

tatctccaga aaccgggtca gagcccgcag ctgctgatct accgtgtatc taagcgcttc 180

tccggcgttc ctgatcgttt cagcggttct ggatccggca ccgactttac tctgaaaatc 240

agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcagttgac ccacgttccg 300

tacaccttcg gtcaaggaan naaactggaa attaaacgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 80
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B03) heavy chain DNA

<400> 80
caggtgcaat tggttcaatc tggtgctgaa gtaaaaaaac cgggcgcttc cgttaaagtg 60

agctgcaaag catctggtta caccttcact gactatatca cgcactgggt tcgtcaggcc 120

ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat 180

accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac 240

atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtacc 300

tactactacg gtccagatct gtttgattac tggggccaag gtaccacggt gaccgtaagc 360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aggggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 81
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B03) light chain

<220>
<221> misc_feature
<222> (107)..(107)
<223> Xaa can be any naturally occurring amino acid

<400> 81

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
            20                  25                  30

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

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

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

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

Thr His Val Pro Tyr Thr Phe Gly Gln Gly Xaa Lys Leu Glu Ile Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160
```

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 82
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B03) heavy chain

<400> 82

Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
20 25 30

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

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

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

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

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

```
Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320
```

```
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys
    450
```

<210> 83
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5A07) light chain DNA

<400> 83
gatattgtta tgactcaaac tccactgtct ctgtccgtga ccccgggtca gccagcgagc 60

atttcttgca aatccagcca atctctggaa acctccaccg gcaacacgta cctgaactgg 120

tatctccaga aaccgggtca gagcccgcag ctgctgatct accgtgtatc taagcgcttc 180

tccggcgttc ctgatcgttt cagcggttct ggatccggca ccgactttac tctgaaaatc 240

agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcagccagg tcattaccca 300

ggtaccttcg gtcaaggaac taaactggaa attaaacgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 84
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5A07) heavy chain DNA

<400> 84
caggtgcaat tggttcaatc tggtgctgaa gtaaaaaaac cgggcgcttc cgttaaagtg 60

agctgcaaag catctggtta caccttcact gactatatca tgcactgggt tcgtcaggcc 120

ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat 180

accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac 240

atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtact 300

tactactacg gttccgccct ctttgattac tggggccaag gtaccacggt gaccgtaagc 360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 85
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5A07) light chain

<400> 85

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
20 25 30

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

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

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

```
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Pro
                85                  90                  95


Gly His Tyr Pro Gly Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125


Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140


Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160


Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175


Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190


Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205


Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210>  86
<211>  451
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD19 (8B8-5A07)  heavy chain

<400>  86

Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
            20                  25                  30
```

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225                 230                 235                 240
```

```
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445
```

Pro Gly Lys
    450

<210> 87
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5D08) light chain DNA

<400> 87
gatattgtta tgactcaaac tccactgtct ctgtccgtga ccccgggtca gccagcgagc 60

atttcttgca aatccagcca atctctggaa acctccaccg gcaacacgta cctgaactgg 120

tatctccaga aaccgggtca gagcccgcag ctgctgatct accgtgtatc taagcgcttc 180

tccggcgttc ctgatcgttt cagcggttct ggatccggca ccgactttac tctgaaaatc 240

agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcagctgac ccatgaacca 300

tacaccttcg gtcaaggaac taaactggaa attaaacgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 88
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5D08) heavy chain DNA

<400> 88
caggtgcaat tggttcaatc tggtgctgaa gtaaaaaaac cgggcgcttc cgttaaagtg 60

agctgcaaag catctggtta caccttcact gactatatca tgcactgggt tcgtcaggcc 120

ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat 180

accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac 240

atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtacc 300

tactactacg gttctgaact gtttgattac tggggccaag gtaccacggt gaccgtaagc 360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 89
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5D08) light chain

<400> 89

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
            20                  25                  30

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

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

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

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

Thr His Glu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205
```

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 90
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5D08) heavy chain

<400> 90

Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
20 25 30

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

```
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365
```

```
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys
    450
```

<210> 91
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5B08) light chain DNA

<400> 91

```
gatattgtta tgactcaaac tccactgtct ctgtccgtga ccccgggtca gccagcgagc       60

atttcttgca aatccagcca atctctggaa acctccaccg gcaacacgta cctgaactgg      120

tatctccaga aaccgggtca gagcccgcag ctgctgatct accgtgtatc taagcgcttc      180

tccggcgttc ctgatcgttt cagcggttct ggatccggca ccgactttac tctgaaaatc      240

agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcagctgga ttcttaccca      300

aacaccttcg gtcaaggaac taaactggaa attaaacgta cggtggctgc accatctgtc      360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg      420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa      480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc      540
```

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 92
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5B08) heavy chain DNA

<400> 92
caggtgcaat tggttcaatc tggtgctgaa gtaaaaaaac cgggcgcttc cgttaaagtg 60

agctgcaaag catctggtta caccttcact gactatatca tgcactgggt tcgtcaggcc 120

ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat 180

accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac 240

atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtacc 300

tactactacg gtccacagct gtttgattac tggggccaag gtaccacggt gaccgtaagc 360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 93
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5B08) light chain

<400> 93

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
20 25 30

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

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

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

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

Asp Ser Tyr Pro Asn Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

```
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 94
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5B08) heavy chain

<400> 94

```
Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
            20                  25                  30

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285
```

```
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys
    450
```

<210> 95
<211> 657
<212> DNA
<213> Artificial Sequence

<220>

<223> CD19 (8B8-5H09) light chain DNA

<400> 95
gatattgtta tgactcaaac tccactgtct ctgtccgtga ccccgggtca gccagcgagc 60

atttcttgca aatccagcca atctctggaa tcttccaccg gcaacacgta cctgaactgg 120

tatctccaga aaccgggtca gagcccgcag ctgctgatct accgtgtatc taagcgcttc 180

tccggcgttc ctgatcgttt cagcggttct ggatccggca ccgactttac tctgaaaatc 240

agccgtgtgg aagctgaaga cgttggcgtc tactattgtc tgcagctgat cgattaccca 300

gttaccttcg gtcaaggaac taaactggaa attaaacgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgt 657

<210> 96
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5H09) heavy chain DNA

<400> 96
caggtgcaat tggttcaatc tggtgctgaa gtaaaaaaac cgggcgcttc cgttaaagtg 60

agctgcaaag catctggtta caccttcact gactatatca tgcactgggt tcgtcaggcc 120

ccgggccagg gtctggagtg gatgggctac attaacccat acaacgacgg ttccaaatat 180

accgagaaat tccagggccg cgtcacgatg accagcgaca cttctatctc caccgcgtac 240

atggaactgt ctagactgcg ttctgacgac accgctgttt actattgtgc acgcggtacc 300

tactactacg gttctgcact gtttgattac tggggccaag gtaccacggt gaccgtaagc 360

tctgctagca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 420

gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 600

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660

cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 97
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5H09) light chain

<400> 97

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Ser Ser
20 25 30

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

```
Pro Gln Leu Leu Ile Tyr Arg Val Ser Lys Arg Phe Ser Gly Val Pro
    50                  55                  60

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

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

Ile Asp Tyr Pro Val Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 98
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5H09) heavy chain

<400> 98

```
Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
            20                  25                  30

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205
```

```
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415
```

```
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430


His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445


Pro Gly Lys
    450


<210>  99
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD19 (8B8-2B11) VH

<400>  99

Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
            20                  25                  30


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


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


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


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


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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 100
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B11) VL

<400> 100

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
20 25 30

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

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

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

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

Leu Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 101
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-7H07) VH

<400> 101

Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
20 25 30

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 102
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-7H07) VL

<400> 102

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
20 25 30

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

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

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

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

Thr His Ile Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 103
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B03) VH

<400> 103

Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
            20   25   30

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 104
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-2B03) VL

<220>
<221> misc_feature
<222> (107)..(107)
<223> Xaa can be any naturally occurring amino acid

<400> 104

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
20 25 30

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

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

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

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

Thr His Val Pro Tyr Thr Phe Gly Gln Gly Xaa Lys Leu Glu Ile Lys
100 105 110

<210> 105
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5A07) VH

<400> 105

Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
20 25 30

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 106
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5A07) VL

<400> 106

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


Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
            20                  25                  30


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


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


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


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


Gly His Tyr Pro Gly Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210>  107
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD19 (8B8-5D08) VH

<400>  107

Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
            20                  25                  30


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


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

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


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


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


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210>  108
<211>  112
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  CD19 (8B8-5D08) VL

<400>  108

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


Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
            20                  25                  30


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


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


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


Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Leu Gln Leu
                85                  90                  95
```

Thr His Glu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 109
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8-5B08) VH

<400> 109

Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
20 25 30

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 110
<211> 112
<212> PRT
<213> Artificial Sequence

<220>

<223> CD19 (8B8-5B08) VL

<400> 110

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


Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Thr Ser
            20                  25                  30


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


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


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


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


Asp Ser Tyr Pro Asn Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

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

<220>
<223> CD19 (8B8-5H09) VH

<400> 111

```
Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
            20                  25                  30


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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

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

<220>
<223> CD19 (8B8-5H09) VL

<400> 112

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Ser Ser
            20   25   30

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

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

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

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

Ile Asp Tyr Pro Val Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 113
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8) VH

<400> 113

Gln Val Gln Leu Val Gln 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 Thr Asp Tyr
20 25 30

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 114
<211> 112

<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 (8B8) VL

<400> 114

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


Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Glu Asn Ser
            20                  25                  30


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


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


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


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


Thr His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 115
<211> 556
<212> PRT
<213> Homo sapiens

<400> 115

```
Met Pro Pro Pro Arg Leu Leu Phe Phe Leu Leu Phe Leu Thr Pro Met
1               5                   10                  15


Glu Val Arg Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu Gly Asp
            20                  25                  30


Asn Ala Val Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln
```

```
        35                  40                  45

Gln Leu Thr Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu
    50                  55                  60

Ser Leu Gly Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile
65                  70                  75                  80

Trp Leu Phe Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu
                85                  90                  95

Cys Gln Pro Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr
            100                 105                 110

Val Asn Val Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp
        115                 120                 125

Leu Gly Gly Leu Gly Cys Gly Leu Lys Asn Arg Ser Ser Glu Gly Pro
    130                 135                 140

Ser Ser Pro Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala
145                 150                 155                 160

Lys Asp Arg Pro Glu Ile Trp Glu Gly Glu Pro Pro Cys Leu Pro Pro
                165                 170                 175

Arg Asp Ser Leu Asn Gln Ser Leu Ser Gln Asp Leu Thr Met Ala Pro
            180                 185                 190

Gly Ser Thr Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser
        195                 200                 205

Arg Gly Pro Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser
    210                 215                 220

Leu Leu Ser Leu Glu Leu Lys Asp Asp Arg Pro Ala Arg Asp Met Trp
225                 230                 235                 240

Val Met Glu Thr Gly Leu Leu Leu Pro Arg Ala Thr Ala Gln Asp Ala
```

```
                245                 250                 255

Gly Lys Tyr Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu
            260                 265                 270

Glu Ile Thr Ala Arg Pro Val Leu Trp His Trp Leu Leu Arg Thr Gly
        275                 280                 285

Gly Trp Lys Val Ser Ala Val Thr Leu Ala Tyr Leu Ile Phe Cys Leu
    290                 295                 300

Cys Ser Leu Val Gly Ile Leu His Leu Gln Arg Ala Leu Val Leu Arg
305                 310                 315                 320

Arg Lys Arg Lys Arg Met Thr Asp Pro Thr Arg Arg Phe Phe Lys Val
                325                 330                 335

Thr Pro Pro Pro Gly Ser Gly Pro Gln Asn Gln Tyr Gly Asn Val Leu
            340                 345                 350

Ser Leu Pro Thr Pro Thr Ser Gly Leu Gly Arg Ala Gln Arg Trp Ala
        355                 360                 365

Ala Gly Leu Gly Gly Thr Ala Pro Ser Tyr Gly Asn Pro Ser Ser Asp
    370                 375                 380

Val Gln Ala Asp Gly Ala Leu Gly Ser Arg Ser Pro Pro Gly Val Gly
385                 390                 395                 400

Pro Glu Glu Glu Glu Gly Glu Gly Tyr Glu Glu Pro Asp Ser Glu Glu
                405                 410                 415

Asp Ser Glu Phe Tyr Glu Asn Asp Ser Asn Leu Gly Gln Asp Gln Leu
            420                 425                 430

Ser Gln Asp Gly Ser Gly Tyr Glu Asn Pro Glu Asp Glu Pro Leu Gly
        435                 440                 445

Pro Glu Asp Glu Asp Ser Phe Ser Asn Ala Glu Ser Tyr Glu Asn Glu
```

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```
    450                 455                 460

Asp Glu Glu Leu Thr Gln Pro Val Ala Arg Thr Met Asp Phe Leu Ser
465                 470                 475                 480

Pro His Gly Ser Ala Trp Asp Pro Ser Arg Glu Ala Thr Ser Leu Gly
                485                 490                 495

Ser Gln Ser Tyr Glu Asp Met Arg Gly Ile Leu Tyr Ala Ala Pro Gln
            500                 505                 510

Leu Arg Ser Ile Arg Gly Gln Pro Gly Pro Asn His Glu Glu Asp Ala
        515                 520                 525

Asp Ser Tyr Glu Asn Met Asp Asn Pro Asp Gly Pro Asp Pro Ala Trp
    530                 535                 540

Gly Gly Gly Gly Arg Met Gly Thr Trp Ser Thr Arg
545                 550                 555
```