SEQUENCE LISTING

<110> KITE PHARMA, INC.

<120> CHIMERIC ANTIGEN AND T CELL RECEPTORS AND METHODS OF USE

<130> K-1031.02US

<140> 15/475,681
<141> 2017-03-31

<150> 62/317,258
<151> 2016-04-01

<160> 284

<170> PatentIn version 3.5

<210> 1
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<213> Homo sapiens

<400> 1

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Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
            20                  25                  30


Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
        35                  40                  45


Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
    50                  55                  60


Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65                  70                  75                  80


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


Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
            100                 105                 110


Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
        115                 120                 125
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Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
130 135 140

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145 150 155 160

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
165 170 175

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
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Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
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210 215 220

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tcacccttgt tccctggtcc atccaagcca 90

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<210> 5
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<210> 6
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cgggaccctg agatgggtgg caaaccaaga cgaaaaaacc cccaggaggg tctctataat 180

gagctgcaga aggataagat ggctgaagcc tattctgaaa taggcatgaa aggagagcgg 240

agaaggggaa aagggcacga cggtttgtac cagggactca gcactgctac gaaggatact 300

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Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

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<220>
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<220>
<223> VL CDR1

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<400> 40
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ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgc aagagccgag 300

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caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc cagaactcct 300

gaatactcct ccagcatatg gcactattac tacggcatgg acgtatgggg ccagggaaca 360

actgtcaccg tctcctca 378

<210> 68
<211> 369
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VH DNA

<400> 68
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcgtatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggcggtgt actactgcgt caaggggccg 300

ttgcaggagc cgccatacga ttatggaatg gacgtatggg gccagggaac aactgtcacc 360

gtctcctca 369

<210> 69
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VL DNA

<400> 69
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc aggtacttag cctggtacca acagaaacct 120

ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtcagcag agaatctcct ggcctttcac ttttggcgga 300

gggaccaagg ttgagatcaa a 321

<210> 70
<211> 336
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VL DNA

<400> 70
gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60

atctcctgca ggtctagtca gagcctcctg catagtaatg gatacaacta tttggattgg 120

tacctgcaga agccagggca gtctccacag ctcctgatct atttgggttc taatcgggcc 180

tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240

agcagagtgg aggctgagga tgttggggtt tattactgca tgcagggact cggcctccct 300

ctcacttttg gcggagggac caaggttgag atcaaa 336

<210> 71
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VL DNA

<400> 71
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcag tacgccgcct accctacttt tggcggaggg 300

accaaggttg agatcaaa 318

<210> 72
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VL DNA

<400> 72
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agctacttag cctggtacca acagaaacct 120

ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtcagcag agacacgtct ggcctcctac ttttggcgga 300

gggaccaagg ttgagatcaa a 321

<210> 73
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VL DNA

<400> 73
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc aggtacttag cctggtacca acagaaacct 120

ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtcagcag agattctact acccttggac ttttggcgga 300

gggaccaagg ttgagatcaa a 321

<210> 74
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>

<223> VL DNA

<400> 74
gacatccagt tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcacttgtc gggcgagtca gggtattagc agctggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatggt gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcagcag atatacacct tccctttcac ttttggcgga 300

gggaccaagg ttgagatcaa a 321

<210> 75
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VL DNA

<400> 75
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcagtt cgcccacact 300

cctttcactt ttggcggagg gaccaaggtt gagatcaaa 339

<210> 76
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VL DNA

<400> 76
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatagc gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcag caccacgtct ggcctctcac ttttggcgga 300

gggaccaagg ttgagatcaa a 321

<210> 77
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> VH Protein

<400> 77
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

Ala Arg Ala Glu Met Gly Ala Val Phe Asp Ile Trp Gly Gln Gly Thr
100 105 110

Met Val Thr Val Ser Ser
        115

<210> 78
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<220>
<223> VH Protein

<400> 78
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1   5   10   15

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

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

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

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

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

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

Gly Arg Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 79
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> VH Protein

<400> 79
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 Ser Tyr
20 25 30

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

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

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

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

Ala Arg Glu Ser Trp Pro Met Asp Val Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 80
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> VH Protein

<400> 80

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

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

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

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

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

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

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

Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 81
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> VH Protein

<400> 81
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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        35                  40                  45

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

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

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

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

Thr Leu Val Thr Val Ser Ser
        115


<210> 82
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<220>
<223> VH Protein

<400> 82
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

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

<210> 83
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> VH Protein

<400> 83
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

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

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

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

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

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

Ala Arg Thr Pro Glu Tyr Ser Ser Ser Ile Trp His Tyr Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 84
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> VH Protein

<400> 84
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

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

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

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

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

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

Val Lys Gly Pro Leu Gln Glu Pro Pro Tyr Asp Tyr Gly Met Asp Val
100 105 110

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

<210> 85
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> VL Protein

<400> 85
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

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

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ile Ser Trp Pro Phe
85 90 95

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

<210> 86
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> VL Protein

<400> 86
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
            20   25   30

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

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala 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 Met Gln Gly
                85   90   95

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

<210> 87
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<220>
<223> VL Protein

<400> 87
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1   5   10   15

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

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

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser

65 70 75 80

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

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

<210> 88
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> VL Protein

<400> 88
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

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

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

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

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

<210> 89
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> VL Protein

<400> 89
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

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

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

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

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

<210> 90
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> VL Protein

<400> 90
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

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

<210> 91
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<220>
<223> VL Protein

<400> 91
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1   5   10   15

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

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

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

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

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

Phe Ala His Thr Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 92
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> VL Protein

<400> 92
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

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

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

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

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

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

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

<210> 93
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VH CDR1

<400> 93
Gly Gly Ser Ile Ser Ser Tyr
1 5

<210> 94
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VH CDR1

<400> 94
Gly Gly Ser Ile Ser Ser Gly Gly Phe
1 5

<210> 95
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VH CDR1

<400> 95
Gly Tyr Thr Leu Thr Glu Leu
1 5

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

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VH CDR1

<400> 96
Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 97
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VH CDR2

<400> 97
Tyr Tyr Ser Gly Ser
1 5

<210> 98
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VH CDR2

<400> 98
His His Ser Gly Ser
1 5

<210> 99
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VH CDR2

<400> 99
Asp Pro Glu Asp Gly Glu
1 5

<210> 100
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VH CDR2

<400> 100
Ser Tyr Asp Gly Ser Asp
1 5

<210> 101
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VH CDR3

<400> 101
Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr
1 5 10

<210> 102
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VH CDR3

<400> 102
Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr
1 5 10

<210> 103
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VH CDR3

<400> 103
Glu Ser Arg Gly Ile Gly Trp Pro Tyr Phe Asp Tyr
1 5 10

<210> 104
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VH CDR3

<400> 104
Glu Arg Tyr Ser Gly Arg Asp Tyr
1 5

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

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VL CDR1

<400> 105
Gln Ala Ser Gln Asp Ile Asn Asn Phe Leu Asn
1   5   10

<210> 106
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<223> VL CDR1

<400> 106
Gln Ala Ser Gln Asp Ile Asn Asn Phe Leu Asn
1   5   10

<210> 107
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<223> VL CDR1

<400> 107
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1   5   10

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

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<223> VL CDR1

<400> 108
Arg Ala Ser Gln Ser Val Ser Ser Leu Leu Thr
1   5   10

<210> 109
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<223> VL CDR2

<400> 109
Asp Ala Ser Asn Leu Glu Thr
1   5

<210> 110
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<223> VL CDR2

<400> 110
Asp Ala Ser Asn Leu Glu Thr
1   5

<210> 111
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<223> VL CDR2

<400> 111
Gly Ala Ser Ser Leu Lys Ser

1 5

<210> 112
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VL CDR2

<400> 112
Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 113
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VL CDR3

<400> 113
Gln Gln Tyr Gly Asn Leu Pro Phe Thr
1 5

<210> 114
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> VL CDR3

<400> 114
Gln Gln Tyr Gly Asn Leu Pro Phe Thr
1 5

<210> 115
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VL CDR3

<400> 115
Gln Gln Ser Tyr Ser Thr Pro Ile Thr
1 5

<210> 116
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<223> VL CDR3

<400> 116
Gln Gln Tyr Asp Thr Trp Pro Phe Thr
1 5

<210> 117
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VH DNA

<400> 117
caggtgcagc tgcaggaatc cggaccgggg ctggtgaagc ccagcgagac tctgagtctc 60

acgtgtacag tttctggagg tagcattagc tcctactatt ggtcatggat aaggcagccc 120

cccgggaagg gattggaatg gatcggctat atttactaca gtgggagcac caattacaac 180

ccctcactga agtctagagt tacaatcagc gttgacacct caaagaatca gttcagtttg 240

aaattgtcta gcgtcacagc agctgataca gccgtctatt attgtgtttc tctggtctat 300

tgcggtgggg attgttacag tggctttgac tattgggggc agggtactct ggttacagtt 360

tcttcc 366

<210> 118
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VH DNA

<400> 118
caggtacagc tgcaggaatc tgggcccgga cttgtcaagc caagtcagac actttctctt 60

acatgtaccg tgagcggcgg aagtataagc agtggaggct tttactggtc ttggatacgg 120

cagcacccag gcaaaggctt ggagtggatt ggatacattc atcattcagg atctacacac 180

tataatccat cccttaagtc ccgggtcacc attagcattg atacgtctaa gaatctgttc 240

agtctcaggc tgtcctccgt cactgctgcc gacacagccg tgtactactg cgcctccttg 300

gtttactgcg gaggcgactg ttatagcggc tttgattatt gggggcaggg gaccctcgta 360

accgtgagct ct 372

<210> 119
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VH DNA

<400> 119
caggtccaac tggtgcagtc cggagccgaa gtcaagaaac caggtgcctc cgttaaagtg 60

agttgcaaag tctctggata cactctgacc gagctctcta tgcactgggt ccggcaggcc 120

cccggcaagg gattggaatg gatgggcggg ttcgatcctg aggacggaga gactatctac 180

gctcaaaaat tccagggacg agtgactgtg accgaagaca ctagtaccga cactgcctac 240

atggaacttt cctctctgcg atcagaagat accgcagtgt actactgtgc tactgaatct 300

aggggcattg gatggcccta cttcgattac tggggtcagg gaactctggt gactgtctcc 360

agc 363

<210> 120
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VH DNA

<400> 120
caggtccagt tggtcgaaag tggcggtggt gtagtgcagc cgggccgcag tttgaggctt 60

tcctgtgcgg cttcaggctt tacttttcc agctatggaa tgcactgggt gcggcaggcc 120

cccggcaaag gacttgagtg ggtggccgtc atttcttatg acggatcaga taagtactac 180

gtggacagcg tcaagggcag attcaccatc tctagggaca acagtaaaaa tagactctac 240

ctccagatga atagcctcag agctgaagac acggccgtct actattgtgc tcgggagcgg 300

tatagtggca gagactactg ggggcagggc acactcgtta cagtgagtag c 351

<210> 121
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VL DNA

<400> 121
gacatccagt tgacacagag cccgagttcc ttgtccgcct ccgtcgggga tagagtgtca 60

tttacctgtc aggcctctca ggatattaat aactttctga attggtatca gcaaaagccc 120

ggaaaggcac ccaagctgtt gatttacgac gccagtaacc tggagacagg cgtgccctcc 180

cggtttagtg gtagcggaag cggtacggat tttaccttta ctatcagctc tctccaaccc 240

gaagacattg caacctacta ttgtcaacaa tatggaaacc tgccttttac atttggcggc 300

ggcaccaagg tggagattaa gcgg 324

<210> 122
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VL DNA

<400> 122
gatatccagc tcactcaaag cccctctagt ctctctgcct cagtggggga tcgggtcagt 60

tttacttgtc aagcttcaca ggatatcaac aacttcctta attggtatca gcagaagcca 120

ggaaaagcac ccaagctgct catctatgat gcctcaaatt tggagacggg tgttcccagt 180

cgattctctg ggtcagggtc cgggaccgac tttacgttta cgatctcctc tctgcagccc 240

gaagacatcg ccacatacta ttgtcaacag tacggcaact tgcctttcac atttgggggc 300

gggactaagg ttgaaatcaa gagg 324

<210> 123
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VL DNA

<400> 123
gatattcaga tgactcaatc tccttcttct ctgtccgctt ccgtgggcga tagagtgacc 60

attacttgta gggcgtccca gtcaatctcc agttatttga attggtatca gcagaagccc 120

gggaaagcac ctaagctgtt gatcagcggg gcttctagcc tgaagagtgg ggtaccttca 180

cggttcagcg gaagcggaag cggaaccgat ttcaccctga ctatcagcag cctgccacct 240

gaggactttg caacttacta ctgccaacag tcatacagca ctccgatcac tttcggccag 300

ggcacccggc tcgaaatcaa gcgc 324

<210> 124
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> VL DNA

<400> 124
gagattgtta tgacccagag tcctgcgacc ctctcagtca gccccgggga gcgcgcaact 60

ttgtcttgca gagctagtca gtccgtgtcc tctcttctga catggtacca gcaaaagccc 120

gggcaggctc cgcgcctttt gatctttggg gcttcaacaa gagccactgg gattcccgca 180

cgattctctg gctccgggag cggtactggt ttcaccctga cgattagcag tctccagagc 240

gaggacttcg ccgtatacta ctgccagcag tacgatacgt ggccattcac ttttggacca 300

gggactaaag tggattttaa gcgc 324

<210> 125
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> VH AA

<400> 125
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

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

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

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

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

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

Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr Trp
100 105 110

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

<210> 126
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> VH AA

<400> 126
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

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

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

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

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

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

Cys Ala Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp
100 105 110

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

<210> 127
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> VH AA

<400> 127
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 Val Ser Gly Tyr Thr Leu Thr Glu Leu
20 25 30

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 128
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<220>
<223> VH AA

<400> 128
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1   5   10   15

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

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

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

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

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

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

Val Thr Val Ser Ser
        115

<210> 129
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> VL AA

<400> 129
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

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

<210> 130
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> VL AA

<400> 130
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
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<210> 131
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> VL AA

<400> 131

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

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

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

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

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

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

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

<210> 132
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> VL AA

<400> 132
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

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

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

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

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

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

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

<210> 133
<211> 1437

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> FS-21495CARDNAHxL

<400> 133
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaggtgc agctgttgga gtctggggga ggcttggtac agcctggggg gtccctgaga 120

ctctcctgtg cagcctctgg attcaccttt agcagctatg ccatgagctg ggtccgccag 180

gctccaggga aggggctgga gtgggtctca gctattagtg gtagtggtgg tagcacatac 240

tacgcagact ccgtgaaggg ccggttcacc atctccagag acaattccaa gaacacgctg 300

tatctgcaaa tgaacagcct gagagccgag gacacggcgg tgtactactg cgcaagagcc 360

gagatgggag ccgtattcga catatggggt cagggtacaa tggtcaccgt ctcctcaggg 420

tctacatccg gctccgggaa gcccggaagt ggcgaaggta gtacaaaggg ggaaattgtg 480

ttgacacagt ctccagccac cctgtctttg tctccagggg aaagagccac cctctcctgc 540

agggccagtc agagtgttag caggtactta gcctggtacc aacagaaacc tggccaggct 600

cccaggctcc tcatctatga tgcatccaac agggccactg gcatcccagc caggttcagt 660

ggcagtgggt ctgggacaga cttcactctc accatcagca gcctagagcc tgaagatttt 720

gcagtttatt actgtcagca gagaatctcc tggcctttca cttttggcgg agggaccaag 780

gttgagatca aacgggccgc tgcccttgat aatgaaaagt caaacggaac aatcattcac 840

gtgaagggca agcacctctg tccgtcaccc ttgttccctg gtccatccaa gccattctgg 900

gtgttggtcg tagtgggtgg agtcctcgct tgttactctc tgctcgtcac cgtggctttt 960

ataatcttct gggttagatc caaaagaagc cgcctgctcc atagcgatta catgaatatg 1020

actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat 1080

ttcgctgcct atcggagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag 1140

cagggccaga accaactgta taacgagctc aacctgggac gcagggaaga gtatgacgtt 1200

ttggacaagc gcagaggacg ggaccctgag atgggtggca aaccaagacg aaaaaacccc 1260

caggagggtc tctataatga gctgcagaag gataagatgg ctgaagccta ttctgaaata 1320

ggcatgaaag gagagcggag aaggggaaaa gggcacgacg gtttgtacca gggactcagc 1380

actgctacga aggatactta tgacgctctc cacatgcaag ccctgccacc taggtaa 1437

<210> 134
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> FS-21495CARHxL

<400> 134
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Ala Glu Met Gly Ala Val Phe Asp Ile
115 120 125

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Ser Thr Ser Gly
130 135 140

```
Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Ile Val
145                 150                 155                 160

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
                165                 170                 175

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Ala Trp
            180                 185                 190

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala
        195                 200                 205

Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
    210                 215                 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
225                 230                 235                 240

Ala Val Tyr Tyr Cys Gln Gln Arg Ile Ser Trp Pro Phe Thr Phe Gly
                245                 250                 255

Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Leu Asp Asn Glu
            260                 265                 270

Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro
        275                 280                 285

Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val
    290                 295                 300

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
305                 310                 315                 320

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
                325                 330                 335

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
            340                 345                 350

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
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        355                 360                 365

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
    370                 375                 380

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
385                 390                 395                 400

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
                405                 410                 415

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
            420                 425                 430

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
        435                 440                 445

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
    450                 455                 460

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465                 470                 475


<210> 135
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<220>
<223> FS-21495CARDNALxH

<400> 135
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc       60

ccggaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc      120

accctctcct gcagggccag tcagagtgtt agcaggtact tagcctggta ccaacagaaa      180

cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca      240

gccaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagcctagag      300
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cctgaagatt ttgcagttta ttactgtcag cagagaatct cctggccttt cacttttggc 360

ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420

ggcgaaggta gtacaaaggg ggaggtgcag ctgttggagt ctgggggagg cttggtacag 480

cctgggggt ccctgagact ctcctgtgca gcctctggat tcacctttag cagctatgcc 540

atgagctggg tccgccaggc tccagggaag gggctggagt gggtctcagc tattagtggt 600

agtggtggta gcacatacta cgcagactcc gtgaagggcc ggttcaccat ctccagagac 660

aattccaaga acacgctgta tctgcaaatg aacagcctga gagccgagga cacggcggtg 720

tactactgcg caagagccga gatgggagcc gtattcgaca tatggggtca gggtacaatg 780

gtcaccgtct cctcagccgc tgcccttgat aatgaaaagt caaacggaac aatcattcac 840

gtgaagggca agcacctctg tccgtcaccc ttgttccctg gtccatccaa gccattctgg 900

gtgttggtcg tagtgggtgg agtcctcgct tgttactctc tgctcgtcac cgtggctttt 960

ataatcttct gggttagatc caaaagaagc cgcctgctcc atagcgatta catgaatatg 1020

actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat 1080

ttcgctgcct atcggagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag 1140

cagggccaga accaactgta taacgagctc aacctgggac gcagggaaga gtatgacgtt 1200

ttggacaagc gcagaggacg ggaccctgag atgggtggca aaccaagacg aaaaaacccc 1260

caggagggtc tctataatga gctgcagaag gataagatgg ctgaagccta ttctgaaata 1320

ggcatgaaag gagagcggag aaggggaaaa gggcacgacg gtttgtacca gggactcagc 1380

actgctacga aggatactta tgacgctctc cacatgcaag ccctgccacc taggtaa 1437

<210> 136
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> FS-21495CARLxH

<400> 136
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

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

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

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

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

Ile Ser Trp Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

Arg Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser
    130                 135                 140

Thr Lys Gly Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
145                 150                 155                 160

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
                165                 170                 175

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
            180                 185                 190

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
        195                 200                 205

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
    210                 215                 220
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Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225                 230                 235                 240

Tyr Tyr Cys Ala Arg Ala Glu Met Gly Ala Val Phe Asp Ile Trp Gly
                245                 250                 255

Gln Gly Thr Met Val Thr Val Ser Ser Ala Ala Ala Leu Asp Asn Glu
            260                 265                 270

Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro
        275                 280                 285

Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val
    290                 295                 300

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
305                 310                 315                 320

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
                325                 330                 335

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
            340                 345                 350

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
        355                 360                 365

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
    370                 375                 380

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
385                 390                 395                 400

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
                405                 410                 415

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
            420                 425                 430

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
        435                 440                 445
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Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
450 455 460

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 137
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> PC-21497CARDNAHxL

<400> 137
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgga gtctggggga ggcgtggtcc agcctgggag gtccctgaga 120

ctctcctgtg cagcgtctgg attcaccttc agtagctatg gcatgcactg ggtccgccag 180

gctccaggca aggggctgga gtgggtggca gttatatcgt atgatggaag taataaatac 240

tatgcagact ccgtgaaggg ccgattcacc atctccagag acaattccaa gaacacgctg 300

tatctgcaaa tgaacagcct gagagccgag gacacggcgg tgtactactg cgccagagac 360

ggtacttatc taggtggtct ctggtacttc gacttatggg ggagaggtac cttggtcacc 420

gtctcctcag ggtctacatc cggctccggg aagcccggaa gtggcgaagg tagtacaaag 480

ggggatattg tgatgactca gtctccactc tccctgcccg tcacccctgg agagccggcc 540

tccatctcct gcaggtctag tcagagcctc ctgcatagta atggatacaa ctatttggat 600

tggtacctgc agaagccagg gcagtctcca cagctcctga tctatttggg ttctaatcgg 660

gcctccgggg tccctgacag gttcagtggc agtggatcag gcacagattt tacactgaaa 720

atcagcagag tggaggctga ggatgttggg gtttattact gcatgcaggg actcggcctc 780

cctctcactt ttggcggagg gaccaaggtt gagatcaaac gggccgctgc ccttgataat 840

gaaaagtcaa acggaacaat cattcacgtg aagggcaagc acctctgtcc gtcacccttg 900

ttccctggtc catccaagcc attctgggtg ttggtcgtag tgggtggagt cctcgcttgt 960

tactctctgc tcgtcaccgt ggcttttata atcttctggg ttagatccaa aagaagccgc 1020

ctgctccata gcgattacat gaatatgact ccacgccgcc ctggccccac aaggaaacac 1080

taccagcctt acgcaccacc tagagatttc gctgcctatc ggagcagggt gaagttttcc 1140

agatctgcag atgcaccagc gtatcagcag ggccagaacc aactgtataa cgagctcaac 1200

ctgggacgca gggaagagta tgacgttttg gacaagcgca gaggacggga ccctgagatg 1260

ggtggcaaac caagacgaaa aaacccccag gagggtctct ataatgagct gcagaaggat 1320

aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1380

cacgacggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1440

atgcaagccc tgccacctag gtaa 1464

<210> 138
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> PC-21497CARHxL

<400> 138
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr
65 70 75 80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser

```
                85                  90                  95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Asp Gly Thr Tyr Leu Gly Gly Leu Trp
        115                 120                 125

Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly
    130                 135                 140

Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys
145                 150                 155                 160

Gly Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro
                165                 170                 175

Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His
            180                 185                 190

Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
        195                 200                 205

Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val
    210                 215                 220

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

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
                245                 250                 255

Gly Leu Gly Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
            260                 265                 270

Lys Arg Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile
        275                 280                 285

His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro
    290                 295                 300
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Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
305                 310                 315                 320

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
                325                 330                 335

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
            340                 345                 350

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
        355                 360                 365

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
    370                 375                 380

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385                 390                 395                 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
                405                 410                 415

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
            420                 425                 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
        435                 440                 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
    450                 455                 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465                 470                 475                 480

Met Gln Ala Leu Pro Pro Arg
                485
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<210> 139
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> PC-21497CARDNALxH

<400> 139
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ccggatattg tgatgactca gtctccactc tccctgcccg tcacccctgg agagccggcc 120

tccatctcct gcaggtctag tcagagcctc ctgcatagta atggatacaa ctatttggat 180

tggtacctgc agaagccagg gcagtctcca cagctcctga tctatttggg ttctaatcgg 240

gcctccgggg tccctgacag gttcagtggc agtggatcag gcacagattt tacactgaaa 300

atcagcagag tggaggctga ggatgttggg gtttattact gcatgcaggg actcggcctc 360

cctctcactt ttggcggagg gaccaaggtt gagatcaaac gggggtctac atccggctcc 420

gggaagcccg gaagtggcga aggtagtaca aaggggcagg tgcagctggt ggagtctggg 480

ggaggcgtgg tccagcctgg gaggtccctg agactctcct gtgcagcgtc tggattcacc 540

ttcagtagct atggcatgca ctgggtccgc caggctccag gcaaggggct ggagtgggtg 600

gcagttatat cgtatgatgg aagtaataaa tactatgcag actccgtgaa gggccgattc 660

accatctcca gagacaattc caagaacacg ctgtatctgc aaatgaacag cctgagagcc 720

gaggacacgg cggtgtacta ctgcgccaga gacggtactt atctaggtgg tctctggtac 780

ttcgacttat gggggagagg taccttggtc accgtctcct cagccgctgc ccttgataat 840

gaaaagtcaa acggaacaat cattcacgtg aagggcaagc acctctgtcc gtcacccttg 900

ttccctggtc catccaagcc attctgggtg ttggtcgtag tgggtggagt cctcgcttgt 960

tactctctgc tcgtcaccgt ggcttttata atcttctggg ttagatccaa aagaagccgc 1020

ctgctccata gcgattacat gaatatgact ccacgccgcc ctggccccac aaggaaacac 1080

taccagcctt acgcaccacc tagagatttc gctgcctatc ggagcagggt gaagttttcc 1140

agatctgcag atgcaccagc gtatcagcag ggccagaacc aactgtataa cgagctcaac 1200

ctgggacgca gggaagagta tgacgttttg gacaagcgca gaggacggga ccctgagatg 1260

ggtggcaaac caagacgaaa aaacccccag gagggtctct ataatgagct gcagaaggat 1320

aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1380

cacgacggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1440

atgcaagccc tgccacctag gtaa 1464

<210> 140
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> PC-21497CARHxL

<400> 140
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln
50 55 60

Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg
65 70 75 80

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

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

Tyr Cys Met Gln Gly Leu Gly Leu Pro Leu Thr Phe Gly Gly Gly Thr
115 120 125

Lys Val Glu Ile Lys Arg Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly
130 135 140

```
Ser Gly Glu Gly Ser Thr Lys Gly Gln Val Gln Leu Val Glu Ser Gly
145                 150                 155                 160

Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala
                165                 170                 175

Ser Gly Phe Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala
            180                 185                 190

Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser
        195                 200                 205

Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
    210                 215                 220

Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
225                 230                 235                 240

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Gly Thr Tyr Leu Gly
                245                 250                 255

Gly Leu Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val
            260                 265                 270

Ser Ser Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile
        275                 280                 285

His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro
    290                 295                 300

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

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
                325                 330                 335

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
            340                 345                 350

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
        355                 360                 365
```

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
370 375 380

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385 390 395 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
405 410 415

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
420 425 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
435 440 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
450 455 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465 470 475 480

Met Gln Ala Leu Pro Pro Arg
485

<210> 141
<211> 1428
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> AJ-21508CARDNAHxL

<400> 141
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctggggc ctcagtgaag 120

gtttcctgca aggcatctgg atacaccttc accagctact atatgcactg ggtgcgacag 180

gcccctggac aagggcttga gtggatggga ataatcaacc ctggtggtgg tagcacaagc 240

tacgcacaga agttccaggg cagagtcacc atgaccaggg acacgtccac gagcacagtc 300

tacatggagc tgagcagcct gagatctgag gacacggcgg tgtactactg cgccagagag 360

agttggccaa tggacgtatg gggccaggga acaactgtca ccgtctcctc agggtctaca 420

tccggctccg ggaagcccgg aagtggcgaa ggtagtacaa agggggaaat agtgatgacg 480

cagtctccag ccaccctgtc tgtgtctcca ggggaaagag ccaccctctc ctgcagggcc 540

agtcagagtg ttagcagcaa cttagcctgg taccagcaga aacctggcca ggctcccagg 600

ctcctcatct atggtgcatc caccagggcc actggtatcc cagccaggtt cagtggcagt 660

gggtctggga cagagttcac tctcaccatc agcagcctgc agtctgaaga ttttgcagtt 720

tattactgtc agcagtacgc cgcctaccct acttttggcg gagggaccaa ggttgagatc 780

aaacgggccg ctgcccttga taatgaaaag tcaaacggaa caatcattca cgtgaagggc 840

aagcacctct gtccgtcacc cttgttccct ggtccatcca agccattctg ggtgttggtc 900

gtagtgggtg gagtcctcgc ttgttactct ctgctcgtca ccgtggcttt tataatcttc 960

tgggttagat ccaaaagaag ccgcctgctc catagcgatt acatgaatat gactccacgc 1020

cgccctggcc ccacaaggaa acactaccag ccttacgcac cacctagaga tttcgctgcc 1080

tatcggagca gggtgaagtt ttccagatct gcagatgcac cagcgtatca gcagggccag 1140

aaccaactgt ataacgagct caacctggga cgcagggaag agtatgacgt tttggacaag 1200

cgcagaggac gggaccctga gatgggtggc aaaccaagac gaaaaaaccc ccaggagggt 1260

ctctataatg agctgcagaa ggataagatg gctgaagcct attctgaaat aggcatgaaa 1320

ggagagcgga gaaggggaaa agggcacgac ggtttgtacc agggactcag cactgctacg 1380

aaggatactt atgacgctct ccacatgcaa gccctgccac ctaggtaa 1428

<210> 142
<211> 475
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> AJ-21508CARHxL

<400> 142
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
            20   25   30

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

Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
    50   55   60

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

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
                85   90   95

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

Ala Val Tyr Tyr Cys Ala Arg Glu Ser Trp Pro Met Asp Val Trp Gly
        115   120   125

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly
    130   135   140

Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Ile Val Met Thr
145   150   155   160

Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu
                165   170   175

Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln
            180   185   190

Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr
        195   200   205

Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr

```
    210                 215                 220

Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val
225                 230                 235                 240

Tyr Tyr Cys Gln Gln Tyr Ala Ala Tyr Pro Thr Phe Gly Gly Gly Thr
                245                 250                 255

Lys Val Glu Ile Lys Arg Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn
            260                 265                 270

Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu
        275                 280                 285

Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly
    290                 295                 300

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
305                 310                 315                 320

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
                325                 330                 335

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
            340                 345                 350

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser
        355                 360                 365

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
    370                 375                 380

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
385                 390                 395                 400

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
                405                 410                 415

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
            420                 425                 430
```

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
435 440 445

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
450 455 460

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 143
<211> 1428
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> AJ-21508CARDNALxH

<400> 143
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaaatag tgatgacgca gtctccagcc accctgtctg tgtctccagg ggaaagagcc 120

accctctcct gcagggccag tcagagtgtt agcagcaact tagcctggta ccagcagaaa 180

cctggccagg ctcccaggct cctcatctat ggtgcatcca ccagggccac tggtatccca 240

gccaggttca gtggcagtgg gtctgggaca gagttcactc tcaccatcag cagcctgcag 300

tctgaagatt ttgcagttta ttactgtcag cagtacgccg cctaccctac ttttggcgga 360

gggaccaagg ttgagatcaa acgggggtct acatccggct ccgggaagcc cggaagtggc 420

gaaggtagta caaaggggca ggtgcagctg gtgcagtctg gggctgaggt gaagaagcct 480

ggggcctcag tgaaggtttc ctgcaaggca tctggataca ccttcaccag ctactatatg 540

cactgggtgc gacaggcccc tggacaaggg cttgagtgga tgggaataat caaccctggt 600

ggtggtagca caagctacgc acagaagttc cagggcagag tcaccatgac cagggacacg 660

tccacgagca cagtctacat ggagctgagc agcctgagat ctgaggacac ggcggtgtac 720

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aagcacctct gtccgtcacc cttgttccct ggtccatcca agccattctg ggtgttggtc 900

gtagtgggtg gagtcctcgc ttgttactct ctgctcgtca ccgtggcttt tataatcttc 960

tgggttagat ccaaaagaag ccgcctgctc catagcgatt acatgaatat gactccacgc 1020

cgccctggcc ccacaaggaa acactaccag ccttacgcac cacctagaga tttcgctgcc 1080

tatcggagca gggtgaagtt ttccagatct gcagatgcac cagcgtatca gcagggccag 1140

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cgcagaggac gggaccctga gatgggtggc aaaccaagac gaaaaaaccc ccaggagggt 1260

ctctataatg agctgcagaa ggataagatg gctgaagcct attctgaaat aggcatgaaa 1320

ggagagcgga gaaggggaaa agggcacgac ggtttgtacc agggactcag cactgctacg 1380

aaggatactt atgacgctct ccacatgcaa gccctgccac ctaggtaa 1428

<210> 144
<211> 475
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> AJ-21508CARLxH

<400> 144
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

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

```
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
                85                  90                  95

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

Ala Ala Tyr Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
        115                 120                 125

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
    130                 135                 140

Lys Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
145                 150                 155                 160

Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
                165                 170                 175

Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
            180                 185                 190

Trp Met Gly Ile Ile Asn Pro Gly Gly Gly Ser Thr Ser Tyr Ala Gln
        195                 200                 205

Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr
    210                 215                 220

Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
225                 230                 235                 240

Tyr Cys Ala Arg Glu Ser Trp Pro Met Asp Val Trp Gly Gln Gly Thr
                245                 250                 255

Thr Val Thr Val Ser Ser Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn
            260                 265                 270

Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu
        275                 280                 285

Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly
    290                 295                 300
```

```
Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
305                 310                 315                 320

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
                325                 330                 335

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
            340                 345                 350

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser
        355                 360                 365

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
    370                 375                 380

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
385                 390                 395                 400

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
                405                 410                 415

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
            420                 425                 430

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
        435                 440                 445

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
    450                 455                 460

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465                 470                 475
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<210> 145
<211> 1449
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> NM-21517CARDNAHxL

<400> 145
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ccgcagctgc agctgcagga gtcgggccca ggactggtga agccttcgga gaccctgtcc 120

ctcacctgca ctgtctctgg tggctccatc agcagtagta gttactactg gggctggatc 180

cgccagcccc cagggaaggg gctggagtgg attgggagta tctcctatag tgggagcacc 240

tactacaacc cgtccctcaa gagtcgagtc accatatccg tagacacgtc caagaaccag 300

ttctccctga agctgagttc tgtgaccgcc gcagacacgg cggtgtacta ctgcgccaga 360

ggcaggggat atgcaaccag cttagccttc gatatctggg gtcagggtac aatggtcacc 420

gtctcctcag ggtctacatc cggctccggg aagcccggaa gtggcgaagg tagtacaaag 480

ggggaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc 540

accctctcct gcagggccag tcagagtgtt agcagctact tagcctggta ccaacagaaa 600

cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 660

gccaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagcctagag 720

cctgaagatt ttgcagttta ttactgtcag cagagacacg tctggcctcc tacttttggc 780

ggagggacca aggttgagat caaacgggcc gctgcccttg ataatgaaaa gtcaaacgga 840

acaatcattc acgtgaaggg caagcacctc tgtccgtcac ccttgttccc tggtccatcc 900

aagccattct gggtgttggt cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc 960

accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat 1020

tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1080

ccacctagag atttcgctgc ctatcggagc agggtgaagt tttccagatc tgcagatgca 1140

ccagcgtatc agcagggcca gaaccaactg tataacgagc tcaacctggg acgcagggaa 1200

gagtatgacg ttttggacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga 1260

cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc 1320

tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac 1380

cagggactca gcactgctac gaaggatact tatgacgctc tccacatgca agccctgcca 1440

cctaggtaa 1449

<210> 146
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> NM-21517CARHxL

<400> 146
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu
20 25 30

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

Ser Ile Ser Ser Ser Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro
50 55 60

Gly Lys Gly Leu Glu Trp Ile Gly Ser Ile Ser Tyr Ser Gly Ser Thr
65 70 75 80

Tyr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr
85 90 95

Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Arg Gly Tyr Ala Thr Ser Leu
115 120 125

Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly
130 135 140

Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys
145 150 155 160

```
Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
                165                 170                 175

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser
            180                 185                 190

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        195                 200                 205

Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
    210                 215                 220

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
225                 230                 235                 240

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg His Val Trp Pro
                245                 250                 255

Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala
            260                 265                 270

Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys
        275                 280                 285

His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp
    290                 295                 300

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
305                 310                 315                 320

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
                325                 330                 335

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
            340                 345                 350

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
        355                 360                 365

Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
```

```
    370                 375                 380

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
385                 390                 395                 400

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
                405                 410                 415

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
            420                 425                 430

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
        435                 440                 445

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
    450                 455                 460

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
465                 470                 475                 480

Pro Arg
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<210> 147
<211> 1449
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> NM-21517CARDNALxH

<400> 147

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ccggaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc      120

accctctcct gcagggccag tcagagtgtt agcagctact tagcctggta ccaacagaaa      180

cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca      240

gccaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagcctagag      300
```

cctgaagatt ttgcagttta ttactgtcag cagagacacg tctggcctcc tacttttggc 360

ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420

ggcgaaggta gtacaaaggg gcagctgcag ctgcaggagt cgggcccagg actggtgaag 480

ccttcggaga ccctgtccct cacctgcact gtctctggtg gctccatcag cagtagtagt 540

tactactggg gctggatccg ccagccccca gggaaggggc tggagtggat tgggagtatc 600

tcctatagtg ggagcaccta ctacaacccg tccctcaaga gtcgagtcac catatccgta 660

gacacgtcca agaaccagtt ctccctgaag ctgagttctg tgaccgccgc agacacggcg 720

gtgtactact gcgccagagg caggggatat gcaaccagct tagccttcga tatctggggt 780

cagggtacaa tggtcaccgt ctcctcagcc gctgcccttg ataatgaaaa gtcaaacgga 840

acaatcattc acgtgaaggg caagcacctc tgtccgtcac ccttgttccc tggtccatcc 900

aagccattct gggtgttggt cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc 960

accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat 1020

tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1080

ccacctagag atttcgctgc ctatcggagc agggtgaagt tttccagatc tgcagatgca 1140

ccagcgtatc agcagggcca gaaccaactg tataacgagc tcaacctggg acgcagggaa 1200

gagtatgacg ttttggacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga 1260

cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc 1320

tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac 1380

cagggactca gcactgctac gaaggatact tatgacgctc tccacatgca agccctgcca 1440

cctaggtaa 1449

<210> 148
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> NM-21517CARLxH

<400> 148

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Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

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

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

Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60

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

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

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

His Val Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

Arg Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser
    130                 135                 140

Thr Lys Gly Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
145                 150                 155                 160

Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
                165                 170                 175

Ser Ser Ser Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys
            180                 185                 190

Gly Leu Glu Trp Ile Gly Ser Ile Ser Tyr Ser Gly Ser Thr Tyr Tyr
        195                 200                 205

Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
    210                 215                 220
```

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Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
225                 230                 235                 240

Val Tyr Tyr Cys Ala Arg Gly Arg Gly Tyr Ala Thr Ser Leu Ala Phe
                245                 250                 255

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ala Ala
            260                 265                 270

Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys
        275                 280                 285

His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp
    290                 295                 300

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
305                 310                 315                 320

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
                325                 330                 335

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
            340                 345                 350

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
        355                 360                 365

Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
    370                 375                 380

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
385                 390                 395                 400

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
                405                 410                 415

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
            420                 425                 430
```

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
435 440 445

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
450 455 460

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
465 470 475 480

Pro Arg

<210> 149
<211> 1440
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> TS-21522CARDNAHxL

<400> 149
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ccggaggtgc agctggtgga gtctggggga ggcttggtac agcctggggg gtccctgaga 120

ctctcctgtg cagcctctgg attcaccttc agtagctata gcatgaactg ggtccgccag 180

gctccaggga aggggctgga gtgggtttca accattagta gtagtagtag taccatatac 240

tacgcagact ctgtgaaggg ccgattcacc atctccagag acaatgccaa gaactcactg 300

tatctgcaaa tgaacagcct gagagctgag gacacggcgg tgtactactg cgccagaggt 360

tctcaggagc acctgatttt cgattattgg ggacagggta cattggtcac cgtctcctca 420

gggtctacat ccggctccgg gaagcccgga agtggcgaag gtagtacaaa gggggaaatt 480

gtgttgacac agtctccagc caccctgtct ttgtctccag gggaaagagc caccctctcc 540

tgcagggcca gtcagagtgt tagcaggtac ttagcctggt accaacagaa acctggccag 600

gctcccaggc tcctcatcta tgatgcatcc aacagggcca ctggcatccc agccaggttc 660

agtggcagtg ggtctgggac agacttcact ctcaccatca gcagcctaga gcctgaagat 720

tttgcagttt attactgtca gcagagattc tactaccctt ggacttttgg cggagggacc 780

aaggttgaga tcaaacgggc cgctgccctt gataatgaaa agtcaaacgg aacaatcatt 840

cacgtgaagg gcaagcacct ctgtccgtca cccttgttcc ctggtccatc caagccattc 900

tgggtgttgg tcgtagtggg tggagtcctc gcttgttact ctctgctcgt caccgtggct 960

tttataatct tctgggttag atccaaaaga agccgcctgc tccatagcga ttacatgaat 1020

atgactccac gccgccctgg ccccacaagg aaacactacc agccttacgc accacctaga 1080

gatttcgctg cctatcggag cagggtgaag ttttccagat ctgcagatgc accagcgtat 1140

cagcagggcc agaaccaact gtataacgag ctcaacctgg gacgcaggga agagtatgac 1200

gttttggaca agcgcagagg acgggaccct gagatgggtg gcaaaccaag acgaaaaaac 1260

ccccaggagg gtctctataa tgagctgcag aaggataaga tggctgaagc ctattctgaa 1320

ataggcatga aaggagagcg gagaagggga aaagggcacg acggtttgta ccagggactc 1380

agcactgcta cgaaggatac ttatgacgct ctccacatgc aagccctgcc acctaggtaa 1440

<210> 150
<211> 479
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> TS-21522CARHxL

<400> 150
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ser Thr Ile Ser Ser Ser Ser Ser Thr Ile Tyr

```
65                  70                  75                  80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Gly Ser Gln Glu His Leu Ile Phe Asp
        115                 120                 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Thr Ser
    130                 135                 140

Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Ile
145                 150                 155                 160

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
                165                 170                 175

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Ala
            180                 185                 190

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp
        195                 200                 205

Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly
    210                 215                 220

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp
225                 230                 235                 240

Phe Ala Val Tyr Tyr Cys Gln Gln Arg Phe Tyr Tyr Pro Trp Thr Phe
                245                 250                 255

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Leu Asp Asn
            260                 265                 270

Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys
        275                 280                 285
```

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Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val
    290                 295                 300

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
305                 310                 315                 320

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
                325                 330                 335

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
            340                 345                 350

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
        355                 360                 365

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
    370                 375                 380

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
385                 390                 395                 400

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
                405                 410                 415

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
            420                 425                 430

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
        435                 440                 445

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
    450                 455                 460

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465                 470                 475
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<210> 151
<211> 1440
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> TS-21522CARDNALxH

<400> 151
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ccggaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc 120

accctctcct gcagggccag tcagagtgtt agcaggtact tagcctggta ccaacagaaa 180

cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 240

gccaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagcctagag 300

cctgaagatt ttgcagttta ttactgtcag cagagattct actacccttg gacttttggc 360

ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420

ggcgaaggta gtacaaaggg ggaggtgcag ctggtggagt ctgggggagg cttggtacag 480

cctgggggt ccctgagact ctcctgtgca gcctctggat tcaccttcag tagctatagc 540

atgaactggg tccgccaggc tccagggaag gggctggagt gggtttcaac cattagtagt 600

agtagtagta ccatatacta cgcagactct gtgaagggcc gattcaccat ctccagagac 660

aatgccaaga actcactgta tctgcaaatg aacagcctga gagctgagga cacggcggtg 720

tactactgcg ccagaggttc tcaggagcac ctgattttcg attattgggg acagggtaca 780

ttggtcaccg tctcctcagc cgctgccctt gataatgaaa agtcaaacgg aacaatcatt 840

cacgtgaagg gcaagcacct ctgtccgtca cccttgttcc ctggtccatc caagccattc 900

tgggtgttgg tcgtagtggg tggagtcctc gcttgttact ctctgctcgt caccgtggct 960

tttataatct tctgggttag atccaaaaga agccgcctgc tccatagcga ttacatgaat 1020

atgactccac gccgccctgg ccccacaagg aaacactacc agccttacgc accacctaga 1080

gatttcgctg cctatcggag cagggtgaag ttttccagat ctgcagatgc accagcgtat 1140

cagcagggcc agaaccaact gtataacgag ctcaacctgg gacgcaggga agagtatgac 1200

gttttggaca agcgcagagg acgggaccct gagatgggtg gcaaaccaag acgaaaaaac 1260

ccccaggagg gtctctataa tgagctgcag aaggataaga tggctgaagc ctattctgaa 1320

ataggcatga aaggagagcg gagaagggga aaagggcacg acggtttgta ccagggactc 1380

agcactgcta cgaaggatac ttatgacgct ctccacatgc aagccctgcc acctaggtaa 1440

<210> 152
<211> 479
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> TS-21522CARLxH

<400> 152
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

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

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

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

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

Phe Tyr Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser
130 135 140

Thr Lys Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
145 150 155 160

```
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
                165                 170                 175

Ser Ser Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
            180                 185                 190

Glu Trp Val Ser Thr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala
        195                 200                 205

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
    210                 215                 220

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225                 230                 235                 240

Tyr Tyr Cys Ala Arg Gly Ser Gln Glu His Leu Ile Phe Asp Tyr Trp
                245                 250                 255

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ala Ala Leu Asp Asn
            260                 265                 270

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

Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val
    290                 295                 300

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
305                 310                 315                 320

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
                325                 330                 335

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
            340                 345                 350

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
        355                 360                 365
```

```
Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
    370                 375                 380

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
385                 390                 395                 400

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
                405                 410                 415

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
            420                 425                 430

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
        435                 440                 445

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
    450                 455                 460

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465                 470                 475


<210> 153
<211> 1449
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<220>
<223> RY-21527CARDNAHxL

<400> 153
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ccgcaggtgc agctggtgga gtctggggga ggcgtggtcc agcctgggag gtccctgaga      120

ctctcctgtg cagcgtctgg attcaccttc agtagctatg gcatgcactg ggtccgccag      180

gctccaggca aggggctgga gtgggtggca gttatatcgt atgatggaag taataaatac      240

tatgcagact ccgtgaaggg ccgattcacc atctccagag acaattccaa gaacacgctg      300

tatctgcaaa tgaacagcct gagagccgag gacacggcgg tgtactactg cgccagaact      360

gacttctgga gcggatcccc tccaggctta gattactggg gacagggtac attggtcacc      420
```

gtctcctcag ggtctacatc cggctccggg aagcccggaa gtggcgaagg tagtacaaag 480

ggggacatcc agttgaccca gtctccatct tccgtgtctg catctgtagg agacagagtc 540

accatcactt gtcgggcgag tcagggtatt agcagctggt tagcctggta tcagcagaaa 600

ccagggaaag cccctaagct cctgatctat ggtgcatcca gtttgcaaag tggggtccca 660

tcaaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctgcag 720

cctgaagatt ttgcaactta ttactgtcag cagatataca ccttcccttt cacttttggc 780

ggagggacca aggttgagat caaacgggcc gctgcccttg ataatgaaaa gtcaaacgga 840

acaatcattc acgtgaaggg caagcacctc tgtccgtcac ccttgttccc tggtccatcc 900

aagccattct gggtgttggt cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc 960

accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat 1020

tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1080

ccacctagag atttcgctgc ctatcggagc agggtgaagt tttccagatc tgcagatgca 1140

ccagcgtatc agcagggcca gaaccaactg tataacgagc tcaacctggg acgcagggaa 1200

gagtatgacg ttttggacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga 1260

cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc 1320

tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac 1380

cagggactca gcactgctac gaaggatact tatgacgctc tccacatgca agccctgcca 1440

cctaggtaa 1449

<210> 154
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> RY-21527CARHxL

<400> 154
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

```
His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
            20                  25                  30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
        35                  40                  45

Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr
65                  70                  75                  80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
                85                  90                  95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Thr Asp Phe Trp Ser Gly Ser Pro Pro
        115                 120                 125

Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
    130                 135                 140

Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys
145                 150                 155                 160

Gly Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val
                165                 170                 175

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser
            180                 185                 190

Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        195                 200                 205

Ile Tyr Gly Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
    210                 215                 220

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
```

```
225                 230                 235                 240

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Thr Phe Pro
                245                 250                 255

Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala
            260                 265                 270

Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys
        275                 280                 285

His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp
    290                 295                 300

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
305                 310                 315                 320

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
                325                 330                 335

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
            340                 345                 350

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
        355                 360                 365

Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
    370                 375                 380

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
385                 390                 395                 400

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
                405                 410                 415

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
            420                 425                 430

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
        435                 440                 445
```

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
450 455 460

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
465 470 475 480

Pro Arg

<210> 155
<211> 1449
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> RY-21527CARDNALxH

<400> 155
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggacatcc agttgaccca gtctccatct tccgtgtctg catctgtagg agacagagtc 120

accatcactt gtcgggcgag tcagggtatt agcagctggt tagcctggta tcagcagaaa 180

ccagggaaag cccctaagct cctgatctat ggtgcatcca gtttgcaaag tggggtccca 240

tcaaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctgcag 300

cctgaagatt ttgcaactta ttactgtcag cagatataca ccttcccttt cacttttggc 360

ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420

ggcgaaggta gtacaaaggg gcaggtgcag ctggtggagt ctgggggagg cgtggtccag 480

cctgggaggt ccctgagact ctcctgtgca gcgtctggat tcaccttcag tagctatggc 540

atgcactggg tccgccaggc tccaggcaag gggctggagt gggtggcagt tatatcgtat 600

gatggaagta ataaatacta tgcagactcc gtgaagggcc gattcaccat ctccagagac 660

aattccaaga acacgctgta tctgcaaatg aacagcctga gagccgagga cacggcggtg 720

tactactgcg ccagaactga cttctggagc ggatcccctc caggcttaga ttactgggga 780

cagggtacat tggtcaccgt ctcctcagcc gctgcccttg ataatgaaaa gtcaaacgga 840

acaatcattc acgtgaaggg caagcacctc tgtccgtcac ccttgttccc tggtccatcc 900

aagccattct gggtgttggt cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc 960

accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat 1020

tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1080

ccacctagag atttcgctgc ctatcggagc agggtgaagt tttccagatc tgcagatgca 1140

ccagcgtatc agcagggcca gaaccaactg tataacgagc tcaacctggg acgcagggaa 1200

gagtatgacg ttttggacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga 1260

cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc 1320

tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac 1380

cagggactca gcactgctac gaaggatact tatgacgctc tccacatgca agccctgcca 1440

cctaggtaa 1449

<210> 156
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> RY-21527CARLxH

<400> 156
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Val
20 25 30

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
35 40 45

Gly Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
50 55 60

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

```
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

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

Tyr Thr Phe Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

Arg Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser
    130                 135                 140

Thr Lys Gly Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
145                 150                 155                 160

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
                165                 170                 175

Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
            180                 185                 190

Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
        195                 200                 205

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
    210                 215                 220

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225                 230                 235                 240

Tyr Tyr Cys Ala Arg Thr Asp Phe Trp Ser Gly Ser Pro Pro Gly Leu
                245                 250                 255

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ala Ala
            260                 265                 270

Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys
        275                 280                 285
```

```
His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp
    290                 295                 300

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
305                 310                 315                 320

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
                325                 330                 335

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
            340                 345                 350

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
        355                 360                 365

Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
    370                 375                 380

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
385                 390                 395                 400

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
                405                 410                 415

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
            420                 425                 430

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
        435                 440                 445

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
    450                 455                 460

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
465                 470                 475                 480

Pro Arg
```

<210> 157
<211> 1479

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> PP-21528CARDNAHxL

<400> 157
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgca gtctggggct gaggtgaaga agcctgggtc ctcggtgaag 120

gtctcctgca aggcttctgg aggcaccttc agcagctatg ctatcagctg ggtgcgacag 180

gcccctggac aagggcttga gtggatggga gggatcatcc ctatctttgg tacagcaaac 240

tacgcacaga agttccaggg cagagtcacg attaccgcgg acgaatccac gagcacagcc 300

tacatggagc tgagcagcct gagatctgag gacacggcgg tgtactactg cgccagaact 360

cctgaatact cctccagcat atggcactat tactacggca tggacgtatg gggccaggga 420

acaactgtca ccgtctcctc agggtctaca tccggctccg ggaagcccgg aagtggcgaa 480

ggtagtacaa agggggacat cgtgatgacc cagtctccag actccctggc tgtgtctctg 540

ggcgagaggg ccaccatcaa ctgcaagtcc agccagagtg ttttatacag ctccaacaat 600

aagaactact tagcttggta ccagcagaaa ccaggacagc ctcctaagct gctcatttac 660

tgggcatcta cccgggaatc cggggtccct gaccgattca gtggcagcgg gtctgggaca 720

gatttcactc tcaccatcag cagcctgcag gctgaagatg tggcagttta ttactgtcag 780

cagttcgccc acactccttt cacttttggc ggagggacca aggttgagat caaacgggcc 840

gctgcccttg ataatgaaaa gtcaaacgga acaatcattc acgtgaaggg caagcacctc 900

tgtccgtcac ccttgttccc tggtccatcc aagccattct gggtgttggt cgtagtgggt 960

ggagtcctcg cttgttactc tctgctcgtc accgtggctt ttataatctt ctgggttaga 1020

tccaaaagaa gccgcctgct ccatagcgat tacatgaata tgactccacg ccgccctggc 1080

cccacaagga aacactacca gccttacgca ccacctagag atttcgctgc ctatcggagc 1140

agggtgaagt tttccagatc tgcagatgca ccagcgtatc agcagggcca gaaccaactg 1200

tataacgagc tcaacctggg acgcagggaa gagtatgacg ttttggacaa gcgcagagga 1260

cgggaccctg agatgggtgg caaaccaaga cgaaaaaacc cccaggaggg tctctataat 1320

gagctgcaga aggataagat ggctgaagcc tattctgaaa taggcatgaa aggagagcgg 1380

agaaggggaa aagggcacga cggtttgtac cagggactca gcactgctac gaaggatact 1440

tatgacgctc tccacatgca agccctgcca cctaggtaa 1479

<210> 158
<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> PP-21528CARHxL

<400> 158
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly
35 40 45

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

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

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser
85 90 95

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

Ala Val Tyr Tyr Cys Ala Arg Thr Pro Glu Tyr Ser Ser Ser Ile Trp
115 120 125

His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr

```
    130                 135                 140

Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu
145                 150                 155                 160

Gly Ser Thr Lys Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu
                165                 170                 175

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln
            180                 185                 190

Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln
        195                 200                 205

Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr
    210                 215                 220

Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
225                 230                 235                 240

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val
                245                 250                 255

Tyr Tyr Cys Gln Gln Phe Ala His Thr Pro Phe Thr Phe Gly Gly Gly
            260                 265                 270

Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Leu Asp Asn Glu Lys Ser
        275                 280                 285

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
    290                 295                 300

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
305                 310                 315                 320

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
                325                 330                 335

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
            340                 345                 350
```

```
Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
        355                 360                 365

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe
    370                 375                 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
385                 390                 395                 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
                405                 410                 415

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
            420                 425                 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
        435                 440                 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
    450                 455                 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465                 470                 475                 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490
```

<210> 159
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> PP-21528CARDNALxH

<400> 159

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atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc       60

ccggacatcg tgatgaccca gtctccagac tccctggctg tgtctctggg cgagagggcc      120
```

accatcaact gcaagtccag ccagagtgtt ttatacagct ccaacaataa gaactactta 180

gcttggtacc agcagaaacc aggacagcct cctaagctgc tcatttactg ggcatctacc 240

cgggaatccg gggtccctga ccgattcagt ggcagcgggt ctgggacaga tttcactctc 300

accatcagca gcctgcaggc tgaagatgtg gcagtttatt actgtcagca gttcgcccac 360

actcctttca cttttggcgg agggaccaag gttgagatca aacgggggtc tacatccggc 420

tccgggaagc ccggaagtgg cgaaggtagt acaaaggggc aggtgcagct ggtgcagtct 480

ggggctgagg tgaagaagcc tgggtcctcg gtgaaggtct cctgcaaggc ttctggaggc 540

accttcagca gctatgctat cagctgggtg cgacaggccc ctggacaagg gcttgagtgg 600

atgggaggga tcatccctat ctttggtaca gcaaactacg cacagaagtt ccagggcaga 660

gtcacgatta ccgcggacga atccacgagc acagcctaca tggagctgag cagcctgaga 720

tctgaggaca cggcggtgta ctactgcgcc agaactcctg aatactcctc cagcatatgg 780

cactattact acggcatgga cgtatggggc cagggaacaa ctgtcaccgt ctcctcagcc 840

gctgcccttg ataatgaaaa gtcaaacgga acaatcattc acgtgaaggg caagcacctc 900

tgtccgtcac ccttgttccc tggtccatcc aagccattct gggtgttggt cgtagtgggt 960

ggagtcctcg cttgttactc tctgctcgtc accgtggctt ttataatctt ctgggttaga 1020

tccaaaagaa gccgcctgct ccatagcgat tacatgaata tgactccacg ccgccctggc 1080

cccacaagga aacactacca gccttacgca ccacctagag atttcgctgc ctatcggagc 1140

agggtgaagt tttccagatc tgcagatgca ccagcgtatc agcagggcca gaaccaactg 1200

tataacgagc tcaacctggg acgcagggaa gagtatgacg ttttggacaa gcgcagagga 1260

cgggaccctg agatgggtgg caaaccaaga cgaaaaaacc cccaggaggg tctctataat 1320

gagctgcaga aggataagat ggctgaagcc tattctgaaa taggcatgaa aggagagcgg 1380

agaaggggaa aagggcacga cggtttgtac cagggactca gcactgctac gaaggatact 1440

tatgacgctc tccacatgca agccctgcca cctaggtaa 1479

<210> 160
<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<220>
<223> PP-21528CARLxH

<400> 160
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln
35 40 45

Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln
50 55 60

Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr
65 70 75 80

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

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

Tyr Tyr Cys Gln Gln Phe Ala His Thr Pro Phe Thr Phe Gly Gly Gly
115 120 125

Thr Lys Val Glu Ile Lys Arg Gly Ser Thr Ser Gly Ser Gly Lys Pro
130 135 140

Gly Ser Gly Glu Gly Ser Thr Lys Gly Gln Val Gln Leu Val Gln Ser
145 150 155 160

Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys
165 170 175

Ala Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln
180 185 190

```
Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe
        195                 200                 205

Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr
    210                 215                 220

Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
225                 230                 235                 240

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Thr Pro Glu Tyr Ser
                245                 250                 255

Ser Ser Ile Trp His Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly
            260                 265                 270

Thr Thr Val Thr Val Ser Ser Ala Ala Ala Leu Asp Asn Glu Lys Ser
        275                 280                 285

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
    290                 295                 300

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
305                 310                 315                 320

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
                325                 330                 335

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
            340                 345                 350

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
        355                 360                 365

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe
    370                 375                 380

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
385                 390                 395                 400

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
                405                 410                 415
```

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
420 425 430

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
435 440 445

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
450 455 460

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
465 470 475 480

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 161
<211> 1452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> RD-21530CARDNAHxL

<400> 161
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctggtgga gtctgggggа ggcgtggtcc agcctgggag gtccctgaga 120

ctctcctgtg cagcgtctgg attcaccttc agtagctatg gcatgcactg ggtccgccag 180

gctccaggca aggggctgga gtgggtggca gttatatcgt atgatggaag taataaatac 240

tatgcagact ccgtgaaggg ccgattcacc atctccagag acaattccaa gaacacgctg 300

tatctgcaaa tgaacagcct gagagccgag gacacggcgg tgtactactg cgtcaagggg 360

ccgttgcagg agccgccata cgattatgga atggacgtat ggggccaggg aacaactgtc 420

accgtctcct cagggtctac atccggctcc gggaagcccg gaagtggcga aggtagtaca 480

aaggggaaa tagtgatgac gcagtctcca gccaccctgt ctgtgtctcc aggggaaaga 540

gccaccctct cctgcagggc cagtcagagt gttagcagca acttagcctg gtaccagcag 600

aaacctggcc aggctcccag gctcctcatc tatagcgcat ccaccagggc cactggtatc 660

ccagccaggt tcagtggcag tgggtctggg acagagttca ctctcaccat cagcagcctg 720

cagtctgaag attttgcagt ttattactgt cagcagcacc acgtctggcc tctcactttt 780

ggcggaggga ccaaggttga gatcaaacgg gccgctgccc ttgataatga aaagtcaaac 840

ggaacaatca ttcacgtgaa gggcaagcac ctctgtccgt cacccttgtt ccctggtcca 900

tccaagccat tctgggtgtt ggtcgtagtg ggtggagtcc tcgcttgtta ctctctgctc 960

gtcaccgtgg cttttataat cttctgggtt agatccaaaa gaagccgcct gctccatagc 1020

gattacatga atatgactcc acgccgccct ggccccacaa ggaaacacta ccagccttac 1080

gcaccaccta gagatttcgc tgcctatcgg agcagggtga agttttccag atctgcagat 1140

gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg 1200

gaagagtatg acgttttgga caagcgcaga ggacgggacc ctgagatggg tggcaaacca 1260

agacgaaaaa acccccagga gggtctctat aatgagctgc agaaggataa gatggctgaa 1320

gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg 1380

taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440

ccacctaggt aa 1452

<210> 162
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> RD-21530CARHxL

<400> 162
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe

```
        35                  40                  45

Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr
65                  70                  75                  80

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
                85                  90                  95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Val Lys Gly Pro Leu Gln Glu Pro Pro Tyr Asp
        115                 120                 125

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
    130                 135                 140

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
145                 150                 155                 160

Lys Gly Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser
                165                 170                 175

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser
            180                 185                 190

Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu
        195                 200                 205

Leu Ile Tyr Ser Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe
    210                 215                 220

Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu
225                 230                 235                 240

Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His His Val Trp
                245                 250                 255
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Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala
            260                 265                 270

Ala Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly
        275                 280                 285

Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe
    290                 295                 300

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
305                 310                 315                 320

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
                325                 330                 335

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
            340                 345                 350

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
        355                 360                 365

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
    370                 375                 380

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
385                 390                 395                 400

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
                405                 410                 415

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
            420                 425                 430

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
        435                 440                 445

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
    450                 455                 460

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
```

465 470 475 480

Pro Pro Arg

<210> 163
<211> 1452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> RD-21530CARDNALxH

<400> 163
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaaatag tgatgacgca gtctccagcc accctgtctg tgtctccagg ggaaagagcc 120

accctctcct gcagggccag tcagagtgtt agcagcaact tagcctggta ccagcagaaa 180

cctggccagg ctcccaggct cctcatctat agcgcatcca ccagggccac tggtatccca 240

gccaggttca gtggcagtgg gtctgggaca gagttcactc tcaccatcag cagcctgcag 300

tctgaagatt ttgcagttta ttactgtcag cagcaccacg tctggcctct cacttttggc 360

ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420

ggcgaaggta gtacaaaggg gcaggtgcag ctggtggagt ctgggggagg cgtggtccag 480

cctgggaggt ccctgagact ctcctgtgca gcgtctggat tcaccttcag tagctatggc 540

atgcactggg tccgccaggc tccaggcaag gggctggagt gggtggcagt tatatcgtat 600

gatggaagta ataaatacta tgcagactcc gtgaagggcc gattcaccat ctccagagac 660

aattccaaga acacgctgta tctgcaaatg aacagcctga gagccgagga cacggcggtg 720

tactactgcg tcaaggggcc gttgcaggag ccgccatacg attatggaat ggacgtatgg 780

ggccagggaa caactgtcac cgtctcctca gccgctgccc ttgataatga aaagtcaaac 840

ggaacaatca ttcacgtgaa gggcaagcac ctctgtccgt caccttgtt ccctggtcca 900

tccaagccat tctgggtgtt ggtcgtagtg ggtggagtcc tcgcttgtta ctctctgctc 960

gtcaccgtgg cttttataat cttctgggtt agatccaaaa gaagccgcct gctccatagc 1020

gattacatga atatgactcc acgccgccct ggccccacaa ggaaacacta ccagccttac 1080

gcaccaccta gagatttcgc tgcctatcgg agcagggtga agttttccag atctgcagat 1140

gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg 1200

gaagagtatg acgttttgga caagcgcaga ggacgggacc ctgagatggg tggcaaacca 1260

agacgaaaaa acccccagga gggtctctat aatgagctgc agaaggataa gatggctgaa 1320

gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg 1380

taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440

ccacctaggt aa 1452

<210> 164
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> RD-21530CARLxH

<400> 164
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
50 55 60

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

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
85 90 95

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Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His
            100                 105                 110

His Val Trp Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

Arg Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser
    130                 135                 140

Thr Lys Gly Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
145                 150                 155                 160

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
                165                 170                 175

Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
            180                 185                 190

Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
        195                 200                 205

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
    210                 215                 220

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
225                 230                 235                 240

Tyr Tyr Cys Val Lys Gly Pro Leu Gln Glu Pro Pro Tyr Asp Tyr Gly
                245                 250                 255

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ala
            260                 265                 270

Ala Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly
        275                 280                 285

Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe
    290                 295                 300

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
305                 310                 315                 320
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Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
325 330 335

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
340 345 350

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
355 360 365

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
370 375 380

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
385 390 395 400

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
405 410 415

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
420 425 430

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
435 440 445

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
450 455 460

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
465 470 475 480

Pro Pro Arg

<210> 165
<211> 1440
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 165
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtcc aactgcaaga aagcggaccc ggactggtga agccttctga gacacttagt 120

ctgacgtgca cggtcagtgg cggctccatc tcctcctatt attggtcatg gatacgacaa 180

cccccaggta agggcctgga atggattggc tatatctact attcaggaag cacgaactac 240

aatcccagcc tgaagtcccg agtgacaatt tcagtagata ccagtaaaaa ccagttcagt 300

cttaaactgt caagcgtgac agctgccgac accgctgtgt attactgcgt ctcactggtg 360

tattgtggag gggattgtta tagcgggttc gattattggg gacagggaac cctggtgact 420

gtatcttccg gcggcggcgg ctcagggggt ggcggtagtg gcggtggggg ttccgatatt 480

caactgacac aatcccccag ctcactcagc gccagcgtgg gggacagggt tagctttacc 540

tgtcaagcct ctcaggatat aaataacttt ctgaactggt atcaacagaa gcctgggaag 600

gcgcccaaac tcctgatcta tgatgcgtcc aacctggaaa ctggcgtgcc ttcacgcttt 660

agcggctctg gcagtggtac agacttcact tttaccatct cttcacttca gccggaggac 720

atcgccacat attactgtca acagtacgga aacttgccct ttacttttgg aggcggcacc 780

aaagttgaaa tcaaaagggc cgctgccctg gataacgaaa agagcaatgg gactataata 840

catgttaaag gaaaacacct gtgtccatct cccctgttcc ctggaccgtc aaagccattt 900

tgggtgctcg tggttgtcgg tggcgttctc gcctgttata gcttgctggt gacagtagcc 960

ttcattatct tttgggtgag atccaaaaga agccgcctgc tccatagcga ttacatgaat 1020

atgactccac gccgccctgg ccccacaagg aaacactacc agccttacgc accacctaga 1080

gatttcgctg cctatcggag cagggtgaag ttttccagat ctgcagatgc accagcgtat 1140

cagcagggcc agaaccaact gtataacgag ctcaacctgg gacgcaggga agagtatgac 1200

gttttggaca agcgcagagg acgggaccct gagatgggtg gcaaaccaag acgaaaaaac 1260

ccccaggagg gtctctataa tgagctgcag aaggataaga tggctgaagc ctattctgaa 1320

ataggcatga aaggagagcg gagaagggga aaagggcacg acggtttgta ccagggactc 1380

agcactgcta cgaaggatac ttatgacgct ctccacatgc aagccctgcc acctaggtaa 1440

<210> 166
<211> 479
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 166
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
20 25 30

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

Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys
50 55 60

Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr
65 70 75 80

Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
85 90 95

Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
100 105 110

Val Tyr Tyr Cys Val Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser
115 120 125

Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
145 150 155 160

Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

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                165                 170                 175

Val Ser Phe Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe Leu Asn
            180                 185                 190

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
        195                 200                 205

Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    210                 215                 220

Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp
225                 230                 235                 240

Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Gly Asn Leu Pro Phe Thr Phe
                245                 250                 255

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Leu Asp Asn
            260                 265                 270

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

Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val
    290                 295                 300

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
305                 310                 315                 320

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
                325                 330                 335

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
            340                 345                 350

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
        355                 360                 365

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
    370                 375                 380
```

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Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
385                 390                 395                 400

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
                405                 410                 415

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
            420                 425                 430

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
        435                 440                 445

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
    450                 455                 460

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465                 470                 475
```

<210> 167
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 167
caggtccaac tgcaagaaag cggacccgga ctggtgaagc cttctgagac acttagtctg 60

acgtgcacgg tcagtggcgg ctccatctcc tcctattatt ggtcatggat acgacaaccc 120

ccaggtaagg gcctggaatg gattggctat atctactatt caggaagcac gaactacaat 180

cccagcctga agtcccgagt gacaatttca gtagatacca gtaaaaacca gttcagtctt 240

aaactgtcaa gcgtgacagc tgccgacacc gctgtgtatt actgcgtctc actggtgtat 300

tgtggagggg attgttatag cgggttcgat tattggggac agggaaccct ggtgactgta 360

tcttccggcg gcggcggctc agggggtggc ggtagtggcg gtgggggttc cgatattcaa 420

ctgacacaat cccccagctc actcagcgcc agcgtggggg acagggttag ctttacctgt 480

caagcctctc aggatataaa taactttctg aactggtatc aacagaagcc tgggaaggcg 540

cccaaactcc tgatctatga tgcgtccaac ctggaaactg gcgtgccttc acgctttagc 600

ggctctggca gtggtacaga cttcactttt accatctctt cacttcagcc ggaggacatc 660

gccacatatt actgtcaaca gtacggaaac ttgcccttta cttttggagg cggcaccaaa 720

gttgaaatca aaagggccgc tgccctggat aacgaaaaga gcaatgggac tataatacat 780

gttaaaggaa aacacctgtg tccatctccc ctgttccctg gaccgtcaaa gccattttgg 840

gtgctcgtgg ttgtcggtgg cgttctcgcc tgttatagct tgctggtgac agtagccttc 900

attatctttt gggtgagatc caaaagaagc cgcctgctcc atagcgatta catgaatatg 960

actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat 1020

ttcgctgcct atcggagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag 1080

cagggccaga accaactgta taacgagctc aacctgggac gcagggaaga gtatgacgtt 1140

ttggacaagc gcagaggacg ggaccctgag atgggtggca aaccaagacg aaaaaacccc 1200

caggagggtc tctataatga gctgcagaag gataagatgg ctgaagccta ttctgaaata 1260

ggcatgaaag gagagcggag aaggggaaaa gggcacgacg gtttgtacca gggactcagc 1320

actgctacga aggatactta tgacgctctc cacatgcaag ccctgccacc tagg 1374

<210> 168
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 168
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

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

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

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

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

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

Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
    130                 135                 140

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

Gln Ala Ser Gln Asp Ile Asn Asn Phe Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu
            180                 185                 190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Tyr Gly Asn Leu Pro Phe Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys Arg Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn Gly
                245                 250                 255
```

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Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
            260                 265                 270

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
        275                 280                 285

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
    290                 295                 300

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
305                 310                 315                 320

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
                325                 330                 335

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg
    450                 455
```

<210> 169
<211> 1467

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 169
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctgcagga atccggaccg gggctggtga agcccagcga gactctgagt 120

ctcacgtgta cagtttctgg aggtagcatt agctcctact attggtcatg gataaggcag 180

ccccccggga agggattgga atggatcggc tatatttact acagtgggag caccaattac 240

aacccctcac tgaagtctag agttacaatc agcgttgaca cctcaaagaa tcagttcagt 300

ttgaaattgt ctagcgtcac agcagctgat acagccgtct attattgtgt ttctctggtc 360

tattgcggtg gggattgtta cagtggcttt gactattggg ggcagggtac tctggttaca 420

gtttcttccg gggggggagg ctctgggggc ggaggctcag gtggtggagg cagcgacatc 480

cagttgacac agagcccgag ttccttgtcc gcctccgtcg gggatagagt gtcatttacc 540

tgtcaggcct ctcaggatat taataacttt ctgaattggt atcagcaaaa gcccggaaag 600

gcacccaagc tgttgattta cgacgccagt aacctggaga caggcgtgcc ctcccggttt 660

agtggtagcg gaagcggtac ggattttacc tttactatca gctctctcca acccgaagac 720

attgcaacct actattgtca acaatatgga aacctgcctt ttacatttgg cggcggcacc 780

aaggtggaga ttaagcgggc ggcagctatt gaggtgatgt atccaccgcc ttacctggat 840

aacgaaaaga gtaacggtac catcattcac gtgaaaggta aacacctgtg tccttctccc 900

ctcttccccg ggccatcaaa gcccttctgg gttcttgtgg tcgtgggagg cgtgcttgct 960

tgttattctc tgctcgttac cgtggcgttt atcatttttt gggttagatc caaaagaagc 1020

cgcctgctcc atagcgatta catgaatatg actccacgcc gccctggccc cacaaggaaa 1080

cactaccagc cttacgcacc acctagagat ttcgctgcct atcggagcag ggtgaagttt 1140

tccagatctg cagatgcacc agcgtatcag cagggccaga accaactgta taacgagctc 1200

aacctgggac gcagggaaga gtatgacgtt ttggacaagc gcagaggacg ggaccctgag 1260

atgggtggca aaccaagacg aaaaaacccc caggagggtc tctataatga gctgcagaag 1320

gataagatgg ctgaagccta ttctgaaata ggcatgaaag gagagcggag aaggggaaaa 1380

gggcacgacg gtttgtacca gggactcagc actgctacga aggatactta tgacgctctc 1440

cacatgcaag ccctgccacc taggtaa 1467

<210> 170
<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 170
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
20 25 30

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

Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys
50 55 60

Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr
65 70 75 80

Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
85 90 95

Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
100 105 110

Val Tyr Tyr Cys Val Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser
115 120 125

Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly

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    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
145                 150                 155                 160

Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
                165                 170                 175

Val Ser Phe Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe Leu Asn
            180                 185                 190

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
        195                 200                 205

Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    210                 215                 220

Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp
225                 230                 235                 240

Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Gly Asn Leu Pro Phe Thr Phe
                245                 250                 255

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Ile Glu Val
            260                 265                 270

Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile
        275                 280                 285

Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly
    290                 295                 300

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

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
                325                 330                 335

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
            340                 345                 350
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Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
355 360 365

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala
370 375 380

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
385 390 395 400

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
405 410 415

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
420 425 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
435 440 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
450 455 460

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
465 470 475 480

His Met Gln Ala Leu Pro Pro Arg
485

<210> 171
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 171
caggtgcagc tgcaggaatc cggaccgggg ctggtgaagc ccagcgagac tctgagtctc 60

acgtgtacag tttctggagg tagcattagc tcctactatt ggtcatggat aaggcagccc 120

cccgggaagg gattggaatg gatcggctat atttactaca gtgggagcac caattacaac 180

ccctcactga agtctagagt tacaatcagc gttgacacct caaagaatca gttcagtttg 240

aaattgtcta gcgtcacagc agctgataca gccgtctatt attgtgtttc tctggtctat 300

tgcggtgggg attgttacag tggctttgac tattgggggc agggtactct ggttacagtt 360

tcttccgggg ggggaggctc tgggggcgga ggctcaggtg gtggaggcag cgacatccag 420

ttgacacaga gcccgagttc cttgtccgcc tccgtcgggg atagagtgtc atttacctgt 480

caggcctctc aggatattaa taactttctg aattggtatc agcaaaagcc cggaaaggca 540

cccaagctgt tgatttacga cgccagtaac ctggagacag gcgtgccctc ccggtttagt 600

ggtagcggaa gcggtacgga ttttaccttt actatcagct ctctccaacc cgaagacatt 660

gcaacctact attgtcaaca atatggaaac ctgcctttta catttggcgg cggcaccaag 720

gtggagatta agcgggcggc agctattgag gtgatgtatc caccgcctta cctggataac 780

gaaaagagta acggtaccat cattcacgtg aaaggtaaac acctgtgtcc ttctcccctc 840

ttccccgggc catcaaagcc cttctgggtt cttgtggtcg tgggaggcgt gcttgcttgt 900

tattctctgc tcgttaccgt ggcgtttatc atttttttggg ttagatccaa aagaagccgc 960

ctgctccata gcgattacat gaatatgact ccacgccgcc ctggccccac aaggaaacac 1020

taccagcctt acgcaccacc tagagatttc gctgcctatc ggagcagggt gaagttttcc 1080

agatctgcag atgcaccagc gtatcagcag ggccagaacc aactgtataa cgagctcaac 1140

ctgggacgca gggaagagta tgacgttttg gacaagcgca gaggacggga ccctgagatg 1200

ggtggcaaac caagacgaaa aaacccccag gagggtctct ataatgagct gcagaaggat 1260

aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1320

cacgacggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1380

atgcaagccc tgccacctag g 1401

<210> 172
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 172
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1   5   10   15

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

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

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

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

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

Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr Trp
            100   105   110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115   120   125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
    130   135   140

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

Gln Ala Ser Gln Asp Ile Asn Asn Phe Leu Asn Trp Tyr Gln Gln Lys
                165   170   175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu
            180   185   190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195   200   205

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Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Tyr Gly Asn Leu Pro Phe Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys Arg Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro
                245                 250                 255

Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly
            260                 265                 270

Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe
        275                 280                 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
    290                 295                 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305                 310                 315                 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
                325                 330                 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
            340                 345                 350

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
        355                 360                 365

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
    370                 375                 380

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
385                 390                 395                 400

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
                405                 410                 415
```

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
            420   425   430

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
        435   440   445

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
    450   455   460

Pro Pro Arg
465

<210> 173
<211> 1548
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 173
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc   60

ccgcaggtgc aattgcaaga gtccggcccc ggactcgtta aacccagtga gacgcttagc   120

ctgacctgta ccgtctcagg gggcagcatc tcctcttatt actggagctg gatcaggcag   180

cctccaggaa aaggccttga atggattggg tacatctact actctggctc aacaaattat   240

aatccatccc tgaagtcccg cgtgactatc tctgtggaca ccagcaagaa tcagttttca   300

ctgaagttgt ctagtgttac cgcggccgac accgccgtat actactgtgt gtctcttgtg   360

tactgtggcg gcgactgcta ttccgggttc gactactggg gccaagggac tctggtaacc   420

gtgtcctcag gcggcggcgg gtcaggagga ggcggcagtg gaggtggcgg ctccgacatc   480

cagctgacac aatcaccatc ttccctttca gcttcagtcg gggacagagt gtccttcaca   540

tgccaggcca gccaggatat caataacttc ctgaactggt accaacagaa acccggaaag   600

gctccaaagc tcctgatcta tgatgcttcc aacctggaga ccggcgtgcc ctccaggttc   660

agtggttcag gatcaggcac tgactttacg ttcaccatat ccagtcttca gcccgaagac   720

attgcaacct attactgcca acaatacggg aaccttccct ttacattcgg aggcggcacc   780

aaggtggaaa tcaaaagggc tgcagcattg agcaactcaa taatgtattt tagtcacttt 840

gtaccagtgt tcttgccggc taagcctact accacacccg ctccacggcc acctacccca 900

gctcctacca tcgcttcaca gcctctgtcc ctgcgcccag aggcttgccg accggccgca 960

gggggcgctg ttcataccag aggactggat ttcgcctgcg atatctatat ctgggcaccc 1020

ctggccggaa cctgcggcgt actcctgctg tccctggtca tcacgctcta ttgtaatcac 1080

aggaacagat ccaaaagaag ccgcctgctc catagcgatt acatgaatat gactccacgc 1140

cgccctggcc ccacaaggaa acactaccag ccttacgcac cacctagaga tttcgctgcc 1200

tatcggagca gggtgaagtt ttccagatct gcagatgcac cagcgtatca gcagggccag 1260

aaccaactgt ataacgagct caacctggga cgcagggaag agtatgacgt tttggacaag 1320

cgcagaggac gggaccctga gatgggtggc aaaccaagac gaaaaaaccc ccaggagggt 1380

ctctataatg agctgcagaa ggataagatg gctgaagcct attctgaaat aggcatgaaa 1440

ggagagcgga gaaggggaaa agggcacgac ggtttgtacc agggactcag cactgctacg 1500

aaggatactt atgacgctct ccacatgcaa gccctgccac ctaggtaa 1548

<210> 174
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 174
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
20 25 30

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

Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys

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    50                  55                  60

Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr
65                  70                  75                  80

Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
                85                  90                  95

Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
            100                 105                 110

Val Tyr Tyr Cys Val Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser
        115                 120                 125

Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
145                 150                 155                 160

Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
                165                 170                 175

Val Ser Phe Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe Leu Asn
            180                 185                 190

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
        195                 200                 205

Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    210                 215                 220

Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp
225                 230                 235                 240

Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Gly Asn Leu Pro Phe Thr Phe
                245                 250                 255

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Leu Ser Asn
            260                 265                 270
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Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe Leu Pro Ala Lys
        275                 280                 285

Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
    290                 295                 300

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
305                 310                 315                 320

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
                325                 330                 335

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
            340                 345                 350

Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg
        355                 360                 365

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
    370                 375                 380

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
385                 390                 395                 400

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
                405                 410                 415

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
            420                 425                 430

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
        435                 440                 445

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
    450                 455                 460

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
465                 470                 475                 480

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
```

485 490 495

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
500 505 510

Pro Pro Arg
515

<210> 175
<211> 1482
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 175
caggtgcaat tgcaagagtc cggccccgga ctcgttaaac ccagtgagac gcttagcctg 60

acctgtaccg tctcaggggg cagcatctcc tcttattact ggagctggat caggcagcct 120

ccaggaaaag gccttgaatg gattgggtac atctactact ctggctcaac aaattataat 180

ccatccctga agtcccgcgt gactatctct gtggacacca gcaagaatca gttttcactg 240

aagttgtcta gtgttaccgc ggccgacacc gccgtatact actgtgtgtc tcttgtgtac 300

tgtggcggcg actgctattc cgggttcgac tactggggcc aagggactct ggtaaccgtg 360

tcctcaggcg gcggcgggtc aggaggaggc ggcagtggag gtggcggctc cgacatccag 420

ctgacacaat caccatcttc cctttcagct tcagtcgggg acagagtgtc cttcacatgc 480

caggccagcc aggatatcaa taacttcctg aactggtacc aacagaaacc cggaaaggct 540

ccaaagctcc tgatctatga tgcttccaac ctggagaccg gcgtgccctc caggttcagt 600

ggttcaggat caggcactga ctttacgttc accatatcca gtcttcagcc cgaagacatt 660

gcaacctatt actgccaaca atacgggaac cttcccttta cattcggagg cggcaccaag 720

gtggaaatca aaagggctgc agcattgagc aactcaataa tgtattttag tcactttgta 780

ccagtgttct tgccggctaa gcctactacc acacccgctc cacggccacc taccccagct 840

cctaccatcg cttcacagcc tctgtccctg cgcccagagg cttgccgacc ggccgcaggg 900

ggcgctgttc ataccagagg actggatttc gcctgcgata tctatatctg ggcacccctg 960

gccggaacct gcggcgtact cctgctgtcc ctggtcatca cgctctattg taatcacagg 1020

aacagatcca aaagaagccg cctgctccat agcgattaca tgaatatgac tccacgccgc 1080

cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat 1140

cggagcaggg tgaagttttc cagatctgca gatgcaccag cgtatcagca gggccagaac 1200

caactgtata acgagctcaa cctgggacgc agggaagagt atgacgtttt ggacaagcgc 1260

agaggacggg accctgagat gggtggcaaa ccaagacgaa aaaaccccca ggagggtctc 1320

tataatgagc tgcagaagga taagatggct gaagcctatt ctgaaatagg catgaaagga 1380

gagcggagaa ggggaaaagg gcacgacggt ttgtaccagg gactcagcac tgctacgaag 1440

gatacttatg acgctctcca catgcaagcc ctgccaccta gg 1482

<210> 176
<211> 494
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 176
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

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

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

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

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

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

Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
    130                 135                 140

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

Gln Ala Ser Gln Asp Ile Asn Asn Phe Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu
            180                 185                 190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Tyr Gly Asn Leu Pro Phe Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys Arg Ala Ala Ala Leu Ser Asn Ser Ile Met Tyr Phe
                245                 250                 255

Ser His Phe Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro
            260                 265                 270

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
        275                 280                 285

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
    290                 295                 300
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Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
305                 310                 315                 320

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
                325                 330                 335

Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
            340                 345                 350

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
        355                 360                 365

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
    370                 375                 380

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
385                 390                 395                 400

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
                405                 410                 415

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
            420                 425                 430

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
        435                 440                 445

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
    450                 455                 460

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
465                 470                 475                 480

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490
```

<210> 177
<211> 1440
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 177
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggatatcc agctcacgca atccccctca agcttgagtg cctccgtggg cgaccgggtg 120

tccttcacat gtcaggcaag ccaagacata aataatttcc tgaattggta ccaacaaaaa 180

cccggcaagg ctcccaaact cctgatttat gatgcctcca atctggagac cggggtccct 240

tctagattca gcggaagtgg cagcggcaca gactttacat ttactatctc ttctctgcaa 300

ccagaggaca tcgccacata ctattgccag caatacggca atctgccctt caccttcgga 360

ggcggaacca aggtagaaat taaaaggggc ggtggaggct ccggaggggg gggctctggc 420

ggaggggct cccaagtaca attgcaggag tcagggcctg gactcgtgaa gccttcagaa 480

actttgtcac tgacatgtac agtgtccggc ggaagcattt ccagttacta ttggtcctgg 540

attagacagc cacccggcaa aggactggaa tggattggat atatctacta ctctggatct 600

acaaactata atcccagcct caaatccagg gtcactatta gtgtggatac atcaaagaat 660

cagttctcct tgaagctgag ctcagtcact gctgccgaca ccgcagtgta ctattgtgtg 720

agcctggtct actgcggcgg agattgctac agcggtttcg attactgggg ccagggcacc 780

ctggttaccg ttagttccgc ggctgctctt gataacgaga agtccaacgg tacgattatc 840

cacgttaagg gtaagcacct ttgccctagc ccgctgttcc caggccccag taagcccttt 900

tgggtcctcg ttgtggtagg tggggtactc gcctgctact ccctgctcgt cactgtcgca 960

ttcatcatct tctgggtcag atccaaaaga agccgcctgc tccatagcga ttacatgaat 1020

atgactccac gccgccctgg ccccacaagg aaacactacc agccttacgc accacctaga 1080

gatttcgctg cctatcggag cagggtgaag ttttccagat ctgcagatgc accagcgtat 1140

cagcagggcc agaaccaact gtataacgag ctcaacctgg gacgcaggga agagtatgac 1200

gttttggaca agcgcagagg acgggaccct gagatgggtg gcaaaccaag acgaaaaaac 1260

ccccaggagg gtctctataa tgagctgcag aaggataaga tggctgaagc ctattctgaa 1320

ataggcatga aaggagagcg gagaagggga aaagggcacg acggtttgta ccagggactc 1380

agcactgcta cgaaggatac ttatgacgct ctccacatgc aagccctgcc acctaggtaa 1440

<210> 178
<211> 479
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 178
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu
20 25 30

Ser Ala Ser Val Gly Asp Arg Val Ser Phe Thr Cys Gln Ala Ser Gln
35 40 45

Asp Ile Asn Asn Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
50 55 60

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile
85 90 95

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

Gly Asn Leu Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

```
145                 150                 155                 160

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
                165                 170                 175

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
            180                 185                 190

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
        195                 200                 205

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
    210                 215                 220

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Val
225                 230                 235                 240

Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr Trp
                245                 250                 255

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ala Ala Leu Asp Asn
            260                 265                 270

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

Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val
    290                 295                 300

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
305                 310                 315                 320

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
                325                 330                 335

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
            340                 345                 350

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
        355                 360                 365
```

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
370 375 380

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
385 390 395 400

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
405 410 415

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
420 425 430

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
435 440 445

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
450 455 460

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 179
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 179
gatatccagc tcacgcaatc cccctcaagc ttgagtgcct ccgtgggcga ccgggtgtcc 60

ttcacatgtc aggcaagcca agacataaat aatttcctga attggtacca acaaaaaccc 120

ggcaaggctc ccaaactcct gatttatgat gcctccaatc tggagaccgg ggtcccttct 180

agattcagcg gaagtggcag cggcacagac tttacattta ctatctcttc tctgcaacca 240

gaggacatcg ccacatacta ttgccagcaa tacggcaatc tgcccttcac cttcggaggc 300

ggaaccaagg tagaaattaa aaggggcggt ggaggctccg gagggggggg ctctggcgga 360

```
gggggctccc aagtacaatt gcaggagtca gggcctggac tcgtgaagcc ttcagaaact      420

ttgtcactga catgtacagt gtccggcgga agcatttcca gttactattg gtcctggatt      480

agacagccac ccggcaaagg actggaatgg attggatata tctactactc tggatctaca      540

aactataatc ccagcctcaa atccagggtc actattagtg tggatacatc aaagaatcag      600

ttctccttga agctgagctc agtcactgct gccgacaccg cagtgtacta ttgtgtgagc      660

ctggtctact gcggcggaga ttgctacagc ggtttcgatt actggggcca gggcaccctg      720

gttaccgtta gttccgcggc tgctcttgat aacgagaagt ccaacggtac gattatccac      780

gttaagggta agcacctttg ccctagcccg ctgttcccag gccccagtaa gccctttgg       840

gtcctcgttg tggtaggtgg ggtactcgcc tgctactccc tgctcgtcac tgtcgcattc      900

atcatcttct gggtcagatc caaaagaagc cgcctgctcc atagcgatta catgaatatg      960

actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat     1020

ttcgctgcct atcggagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag     1080

cagggccaga accaactgta taacgagctc aacctgggac gcagggaaga gtatgacgtt     1140

ttggacaagc gcagaggacg ggaccctgag atgggtggca aaccaagacg aaaaaacccc     1200

caggagggtc tctataatga gctgcagaag gataagatgg ctgaagccta ttctgaaata     1260

ggcatgaaag gagagcggag aaggggaaaa gggcacgacg gtttgtacca gggactcagc     1320

actgctacga aggatactta tgacgctctc cacatgcaag ccctgccacc tagg           1374
```

<210> 180
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 180

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


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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
            100                 105                 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
        115                 120                 125

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
    130                 135                 140

Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile
145                 150                 155                 160

Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr
                165                 170                 175

Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile
            180                 185                 190

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
        195                 200                 205

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Val Ser Leu Val Tyr Cys
    210                 215                 220

Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
225                 230                 235                 240
```

```
Val Thr Val Ser Ser Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn Gly
                245                 250                 255

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
            260                 265                 270

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
        275                 280                 285

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
    290                 295                 300

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
305                 310                 315                 320

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
                325                 330                 335

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
            340                 345                 350

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
        355                 360                 365

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
    370                 375                 380

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
385                 390                 395                 400

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
                405                 410                 415

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
            420                 425                 430

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
        435                 440                 445

Ala Leu His Met Gln Ala Leu Pro Pro Arg
    450                 455
```

<210> 181
<211> 1467
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 181
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggatatcc agctgaccca gtctccatcc tctttgagtg cctccgtggg tgaccgcgtc 120

tctttcactt gccaagccag ccaagacatc aacaactttc tgaattggta ccagcagaaa 180

ccaggcaaag caccaaagct cctcatctac gacgcctcca acctggaaac cggggtgccc 240

agcaggttta gcgggagcgg ttctggcacg gattttacgt tcaccatctc ctctctgcag 300

cccgaggata tagctactta ttactgtcag cagtacggga atctgccatt tacttttggg 360

ggtggaacta aggtggaaat caaaaggggc ggcgggggaa gcgggggcgg gggctcaggt 420

ggcggaggga gccaggtgca actccaggaa agtggcccag gattggtgaa gcccagcgag 480

acccttccc ttacttgtac tgttagcgga ggcagcataa gcagctacta ttggtcctgg 540

atcagacagc caccagggaa agggcttgaa tggattggct acatttacta ttccgggtcc 600

accaactaca acccatccct caagtcccgc gtgacaattt ccgtcgacac aagcaagaac 660

cagttctccc tgaaacttag tagcgtcact gctgcagata cagcagtgta ctattgtgtc 720

agccttgtct actgtggcgg cgactgctac agtggctttg attactgggg acagggcacg 780

ctcgtgacag tgtccagcgc tgcggctatc gaggtaatgt atccgccacc gtatctggac 840

aacgagaagt ctaatgggac aatcattcac gtgaagggga agcacctgtg tccatccccc 900

ctgtttccgg gtcccagtaa acccttctgg gtgcttgttg tcgttggcgg ggtgctggcc 960

tgctattccc tgctggtgac cgtcgcgttt attattttct gggttagatc caaaagaagc 1020

cgcctgctcc atagcgatta catgaatatg actccacgcc gccctggccc cacaaggaaa 1080

cactaccagc cttacgcacc acctagagat ttcgctgcct atcggagcag ggtgaagttt 1140

tccagatctg cagatgcacc agcgtatcag cagggccaga accaactgta taacgagctc 1200

aacctgggac gcagggaaga gtatgacgtt ttggacaagc gcagaggacg ggaccctgag 1260

atgggtggca aaccaagacg aaaaaacccc caggagggtc tctataatga gctgcagaag 1320

gataagatgg ctgaagccta ttctgaaata ggcatgaaag gagagcggag aaggggaaaa 1380

gggcacgacg gtttgtacca gggactcagc actgctacga aggatactta tgacgctctc 1440

cacatgcaag ccctgccacc taggtaa 1467

<210> 182
<211> 488
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 182
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu
20 25 30

Ser Ala Ser Val Gly Asp Arg Val Ser Phe Thr Cys Gln Ala Ser Gln
35 40 45

Asp Ile Asn Asn Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
50 55 60

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile
85 90 95

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

Gly Asn Leu Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

```
        115                 120                 125

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
145                 150                 155                 160

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
                165                 170                 175

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
            180                 185                 190

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
        195                 200                 205

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
    210                 215                 220

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Val
225                 230                 235                 240

Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr Trp
                245                 250                 255

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ala Ala Ile Glu Val
            260                 265                 270

Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile
        275                 280                 285

Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly
    290                 295                 300

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

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
                325                 330                 335
```

```
Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
            340                 345                 350

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
        355                 360                 365

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala
    370                 375                 380

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
385                 390                 395                 400

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
                405                 410                 415

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
            420                 425                 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
        435                 440                 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
    450                 455                 460

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
465                 470                 475                 480

His Met Gln Ala Leu Pro Pro Arg
                485
```

<210> 183
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 183

gatatccagc tgacccagtc tccatcctct ttgagtgcct ccgtgggtga ccgcgtctct 60

ttcacttgcc aagccagcca agacatcaac aactttctga attggtacca gcagaaacca 120

ggcaaagcac caaagctcct catctacgac gcctccaacc tggaaaccgg ggtgcccagc 180

aggtttagcg ggagcggttc tggcacggat tttacgttca ccatctcctc tctgcagccc 240

gaggatatag ctacttatta ctgtcagcag tacgggaatc tgccatttac ttttgggggt 300

ggaactaagg tggaaatcaa aaggggcggc gggggaagcg ggggcggggg ctcaggtggc 360

ggagggagcc aggtgcaact ccaggaaagt ggcccaggat tggtgaagcc cagcgagacc 420

ctttccctta cttgtactgt tagcggaggc agcataagca gctactattg gtcctggatc 480

agacagccac cagggaaagg gcttgaatgg attggctaca tttactattc cgggtccacc 540

aactacaacc catccctcaa gtcccgcgtg acaatttccg tcgacacaag caagaaccag 600

ttctccctga aacttagtag cgtcactgct gcagatacag cagtgtacta ttgtgtcagc 660

cttgtctact gtggcggcga ctgctacagt ggctttgatt actggggaca gggcacgctc 720

gtgacagtgt ccagcgctgc ggctatcgag gtaatgtatc cgccaccgta tctggacaac 780

gagaagtcta atgggacaat cattcacgtg aaggggaagc acctgtgtcc atccccctg 840

tttccgggtc ccagtaaacc cttctgggtg cttgttgtcg ttggcggggt gctggcctgc 900

tattccctgc tggtgaccgt cgcgtttatt attttctggg ttagatccaa aagaagccgc 960

ctgctccata gcgattacat gaatatgact ccacgccgcc ctggccccac aaggaaacac 1020

taccagcctt acgcaccacc tagagatttc gctgcctatc ggagcagggt gaagttttcc 1080

agatctgcag atgcaccagc gtatcagcag ggccagaacc aactgtataa cgagctcaac 1140

ctgggacgca gggaagagta tgacgttttg gacaagcgca gaggacggga ccctgagatg 1200

ggtggcaaac caagacgaaa aaacccccag gagggtctct ataatgagct gcagaaggat 1260

aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1320

cacgacggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1380

atgcaagccc tgccacctag g 1401

<210> 184
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 184
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
115 120 125

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
130 135 140

Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile
145 150 155 160

Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr
165 170 175

Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile
180 185 190

```
Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
        195                 200                 205

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Val Ser Leu Val Tyr Cys
    210                 215                 220

Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
225                 230                 235                 240

Val Thr Val Ser Ser Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro
                245                 250                 255

Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly
            260                 265                 270

Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe
        275                 280                 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
    290                 295                 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305                 310                 315                 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
                325                 330                 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
            340                 345                 350

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
        355                 360                 365

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
    370                 375                 380

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
385                 390                 395                 400
```

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
405 410 415

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
420 425 430

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
435 440 445

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
450 455 460

Pro Pro Arg
465

<210> 185
<211> 1548
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 185
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggacattc aattgaccca gtcccctagc agtctctcag caagtgtggg agatagggtg 120

tcattcacct gtcaggcttc acaggacatc aacaacttcc tcaattggta tcagcagaag 180

ccagggaagg caccaaagct gctcatatat gacgcttcaa accttgaaac cggagtacct 240

agccgcttca gcggaagcgg atcagggact gacttcactt ttaccatctc ttcactgcag 300

cccgaagaca tcgccacata ctactgccag cagtacggaa acttgccttt tacatttggg 360

ggcggcacca aagtggagat taagcgaggg ggaggcggct caggaggcgg tggctccgga 420

ggcgggggtt cccaggtcca gctccaggaa tccggcccag gtctggttaa gcccagtgaa 480

actttgtccc tcacgtgtac tgtgagcggt ggttcaatct cctcatacta ttggtcttgg 540

atacggcaac ctcctggaaa gggcctcgag tggatcggct atatctacta tagtggctcc 600

actaattaca acccttccct caagtccaga gtcaccattt ccgtggacac atctaagaac 660

cagttcagtc tgaagttgtc cagcgttaca gccgcagaca cagccgttta ttactgtgtg 720

tctcttgttt actgcggggg agactgttat agcggcttcg attactgggg ccagggcacc 780

ttggtcacag tctcttccgc ggccgccctc tctaacagta ttatgtactt ttctcatttt 840

gtacccgtgt tccttcccgc taagccaact actaccccgg ccccacggcc gcctacccct 900

gcacccacaa tagccagtca gcctttgagc ctgagacctg aggcttgtcg gccggctgct 960

gggggtgcag tgcacacacg aggtcttgat tttgcttgcg acatatacat ctgggcccct 1020

ctggccggga cctgtggggt gctgcttctg agcttggtca tcacgctcta ttgcaaccat 1080

cgcaacagat ccaaaagaag ccgcctgctc catagcgatt acatgaatat gactccacgc 1140

cgccctggcc ccacaaggaa acactaccag ccttacgcac cacctagaga tttcgctgcc 1200

tatcggagca gggtgaagtt ttccagatct gcagatgcac cagcgtatca gcagggccag 1260

aaccaactgt ataacgagct caacctggga cgcagggaag agtatgacgt tttggacaag 1320

cgcagaggac gggaccctga gatgggtggc aaaccaagac gaaaaaaccc ccaggagggt 1380

ctctataatg agctgcagaa ggataagatg gctgaagcct attctgaaat aggcatgaaa 1440

ggagagcgga gaaggggaaa agggcacgac ggtttgtacc agggactcag cactgctacg 1500

aaggatactt atgacgctct ccacatgcaa gccctgccac ctaggtaa 1548

<210> 186
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 186
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu
20 25 30

Ser Ala Ser Val Gly Asp Arg Val Ser Phe Thr Cys Gln Ala Ser Gln

```
        35                  40                  45

Asp Ile Asn Asn Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
    50                  55                  60

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile
                85                  90                  95

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

Gly Asn Leu Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
145                 150                 155                 160

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
                165                 170                 175

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
            180                 185                 190

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
        195                 200                 205

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
    210                 215                 220

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Val
225                 230                 235                 240

Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr Trp
                245                 250                 255
```

```
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ala Ala Leu Ser Asn
            260                 265                 270

Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe Leu Pro Ala Lys
        275                 280                 285

Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
    290                 295                 300

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
305                 310                 315                 320

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
                325                 330                 335

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
            340                 345                 350

Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg
        355                 360                 365

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
    370                 375                 380

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
385                 390                 395                 400

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
                405                 410                 415

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
            420                 425                 430

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
        435                 440                 445

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
    450                 455                 460

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
```

465 470 475 480

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
485 490 495

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
500 505 510

Pro Pro Arg
515

<210> 187
<211> 1482
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 187
gacattcaat tgacccagtc ccctagcagt ctctcagcaa gtgtgggaga tagggtgtca 60

ttcacctgtc aggcttcaca ggacatcaac aacttcctca attggtatca gcagaagcca 120

gggaaggcac caaagctgct catatatgac gcttcaaacc ttgaaaccgg agtacctagc 180

cgcttcagcg gaagcggatc agggactgac ttcactttta ccatctcttc actgcagccc 240

gaagacatcg ccacatacta ctgccagcag tacggaaact tgccttttac atttgggggc 300

ggcaccaaag tggagattaa gcgaggggga ggcggctcag gaggcggtgg ctccggaggc 360

gggggttccc aggtccagct ccaggaatcc ggcccaggtc tggttaagcc cagtgaaact 420

ttgtccctca cgtgtactgt gagcggtggt tcaatctcct catactattg gtcttggata 480

cggcaacctc ctggaaaggg cctcgagtgg atcggctata tctactatag tggctccact 540

aattacaacc cttccctcaa gtccagagtc accatttccg tggacacatc taagaaccag 600

ttcagtctga agttgtccag cgttacagcc gcagacacag ccgtttatta ctgtgtgtct 660

cttgtttact gcgggggaga ctgttatagc ggcttcgatt actggggcca gggcaccttg 720

gtcacagtct cttccgcggc cgccctctct aacagtatta tgtacttttc tcattttgta 780

cccgtgttcc ttcccgctaa gccaactact accccggccc cacggccgcc tacccctgca 840

cccacaatag ccagtcagcc tttgagcctg agacctgagg cttgtcggcc ggctgctggg 900

ggtgcagtgc acacacgagg tcttgatttt gcttgcgaca tatacatctg ggcccctctg 960

gccgggacct gtggggtgct gcttctgagc ttggtcatca cgctctattg caaccatcgc 1020

aacagatcca aaagaagccg cctgctccat agcgattaca tgaatatgac tccacgccgc 1080

cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat 1140

cggagcaggg tgaagtttc cagatctgca gatgcaccag cgtatcagca gggccagaac 1200

caactgtata acgagctcaa cctgggacgc agggaagagt atgacgtttt ggacaagcgc 1260

agaggacggg accctgagat gggtggcaaa ccaagacgaa aaaaccccca ggagggtctc 1320

tataatgagc tgcagaagga taagatggct gaagcctatt ctgaaatagg catgaaagga 1380

gagcggagaa ggggaaaagg gcacgacggt ttgtaccagg gactcagcac tgctacgaag 1440

gatacttatg acgctctcca catgcaagcc ctgccaccta gg 1482

<210> 188
<211> 494
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 188
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
            100                 105                 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln
        115                 120                 125

Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr
    130                 135                 140

Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile
145                 150                 155                 160

Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr
                165                 170                 175

Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile
            180                 185                 190

Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val
        195                 200                 205

Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Val Ser Leu Val Tyr Cys
    210                 215                 220

Gly Gly Asp Cys Tyr Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
225                 230                 235                 240

Val Thr Val Ser Ser Ala Ala Ala Leu Ser Asn Ser Ile Met Tyr Phe
                245                 250                 255

Ser His Phe Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro
            260                 265                 270

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
        275                 280                 285
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Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
    290                 295                 300

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
305                 310                 315                 320

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
                325                 330                 335

Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
            340                 345                 350

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
        355                 360                 365

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
    370                 375                 380

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
385                 390                 395                 400

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
                405                 410                 415

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
            420                 425                 430

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
        435                 440                 445

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
    450                 455                 460

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
465                 470                 475                 480

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490
```

<210> 189
<211> 1446
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 189
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtac agctgcagga atctgggccc ggacttgtca agccaagtca gacactttct 120

cttacatgta ccgtgagcgg cggaagtata agcagtggag gcttttactg gtcttggata 180

cggcagcacc caggcaaagg cttggagtgg attggataca ttcatcattc aggatctaca 240

cactataatc catcccttaa gtcccgggtc accattagca ttgatacgtc taagaatctg 300

ttcagtctca ggctgtcctc cgtcactgct gccgacacag ccgtgtacta ctgcgcctcc 360

ttggtttact gcggaggcga ctgttatagc ggctttgatt attgggggca ggggaccctc 420

gtaaccgtga gctctggagg gggtgggagc gggggaggag gttcaggggg gggcggctcc 480

gatatccagc tcactcaaag cccctctagt ctctctgcct cagtgggggа tcgggtcagt 540

tttacttgtc aagcttcaca ggatatcaac aacttcctta attggtatca gcagaagcca 600

ggaaaagcac ccaagctgct catctatgat gcctcaaatt tggagacggg tgttcccagt 660

cgattctctg ggtcagggtc cgggaccgac tttacgttta cgatctcctc tctgcagccc 720

gaagacatcg ccacatacta ttgtcaacag tacggcaact tgcctttcac atttgggggc 780

gggactaagg ttgaaatcaa gagggccgct gcactggaca atgagaagtc caacggcacc 840

atcatccacg tgaagggcaa gcacctgtgc cctagtcctc tgttcccagg cccatccaaa 900

ccttttggg ttcttgttgt ggtcgggggg gtgctggcct gctattctct gctggtcacg 960

gtggccttca taattttctg ggttagatcc aaaagaagcc gcctgctcca tagcgattac 1020

atgaatatga ctccacgccg ccctggcccc acaaggaaac actaccagcc ttacgcacca 1080

cctagagatt tcgctgccta tcggagcagg gtgaagtttt ccagatctgc agatgcacca 1140

gcgtatcagc agggccagaa ccaactgtat aacgagctca acctgggacg cagggaagag 1200

tatgacgttt tggacaagcg cagaggacgg gaccctgaga tgggtggcaa accaagacga 1260

aaaaaccccc aggagggtct ctataatgag ctgcagaagg ataagatggc tgaagcctat 1320

tctgaaatag gcatgaaagg agagcggaga aggggaaaag ggcacgacgg tttgtaccag 1380

ggactcagca ctgctacgaa ggatacttat gacgctctcc acatgcaagc cctgccacct 1440

aggtaa 1446

<210> 190
<211> 481
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 190
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
20 25 30

Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly
35 40 45

Ser Ile Ser Ser Gly Gly Phe Tyr Trp Ser Trp Ile Arg Gln His Pro
50 55 60

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile His His Ser Gly Ser Thr
65 70 75 80

His Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr
85 90 95

Ser Lys Asn Leu Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Ser Leu Val Tyr Cys Gly Gly Asp Cys
115 120 125

```
Tyr Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145                 150                 155                 160

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
                165                 170                 175

Asp Arg Val Ser Phe Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe
            180                 185                 190

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        195                 200                 205

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    210                 215                 220

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
225                 230                 235                 240

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Gly Asn Leu Pro Phe
                245                 250                 255

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Leu
            260                 265                 270

Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His
        275                 280                 285

Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val
    290                 295                 300

Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr
305                 310                 315                 320

Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu
                325                 330                 335

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
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            340                 345                 350

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
        355                 360                 365

Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
    370                 375                 380

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
385                 390                 395                 400

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
                405                 410                 415

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
            420                 425                 430

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
        435                 440                 445

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
    450                 455                 460

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
465                 470                 475                 480

Arg
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<210> 191
<211> 1380
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 191
caggtacagc tgcaggaatc tgggcccgga cttgtcaagc caagtcagac actttctctt 60

acatgtaccg tgagcggcgg aagtataagc agtggaggct tttactggtc ttggatacgg 120

cagcacccag gcaaaggctt ggagtggatt ggatacattc atcattcagg atctacacac 180

tataatccat cccttaagtc ccgggtcacc attagcattg atacgtctaa gaatctgttc 240

agtctcaggc tgtcctccgt cactgctgcc gacacagccg tgtactactg cgcctccttg 300

gtttactgcg gaggcgactg ttatagcggc tttgattatt gggggcaggg gaccctcgta 360

accgtgagct ctggaggggg tgggagcggg ggaggaggtt caggggggggg cggctccgat 420

atccagctca ctcaaagccc ctctagtctc tctgcctcag tgggggatcg ggtcagtttt 480

acttgtcaag cttcacagga tatcaacaac ttccttaatt ggtatcagca gaagccagga 540

aaagcaccca agctgctcat ctatgatgcc tcaaatttgg agacgggtgt tcccagtcga 600

ttctctgggt cagggtccgg gaccgacttt acgtttacga tctcctctct gcagcccgaa 660

gacatcgcca catactattg tcaacagtac ggcaacttgc ctttcacatt tgggggcggg 720

actaaggttg aaatcaagag ggccgctgca ctggacaatg agaagtccaa cggcaccatc 780

atccacgtga agggcaagca cctgtgccct agtcctctgt tcccaggccc atccaaacct 840

ttttgggttc ttgttgtggt cgggggggtg ctggcctgct attctctgct ggtcacggtg 900

gccttcataa ttttctgggt tagatccaaa agaagccgcc tgctccatag cgattacatg 960

aatatgactc cacgccgccc tggccccaca aggaaacact accagcctta cgcaccacct 1020

agagatttcg ctgcctatcg gagcagggtg aagttttcca gatctgcaga tgcaccagcg 1080

tatcagcagg gccagaacca actgtataac gagctcaacc tgggacgcag ggaagagtat 1140

gacgttttgg acaagcgcag aggacgggac cctgagatgg gtggcaaacc aagacgaaaa 1200

aacccccagg agggtctcta taatgagctg cagaaggata agatggctga agcctattct 1260

gaaataggca tgaaaggaga gcggagaagg ggaaaagggc acgacggttt gtaccaggga 1320

ctcagcactg ctacgaagga tacttatgac gctctccaca tgcaagccct gccacctagg 1380

<210> 192
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 192
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1   5   10   15

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

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

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

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

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

Cys Ala Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp
            100   105   110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
        115   120   125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
    130   135   140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Ser Phe
145   150   155   160

Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe Leu Asn Trp Tyr Gln
                165   170   175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn
            180   185   190

Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195   200   205

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Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Tyr Gly Asn Leu Pro Phe Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Leu Asp Asn Glu Lys Ser
                245                 250                 255

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
            260                 265                 270

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
        275                 280                 285

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
    290                 295                 300

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
305                 310                 315                 320

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
                325                 330                 335

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe
            340                 345                 350

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
        355                 360                 365

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
    370                 375                 380

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
385                 390                 395                 400

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
                405                 410                 415
```

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
420 425 430

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
435 440 445

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
450 455 460

<210> 193
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 193
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctgcagga aagcggtccg ggacttgtca agccgtccca aacgctgagt 120

ctgacgtgta ctgtctctgg tggctctatt tcttccgggg gcttttattg gtcttggatc 180

agacaacacc ctggcaaagg gctggagtgg atagggtata ttcaccactc tgggtccact 240

cactacaacc catcattgaa atccagagtg actatctcaa tcgacacatc caagaacctt 300

ttcagcctga ggttgtcatc agttaccgcc gctgacaccg cggtgtatta ttgcgcctct 360

ctcgtgtact gcggtggcga ttgttatagt ggctttgact actgggggca ggggacattg 420

gttaccgttt caagtggagg cggtgggtct ggcgggggcg gtagcggagg tgggggagc 480

gacatacagc ttacgcagag cccctccagc ctttcagcct ccgtgggggga tagggtgtcc 540

tttacctgcc aggcttccca ggacataaac aacttcctca attggtatca gcaaaagccc 600

gggaaagcac caaagctgct catctacgat gccagcaacc tggaaaccgg agtgccgtct 660

cgcttctctg gaagtggcag tgggaccgat ttcactttta caatctcaag tttgcagcca 720

gaagacattg caacatacta ctgtcaacag tacggcaatc tccccttac atttgggggg 780

ggaactaaag tggagattaa gcgcgctgca gccattgaag ttatgtatcc gcccccgtat 840

ctggataacg agaaatctaa tggtaccata atacatgtga aggggaagca cctctgtcca 900

tcaccgctgt tccccggccc ttcaaaacct ttctgggtac tcgttgtcgt gggtggagtt 960

ctggcctgct atagtctgct ggtgaccgtg gcgtttatca tcttctgggt aagatccaaa 1020

agaagccgcc tgctccatag cgattacatg aatatgactc cacgccgccc tggccccaca 1080

aggaaacact accagcctta cgcaccacct agagatttcg ctgcctatcg gagcagggtg 1140

aagttttcca gatctgcaga tgcaccagcg tatcagcagg gccagaacca actgtataac 1200

gagctcaacc tgggacgcag ggaagagtat gacgttttgg acaagcgcag aggacgggac 1260

cctgagatgg gtggcaaacc aagacgaaaa aacccccagg agggtctcta taatgagctg 1320

cagaaggata agatggctga agcctattct gaaataggca tgaaaggaga gcggagaagg 1380

ggaaaagggc acgacggttt gtaccaggga ctcagcactg ctacgaagga tacttatgac 1440

gctctccaca tgcaagccct gccacctagg taa 1473

<210> 194
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 194
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
20 25 30

Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly
35 40 45

Ser Ile Ser Ser Gly Gly Phe Tyr Trp Ser Trp Ile Arg Gln His Pro
50 55 60

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile His His Ser Gly Ser Thr
65 70 75 80

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His Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr
                85                  90                  95

Ser Lys Asn Leu Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp
            100                 105                 110

Thr Ala Val Tyr Tyr Cys Ala Ser Leu Val Tyr Cys Gly Gly Asp Cys
        115                 120                 125

Tyr Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
    130                 135                 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145                 150                 155                 160

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
                165                 170                 175

Asp Arg Val Ser Phe Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe
            180                 185                 190

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        195                 200                 205

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    210                 215                 220

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
225                 230                 235                 240

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Gly Asn Leu Pro Phe
                245                 250                 255

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Ile
            260                 265                 270

Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly
        275                 280                 285

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
```

290 295 300

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
305 310 315 320

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
325 330 335

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
340 345 350

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
355 360 365

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 195
<211> 1407
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 195
caggtgcagc tgcaggaaag cggtccggga cttgtcaagc cgtcccaaac gctgagtctg 60

acgtgtactg tctctggtgg ctctatttct tccgggggct tttattggtc ttggatcaga 120

caacaccctg gcaaagggct ggagtggata gggtatattc accactctgg gtccactcac 180

tacaacccat cattgaaatc cagagtgact atctcaatcg acacatccaa gaacctttc 240

agcctgaggt tgtcatcagt taccgccgct gacaccgcgg tgtattattg cgcctctctc 300

gtgtactgcg gtggcgattg ttatagtggc tttgactact gggggcaggg gacattggtt 360

accgtttcaa gtggaggcgg tgggtctggc gggggcggta gcggaggtgg ggggagcgac 420

atacagctta cgcagagccc ctccagcctt tcagcctccg tgggggatag ggtgtccttt 480

acctgccagg cttcccagga cataaacaac ttcctcaatt ggtatcagca aaagcccggg 540

aaagcaccaa agctgctcat ctacgatgcc agcaacctgg aaaccggagt gccgtctcgc 600

ttctctggaa gtggcagtgg gaccgatttc acttttacaa tctcaagttt gcagccagaa 660

gacattgcaa catactactg tcaacagtac ggcaatctcc cctttacatt tgggggggga 720

actaaagtgg agattaagcg cgctgcagcc attgaagtta tgtatccgcc cccgtatctg 780

gataacgaga aatctaatgg taccataata catgtgaagg ggaagcacct ctgtccatca 840

ccgctgttcc ccggcccttc aaaacctttc tgggtactcg ttgtcgtggg tggagttctg 900

gcctgctata gtctgctggt gaccgtggcg tttatcatct tctgggtaag atccaaaaga 960

agccgcctgc tccatagcga ttacatgaat atgactccac gccgccctgg ccccacaagg 1020

aaacactacc agccttacgc accacctaga gatttcgctg cctatcggag cagggtgaag 1080

ttttccagat ctgcagatgc accagcgtat cagcagggcc agaaccaact gtataacgag 1140

ctcaacctgg gacgcaggga agagtatgac gttttggaca agcgcagagg acgggaccct 1200

gagatgggtg gcaaaccaag acgaaaaaac ccccaggagg gtctctataa tgagctgcag 1260

aaggataaga tggctgaagc ctattctgaa ataggcatga aaggagagcg gagaagggga 1320

aaagggcacg acggtttgta ccagggactc agcactgcta cgaaggatac ttatgacgct 1380

ctccacatgc aagccctgcc acctagg 1407

<210> 196
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 196
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

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

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

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

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

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

Cys Ala Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
130 135 140

```
Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Ser Phe
145                 150                 155                 160

Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe Leu Asn Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn
            180                 185                 190

Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Tyr Gly Asn Leu Pro Phe Thr Phe Gly Gly Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Ile Glu Val Met Tyr Pro
                245                 250                 255

Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val
            260                 265                 270

Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys
        275                 280                 285

Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
    290                 295                 300

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
305                 310                 315                 320

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
                325                 330                 335

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
            340                 345                 350

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
        355                 360                 365
```

```
Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
    370                 375                 380

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
385                 390                 395                 400

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
                405                 410                 415

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
            420                 425                 430

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
        435                 440                 445

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
    450                 455                 460

Ala Leu Pro Pro Arg
465
```

<210> 197
<211> 1554
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 197
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agttgcagga aagcgggcct ggccttgtga aaccaagcca gacactgagc 120

ctgacatgca ctgtgtccgg cgggtccata tcttccgggg gtttttattg gtcctggata 180

cgccagcatc ccgggaaagg acttgaatgg attggatata tccaccattc cggaagcacc 240

cactacaatc caagccttaa atcccgggtg acaatctcca tcgacacctc aaagaatctt 300

ttttccctgc ggttgtcttc agtaactgcc gccgataccg ctgtgtacta ctgtgccagc 360

ctcgtctatt gcggcggaga ttgttattct gggttcgatt attggggtca aggcacactg 420

gtaactgtca gcagcggagg cggcggttcc gggggcgggg gcagtggagg gggcggatct 480

gacattcagc ttacgcagtc cccatcttca cttagcgcca gcgttggcga tcgggtcagc 540

ttcacgtgtc aagcaagtca ggatatcaac aactttctta actggtacca gcagaagcca 600

ggcaaggcac ccaagttgct gatttacgat gcttctaacc tcgagacggg agtgcctagc 660

cgcttctccg ggagcggcag cggcacagac tttaccttta cgatttccag tctgcagcca 720

gaggatatag caacttatta ctgtcagcag tatggcaacc tccctttac cttcggtggt 780

ggcacaaagg tcgagattaa aagagccgca gcgttgtcca actccataat gtatttttct 840

cattttgtgc ccgtctttct gcctgccaaa cctaccacca cccccgcccc acgaccacct 900

actccagccc ccaccatcgc ctcccagccc ctcagcctga ggccagaggc ttgtcgccct 960

gctgcggggg gcgctgtcca taccagagga ctcgacttcg cctgcgatat ttatatatgg 1020

gcccccctcg ccggcacctg cggagtcttg ctcctgagcc ttgtgatcac gctttattgt 1080

aaccatcgga atagatccaa aagaagccgc ctgctccata gcgattacat gaatatgact 1140

ccacgccgcc ctggccccac aaggaaacac taccagcctt acgcaccacc tagagatttc 1200

gctgcctatc ggagcagggt gaagttttcc agatctgcag atgcaccagc gtatcagcag 1260

ggccagaacc aactgtataa cgagctcaac ctgggacgca gggaagagta tgacgttttg 1320

gacaagcgca gaggacggga ccctgagatg ggtggcaaac caagacgaaa aaacccccag 1380

gagggtctct ataatgagct gcagaaggat aagatggctg aagcctattc tgaaataggc 1440

atgaaaggag agcggagaag gggaaaaggg cacgacggtt tgtaccaggg actcagcact 1500

gctacgaagg atacttatga cgctctccac atgcaagccc tgccacctag gtaa 1554

<210> 198
<211> 517
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 198
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
            20   25   30

Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly
        35   40   45

Ser Ile Ser Ser Gly Gly Phe Tyr Trp Ser Trp Ile Arg Gln His Pro
    50   55   60

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile His His Ser Gly Ser Thr
65   70   75   80

His Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr
                85   90   95

Ser Lys Asn Leu Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp
            100   105   110

Thr Ala Val Tyr Tyr Cys Ala Ser Leu Val Tyr Cys Gly Gly Asp Cys
        115   120   125

Tyr Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
    130   135   140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145   150   155   160

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
                165   170   175

Asp Arg Val Ser Phe Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe
            180   185   190

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        195   200   205

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

```
    210                 215                 220

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
225                 230                 235                 240

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Gly Asn Leu Pro Phe
                245                 250                 255

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Leu
            260                 265                 270

Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe Leu Pro
        275                 280                 285

Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
    290                 295                 300

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
305                 310                 315                 320

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
                325                 330                 335

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
            340                 345                 350

Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Ser Lys Arg
        355                 360                 365

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
    370                 375                 380

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
385                 390                 395                 400

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
                405                 410                 415

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
            420                 425                 430
```

```
Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
        435                 440                 445

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
    450                 455                 460

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
465                 470                 475                 480

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
                485                 490                 495

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
            500                 505                 510

Ala Leu Pro Pro Arg
        515
```

<210> 199
<211> 1488
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 199

```
caggtgcagt tgcaggaaag cgggcctggc cttgtgaaac caagccagac actgagcctg       60

acatgcactg tgtccggcgg gtccatatct tccgggggtt tttattggtc ctggatacgc      120

cagcatcccg ggaaaggact tgaatggatt ggatatatcc accattccgg aagcacccac      180

tacaatccaa gccttaaatc ccgggtgaca atctccatcg acacctcaaa gaatcttttt      240

tccctgcggt tgtcttcagt aactgccgcc gataccgctg tgtactactg tgccagcctc      300

gtctattgcg gcggagattg ttattctggg ttcgattatt ggggtcaagg cacactggta      360

actgtcagca gcggaggcgg cggttccggg ggcgggggca gtggaggggg cggatctgac      420

attcagctta cgcagtcccc atcttcactt agcgccagcg ttggcgatcg ggtcagcttc      480
```

acgtgtcaag caagtcagga tatcaacaac tttcttaact ggtaccagca gaagccaggc 540

aaggcaccca agttgctgat ttacgatgct tctaacctcg agacgggagt gcctagccgc 600

ttctccggga gcggcagcgg cacagacttt acctttacga tttccagtct gcagccagag 660

gatatagcaa cttattactg tcagcagtat ggcaacctcc cttttacctt cggtggtggc 720

acaaaggtcg agattaaaag agccgcagcg ttgtccaact ccataatgta tttttctcat 780

tttgtgcccg tctttctgcc tgccaaacct accaccaccc ccgccccacg accacctact 840

ccagccccca ccatcgcctc ccagcccctc agcctgaggc cagaggcttg tcgccctgct 900

gcgggggggcg ctgtccatac cagaggactc gacttcgcct gcgatattta tatatgggcc 960

cccctcgccg gcacctgcgg agtcttgctc ctgagccttg tgatcacgct ttattgtaac 1020

catcggaata gatccaaaag aagccgcctg ctccatagcg attacatgaa tatgactcca 1080

cgccgccctg gccccacaag gaaacactac cagccttacg caccacctag agatttcgct 1140

gcctatcgga gcagggtgaa gttttccaga tctgcagatg caccagcgta tcagcagggc 1200

cagaaccaac tgtataacga gctcaacctg ggacgcaggg aagagtatga cgttttggac 1260

aagcgcagag gacgggaccc tgagatgggt ggcaaaccaa gacgaaaaaa cccccaggag 1320

ggtctctata atgagctgca gaaggataag atggctgaag cctattctga aataggcatg 1380

aaaggagagc ggagaagggg aaaagggcac gacggtttgt accagggact cagcactgct 1440

acgaaggata cttatgacgc tctccacatg caagccctgc cacctagg 1488

<210> 200
<211> 496
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 200
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

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

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

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

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

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

Cys Ala Ser Leu Val Tyr Cys Gly Gly Asp Cys Tyr Ser Gly Phe Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Ser Phe
145                 150                 155                 160

Thr Cys Gln Ala Ser Gln Asp Ile Asn Asn Phe Leu Asn Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn
            180                 185                 190

Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Tyr Gly Asn Leu Pro Phe Thr Phe Gly Gly Gly
225                 230                 235                 240
```

```
Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Leu Ser Asn Ser Ile Met
                245                 250                 255

Tyr Phe Ser His Phe Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr
            260                 265                 270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
        275                 280                 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
    290                 295                 300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
305                 310                 315                 320

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
                325                 330                 335

Leu Tyr Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg Leu Leu His
            340                 345                 350

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
        355                 360                 365

His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
    370                 375                 380

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
385                 390                 395                 400

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
                405                 410                 415

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

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
        435                 440                 445

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
    450                 455                 460
```

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
465 470 475 480

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490 495

<210> 201
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 201
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtcc aactggtgca gtccggagcc gaagtcaaga aaccaggtgc ctccgttaaa 120

gtgagttgca aagtctctgg atacactctg accgagctct ctatgcactg ggtccggcag 180

gcccccggca agggattgga atggatgggc gggttcgatc ctgaggacgg agagactatc 240

tacgctcaaa aattccaggg acgagtgact gtgaccgaag acactagtac cgacactgcc 300

tacatggaac tttcctctct gcgatcagaa gataccgcag tgtactactg tgctactgaa 360

tctaggggca ttggatggcc ctacttcgat tactggggtc agggaactct ggtgactgtc 420

tccagcggtg gaggtggcag cggtggtggc ggaagcgggg ggggcggctc tgatattcag 480

atgactcaat ctccttcttc tctgtccgct tccgtgggcg atagagtgac cattacttgt 540

agggcgtccc agtcaatctc cagttatttg aattggtatc agcagaagcc cgggaaagca 600

cctaagctgt tgatcagcgg ggcttctagc ctgaagagtg gggtaccttc acggttcagc 660

ggaagcggaa gcggaaccga tttcaccctg actatcagca gcctgccacc tgaggacttt 720

gcaacttact actgccaaca gtcatacagc actccgatca ctttcggcca gggcacccgg 780

ctcgaaatca agcgcgctgc tgctttggac aatgagaagt caaacggcac catcatacat 840

gttaaaggta aacatctgtg tccctccccg ctgttccccg gcccttccaa accgttctgg 900

gttctggtgg tggtcggagg cgtactcgct tgctatagtc tgctggtaac tgtcgccttc 960

atcatctttt gggtgagatc caaaagaagc cgcctgctcc atagcgatta catgaatatg 1020

actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat 1080

ttcgctgcct atcggagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag 1140

cagggccaga accaactgta taacgagctc aacctgggac gcagggaaga gtatgacgtt 1200

ttggacaagc gcagaggacg ggaccctgag atgggtggca aaccaagacg aaaaaacccc 1260

caggagggtc tctataatga gctgcagaag gataagatgg ctgaagccta ttctgaaata 1320

ggcatgaaag gagagcggag aaggggaaaa gggcacgacg gtttgtacca gggactcagc 1380

actgctacga aggatactta tgacgctctc cacatgcaag ccctgccacc taggtaa 1437

<210> 202
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 202
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

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

Thr Leu Thr Glu Leu Ser Met His Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

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

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Val Thr Glu Asp Thr Ser
85 90 95

```
Thr Asp Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Thr Glu Ser Arg Gly Ile Gly Trp Pro Tyr
        115                 120                 125

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
145                 150                 155                 160

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

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
            180                 185                 190

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Ser Gly Ala
        195                 200                 205

Ser Ser Leu Lys Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
    210                 215                 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Pro Pro Glu Asp Phe
225                 230                 235                 240

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Ile Thr Phe Gly
                245                 250                 255

Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ala Ala Leu Asp Asn Glu
            260                 265                 270

Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro
        275                 280                 285

Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val
    290                 295                 300

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
```

305 310 315 320

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
325 330 335

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
340 345 350

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
355 360 365

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
370 375 380

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
385 390 395 400

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
405 410 415

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
420 425 430

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
435 440 445

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
450 455 460

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 203
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 203
caggtccaac tggtgcagtc cggagccgaa gtcaagaaac caggtgcctc cgttaaagtg 60

agttgcaaag tctctggata cactctgacc gagctctcta tgcactgggt ccggcaggcc 120

cccggcaagg gattggaatg gatgggcggg ttcgatcctg aggacggaga gactatctac 180

gctcaaaaat tccagggacg agtgactgtg accgaagaca ctagtaccga cactgcctac 240

atggaacttt cctctctgcg atcagaagat accgcagtgt actactgtgc tactgaatct 300

aggggcattg gatggcccta cttcgattac tggggtcagg gaactctggt gactgtctcc 360

agcggtggag gtggcagcgg tggtggcgga agcgggggg gcggctctga tattcagatg 420

actcaatctc cttcttctct gtccgcttcc gtgggcgata gagtgaccat tacttgtagg 480

gcgtcccagt caatctccag ttatttgaat tggtatcagc agaagcccgg gaaagcacct 540

aagctgttga tcagcggggc ttctagcctg aagagtgggg taccttcacg gttcagcgga 600

agcggaagcg gaaccgattt caccctgact atcagcagcc tgccacctga ggactttgca 660

acttactact gccaacagtc atacagcact ccgatcactt tcggccaggg cacccggctc 720

gaaatcaagc gcgctgctgc tttggacaat gagaagtcaa acggcaccat catacatgtt 780

aaaggtaaac atctgtgtcc ctccccgctg ttccccggcc cttccaaacc gttctgggtt 840

ctggtggtgg tcggaggcgt actcgcttgc tatagtctgc tggtaactgt cgccttcatc 900

atcttttggg tgagatccaa aagaagccgc ctgctccata gcgattacat gaatatgact 960

ccacgccgcc ctggccccac aaggaaacac taccagcctt acgcaccacc tagagatttc 1020

gctgcctatc ggagcagggt gaagttttcc agatctgcag atgcaccagc gtatcagcag 1080

ggccagaacc aactgtataa cgagctcaac ctgggacgca gggaagagta tgacgttttg 1140

gacaagcgca gaggacggga ccctgagatg ggtggcaaac caagacgaaa aaacccccag 1200

gagggtctct ataatgagct gcagaaggat aagatggctg aagcctattc tgaaataggc 1260

atgaaaggag agcggagaag gggaaaaggg cacgacggtt tgtaccaggg actcagcact 1320

gctacgaagg atacttatga cgctctccac atgcaagccc tgccacctag g 1371

<210> 204
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 204
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 Val Ser Gly Tyr Thr Leu Thr Glu Leu
20 25 30

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
130 135 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145 150 155 160

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Leu Leu Ile Ser Gly Ala Ser Ser Leu Lys Ser
180 185 190

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Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Pro Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Ser Tyr Ser Thr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu
225                 230                 235                 240

Glu Ile Lys Arg Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn Gly Thr
                245                 250                 255

Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro
            260                 265                 270

Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu
        275                 280                 285

Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
    290                 295                 300

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
305                 310                 315                 320

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
                325                 330                 335

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
            340                 345                 350

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
        355                 360                 365

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
    370                 375                 380

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
385                 390                 395                 400
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Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
405 410 415

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
420 425 430

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
435 440 445

Leu His Met Gln Ala Leu Pro Pro Arg
450 455

<210> 205
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 205
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agcttgtgca gagcggggcc gaggtgaaga agcccggggc cagcgtcaaa 120

gtgtcctgta aggtcagcgg ttacaccctc accgagctga gcatgcactg ggtacggcag 180

gctcccggca aaggtcttga gtggatgggt ggatttgatc cagaagatgg agagactatc 240

tacgcccaga agttccaggg ccgggtcacc gtaacagaag acacctcaac tgacaccgct 300

tacatggagc tgagttcact gcggtccgag gacacggccg tgtattattg tgccaccgag 360

agccgcggaa tcggatggcc ttacttcgac tactggggac agggtacact tgttacagta 420

tcatccgggg gtggcggctc tggtgggggc ggctccggag ggggtggatc agatatccaa 480

atgactcaaa gtccaagttc cctgtctgcc tcagtcggag atagagtcac cataacctgc 540

agggcaagtc agtccatctc ctcctatctg aactggtacc aacagaaacc tggaaaggcg 600

cctaagctcc tgatctccgg agcctcatct ttgaaatccg gtgtcccatc tcgcttcagt 660

ggctctggaa gcggtacaga ttttactttg accattagca gcctcccacc ggaagacttt 720

gctacatatt actgccagca gtcttactca accccaatca ccttcgggca aggcaccaga 780

ctcgaaataa aaagagcagc tgctatcgag gttatgtacc caccgccgta cttggataac 840

gaaaaaagca atgggaccat cattcatgtg aagggtaagc acctttgccc tagcccactg 900

tttcctggcc cgagtaaacc cttttgggta cttgtggtcg tcggcggcgt gctggcctgc 960

tactcactcc tggttaccgt cgcattcatc atcttttggg tgagatccaa aagaagccgc 1020

ctgctccata gcgattacat gaatatgact ccacgccgcc ctggccccac aaggaaacac 1080

taccagcctt acgcaccacc tagagatttc gctgcctatc ggagcagggt gaagttttcc 1140

agatctgcag atgcaccagc gtatcagcag ggccagaacc aactgtataa cgagctcaac 1200

ctgggacgca gggaagagta tgacgttttg gacaagcgca gaggacggga ccctgagatg 1260

ggtggcaaac caagacgaaa aaacccccag gagggtctct ataatgagct gcagaaggat 1320

aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1380

cacgacggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1440

atgcaagccc tgccacctag gtaa 1464

<210> 206
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 206
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
20 25 30

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

Thr Leu Thr Glu Leu Ser Met His Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

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

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Val Thr Glu Asp Thr Ser
                85                  90                  95

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

Ala Val Tyr Tyr Cys Ala Thr Glu Ser Arg Gly Ile Gly Trp Pro Tyr
        115                 120                 125

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
145                 150                 155                 160

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

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
            180                 185                 190

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Ser Gly Ala
        195                 200                 205

Ser Ser Leu Lys Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
    210                 215                 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Pro Pro Glu Asp Phe
225                 230                 235                 240

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Ile Thr Phe Gly
                245                 250                 255

Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ala Ala Ile Glu Val Met
            260                 265                 270

Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile
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        275                 280                 285

His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro
    290                 295                 300

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

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
                325                 330                 335

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
            340                 345                 350

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
        355                 360                 365

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
    370                 375                 380

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385                 390                 395                 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
                405                 410                 415

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
            420                 425                 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
        435                 440                 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
    450                 455                 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465                 470                 475                 480

Met Gln Ala Leu Pro Pro Arg
                485
```

<210> 207
<211> 1398
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 207
caggtgcagc ttgtgcagag cggggccgag gtgaagaagc ccggggccag cgtcaaagtg 60

tcctgtaagg tcagcggtta caccctcacc gagctgagca tgcactgggt acggcaggct 120

cccggcaaag gtcttgagtg gatgggtgga tttgatccag aagatggaga gactatctac 180

gcccagaagt tccagggccg ggtcaccgta acagaagaca cctcaactga caccgcttac 240

atggagctga gttcactgcg gtccgaggac acggccgtgt attattgtgc caccgagagc 300

cgcggaatcg gatggcctta cttcgactac tggggacagg gtacacttgt tacagtatca 360

tccgggggtg gcggctctgg tgggggcggc tccggagggg gtggatcaga tatccaaatg 420

actcaaagtc caagttccct gtctgcctca gtcggagata gagtcaccat aacctgcagg 480

gcaagtcagt ccatctcctc ctatctgaac tggtaccaac agaaacctgg aaaggcgcct 540

aagctcctga tctccggagc ctcatctttg aaatccggtg tcccatctcg cttcagtggc 600

tctggaagcg gtacagattt tactttgacc attagcagcc tcccaccgga agactttgct 660

acatattact gccagcagtc ttactcaacc ccaatcacct tcgggcaagg caccagactc 720

gaaataaaaa gagcagctgc tatcgaggtt atgtacccac cgccgtactt ggataacgaa 780

aaaagcaatg ggaccatcat tcatgtgaag ggtaagcacc tttgccctag cccactgttt 840

cctggcccga gtaaaccctt ttgggtactt gtggtcgtcg gcggcgtgct ggcctgctac 900

tcactcctgg ttaccgtcgc attcatcatc ttttgggtga gatccaaaag aagccgcctg 960

ctccatagcg attacatgaa tatgactcca cgccgccctg gccccacaag gaaacactac 1020

cagccttacg caccacctag agatttcgct gcctatcgga gcagggtgaa gttttccaga 1080

tctgcagatg caccagcgta tcagcagggc cagaaccaac tgtataacga gctcaacctg 1140

ggacgcaggg aagagtatga cgttttggac aagcgcagag gacgggaccc tgagatgggt 1200

ggcaaaccaa gacgaaaaaa ccccccaggag ggtctctata atgagctgca gaaggataag 1260

atggctgaag cctattctga aataggcatg aaaggagagc ggagaagggg aaaagggcac 1320

gacggtttgt accagggact cagcactgct acgaaggata cttatgacgc tctccacatg 1380

caagccctgc cacctagg 1398

<210> 208
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 208
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 Val Ser Gly Tyr Thr Leu Thr Glu Leu
20 25 30

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

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Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Leu Leu Ile Ser Gly Ala Ser Ser Leu Lys Ser
            180                 185                 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Pro Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Ser Tyr Ser Thr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu
225                 230                 235                 240

Glu Ile Lys Arg Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro Tyr
                245                 250                 255

Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys
            260                 265                 270

His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp
        275                 280                 285

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
    290                 295                 300

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
305                 310                 315                 320

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
                325                 330                 335

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
            340                 345                 350
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Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
        355                 360                 365

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
    370                 375                 380

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
385                 390                 395                 400

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
                405                 410                 415

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
            420                 425                 430

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
        435                 440                 445

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
    450                 455                 460

Pro Arg
465
```

<210> 209
<211> 1545
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 209
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agttggtgca aagcggcgca gaagttaaga aacctggggc gtcagttaag 120

gtgtcttgca aagtatctgg ctataccctc actgagctgt ccatgcattg ggtaaggcag 180

gctcctggaa aggggctcga atggatggga ggatttgacc ctgaagacgg agagaccatc 240

tacgcccaga aattccaggg tagagtaaca gtgactgagg acactagcac tgacacagcg 300

tacatggagc tgagttctct gagaagtgag gacacagccg tttactactg cgctaccgag 360

tccagaggta ttggctggcc atacttcgac tattggggtc agggcaccct ggttacagtg 420

agttcaggag gcgggggctc tgggggggc ggttccggag gggggggctc agatatacag 480

atgacgcaga gtccatcaag tctctcagcc agcgtgggag atcgcgtgac tattacttgc 540

cgcgccagcc agagtattag ctcctatctg aattggtacc agcaaaagcc cgggaaggcc 600

cctaagcttc tgatttctgg cgcctcctct ttgaagtcag gtgtgccaag cagatttagc 660

gggtctggaa gtggcactga ctttacactt actatctcca gcctgccccc agaggatttt 720

gccacatatt actgtcagca aagctactct actccaatca ctttcggcca gggcacaaga 780

ttggagatta agagggctgc cgcactttca aattccatca tgtatttcag ccattttgtg 840

cctgtttttc ttccggccaa acctacaacc actcccgccc cacgcccacc tactcccgcc 900

cctaccattg cctcccagcc tctgtctctt agacctgagg cttgtagacc tgctgccggc 960

ggagccgtgc acactcgcgg tctggacttc gcctgcgaca tctatatctg ggcccctctg 1020

gccggcacct gcggcgttct ccttctctca ctcgtaatca cactctattg caatcacagg 1080

aacagatcca aaagaagccg cctgctccat agcgattaca tgaatatgac tccacgccgc 1140

cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat 1200

cggagcaggg tgaagttttc cagatctgca gatgcaccag cgtatcagca gggccagaac 1260

caactgtata acgagctcaa cctgggacgc agggaagagt atgacgtttt ggacaagcgc 1320

agaggacggg accctgagat gggtggcaaa ccaagacgaa aaaaccccca ggagggtctc 1380

tataatgagc tgcagaagga taagatggct gaagcctatt ctgaaatagg catgaaagga 1440

gagcggagaa ggggaaaagg gcacgacggt ttgtaccagg gactcagcac tgctacgaag 1500

gatacttatg acgctctcca catgcaagcc ctgccaccta ggtaa 1545

<210> 210
<211> 514
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 210
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
            20   25   30

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

Thr Leu Thr Glu Leu Ser Met His Trp Val Arg Gln Ala Pro Gly Lys
    50   55   60

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

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Val Thr Glu Asp Thr Ser
                85   90   95

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

Ala Val Tyr Tyr Cys Ala Thr Glu Ser Arg Gly Ile Gly Trp Pro Tyr
        115   120   125

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
    130   135   140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
145   150   155   160

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

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
            180   185   190

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Ser Gly Ala

```
        195                 200                 205

Ser Ser Leu Lys Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
    210                 215                 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Pro Pro Glu Asp Phe
225                 230                 235                 240

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Ile Thr Phe Gly
                245                 250                 255

Gln Gly Thr Arg Leu Glu Ile Lys Arg Ala Ala Ala Leu Ser Asn Ser
            260                 265                 270

Ile Met Tyr Phe Ser His Phe Val Pro Val Phe Leu Pro Ala Lys Pro
        275                 280                 285

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
    290                 295                 300

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
305                 310                 315                 320

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
                325                 330                 335

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
            340                 345                 350

Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg Leu
        355                 360                 365

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
    370                 375                 380

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
385                 390                 395                 400

Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
                405                 410                 415
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Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
420 425 430

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
435 440 445

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
450 455 460

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
465 470 475 480

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
485 490 495

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
500 505 510

Pro Arg

<210> 211
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 211
caggtgcagt tggtgcaaag cggcgcagaa gttaagaaac ctggggcgtc agttaaggtg 60

tcttgcaaag tatctggcta taccctcact gagctgtcca tgcattgggt aaggcaggct 120

cctggaaagg ggctcgaatg gatgggagga tttgaccctg aagacggaga gaccatctac 180

gcccagaaat tccagggtag agtaacagtg actgaggaca ctagcactga cacagcgtac 240

atggagctga gttctctgag aagtgaggac acagccgttt actactgcgc taccgagtcc 300

agaggtattg gctggccata cttcgactat tggggtcagg gcaccctggt tacagtgagt 360

tcaggaggcg ggggctctgg ggggggcggt tccggagggg ggggctcaga tatacagatg 420

acgcagagtc catcaagtct ctcagccagc gtgggagatc gcgtgactat tacttgccgc 480

gccagccaga gtattagctc ctatctgaat tggtaccagc aaaagcccgg gaaggcccct 540

aagcttctga tttctggcgc ctcctctttg aagtcaggtg tgccaagcag atttagcggg 600

tctggaagtg gcactgactt tacacttact atctccagcc tgcccccaga ggattttgcc 660

acatattact gtcagcaaag ctactctact ccaatcactt tcggccaggg cacaagattg 720

gagattaaga gggctgccgc actttcaaat tccatcatgt atttcagcca ttttgtgcct 780

gtttttcttc cggccaaacc tacaaccact cccgccccac gcccacctac tcccgccccc 840

accattgcct cccagcctct gtctcttaga cctgaggctt gtagacctgc tgccggcgga 900

gccgtgcaca ctcgcggtct ggacttcgcc tgcgacatct atatctgggc ccctctggcc 960

ggcacctgcg gcgttctcct tctctcactc gtaatcacac tctattgcaa tcacaggaac 1020

agatccaaaa gaagccgcct gctccatagc gattacatga atatgactcc acgccgccct 1080

ggccccacaa ggaaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 1140

agcagggtga agttttccag atctgcagat gcaccagcgt atcagcaggg ccagaaccaa 1200

ctgtataacg agctcaacct gggacgcagg gaagagtatg acgttttgga caagcgcaga 1260

ggacgggacc ctgagatggg tggcaaacca agacgaaaaa acccccagga gggtctctat 1320

aatgagctgc agaaggataa gatggctgaa gcctattctg aaataggcat gaaaggagag 1380

cggagaaggg gaaaagggca cgacggtttg taccagggac tcagcactgc tacgaaggat 1440

acttatgacg ctctccacat gcaagccctg ccacctagg 1479

<210> 212
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 212
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 Val Ser Gly Tyr Thr Leu Thr Glu Leu
            20                  25                  30

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Leu Leu Ile Ser Gly Ala Ser Ser Leu Lys Ser
            180                 185                 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Pro Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220
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Gln Gln Ser Tyr Ser Thr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu
225                 230                 235                 240

Glu Ile Lys Arg Ala Ala Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser
                245                 250                 255

His Phe Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala
            260                 265                 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
        275                 280                 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
    290                 295                 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305                 310                 315                 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                325                 330                 335

Asn His Arg Asn Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
            340                 345                 350

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
        355                 360                 365

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys
    370                 375                 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
385                 390                 395                 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
                405                 410                 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
            420                 425                 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
        435                 440                 445
```

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
450 455 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465 470 475 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490

<210> 213
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 213
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtcc agttggtcga aagtggcggt ggtgtagtgc agccgggccg cagtttgagg 120

ctttcctgtg cggcttcagg ctttactttt tccagctatg gaatgcactg ggtgcggcag 180

gcccccggca aaggacttga gtgggtggcc gtcatttctt atgacggatc agataagtac 240

tacgtggaca gcgtcaaggg cagattcacc atctctaggg acaacagtaa aaatagactc 300

tacctccaga tgaatagcct cagagctgaa gacacggccg tctactattg tgctcgggag 360

cggtatagtg gcagagacta ctgggggcag ggcacactcg ttacagtgag tagcggcgga 420

ggagggagtg ggggcggtgg ctccggtgga ggaggttctg agattgttat gacccagagt 480

cctgcgaccc tctcagtcag ccccggggag cgcgcaactt tgtcttgcag agctagtcag 540

tccgtgtcct ctcttctgac atggtaccag caaaagcccg ggcaggctcc gcgccttttg 600

atctttgggg cttcaacaag agccactggg attcccgcac gattctctgg ctccgggagc 660

ggtactggtt tcaccctgac gattagcagt ctccagagcg aggacttcgc cgtatactac 720

tgccagcagt acgatacgtg gccattcact tttggaccag ggactaaagt ggattttaag 780

cgcgccgccg ctctcgataa cgaaaagtca aatggcacca taatccacgt caaaggcaag 840

cacctgtgcc cttccccgct cttccccgga cccagtaaac cattttgggt gctggttgtt 900

gtgggggggcg tgctggcctg ctatagcctt ttggtcactg tagccttcat tatttttggg 960

gtcagatcca aaagaagccg cctgctccat agcgattaca tgaatatgac tccacgccgc 1020

cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat 1080

cggagcaggg tgaagttttc cagatctgca gatgcaccag cgtatcagca gggccagaac 1140

caactgtata acgagctcaa cctgggacgc agggaagagt atgacgtttt ggacaagcgc 1200

agaggacggg accctgagat gggtggcaaa ccaagacgaa aaaaccccca ggagggtctc 1260

tataatgagc tgcagaagga taagatggct gaagcctatt ctgaaatagg catgaaagga 1320

gagcggagaa ggggaaaagg gcacgacggt ttgtaccagg gactcagcac tgctacgaag 1380

gatacttatg acgctctcca catgcaagcc ctgccaccta ggtaa 1425

<210> 214
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 214
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asp Lys Tyr
65 70 75 80

```
Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
                85                  90                  95

Lys Asn Arg Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Glu Arg Tyr Ser Gly Arg Asp Tyr Trp
        115                 120                 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser
145                 150                 155                 160

Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                165                 170                 175

Arg Ala Ser Gln Ser Val Ser Ser Leu Leu Thr Trp Tyr Gln Gln Lys
            180                 185                 190

Pro Gly Gln Ala Pro Arg Leu Leu Ile Phe Gly Ala Ser Thr Arg Ala
        195                 200                 205

Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Gly Phe
    210                 215                 220

Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr
225                 230                 235                 240

Cys Gln Gln Tyr Asp Thr Trp Pro Phe Thr Phe Gly Pro Gly Thr Lys
                245                 250                 255

Val Asp Phe Lys Arg Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn Gly
            260                 265                 270

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
        275                 280                 285

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
```

290 295 300

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
305 310 315 320

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
325 330 335

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
340 345 350

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
355 360 365

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
370 375 380

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
385 390 395 400

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
405 410 415

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
420 425 430

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
435 440 445

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
450 455 460

Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470

<210> 215
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 215
caggtccagt tggtcgaaag tggcggtggt gtagtgcagc cgggccgcag tttgaggctt 60

tcctgtgcgg cttcaggctt tacttttttcc agctatggaa tgcactgggt gcggcaggcc 120

cccggcaaag gacttgagtg ggtggccgtc atttcttatg acggatcaga taagtactac 180

gtggacagcg tcaagggcag attcaccatc tctagggaca acagtaaaaa tagactctac 240

ctccagatga atagcctcag agctgaagac acggccgtct actattgtgc tcgggagcgg 300

tatagtggca gagactactg ggggcagggc acactcgtta cagtgagtag cggcggagga 360

gggagtgggg gcggtggctc cggtggagga ggttctgaga ttgttatgac ccagagtcct 420

gcgaccctct cagtcagccc cggggagcgc gcaactttgt cttgcagagc tagtcagtcc 480

gtgtcctctc ttctgacatg gtaccagcaa aagcccgggc aggctccgcg ccttttgatc 540

tttggggctt caacaagagc cactgggatt cccgcacgat tctctggctc cgggagcggt 600

actggtttca ccctgacgat tagcagtctc cagagcgagg acttcgccgt atactactgc 660

cagcagtacg atacgtggcc attcactttt ggaccaggga ctaaagtgga ttttaagcgc 720

gccgccgctc tcgataacga aaagtcaaat ggcaccataa tccacgtcaa aggcaagcac 780

ctgtgccctt ccccgctctt ccccggaccc agtaaaccat tttgggtgct ggttgttgtg 840

gggggcgtgc tggcctgcta tagccttttg gtcactgtag ccttcattat tttttgggtc 900

agatccaaaa gaagccgcct gctccatagc gattacatga atatgactcc acgccgccct 960

ggccccacaa ggaaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 1020

agcagggtga agttttccag atctgcagat gcaccagcgt atcagcaggg ccagaaccaa 1080

ctgtataacg agctcaacct gggacgcagg gaagagtatg acgttttgga caagcgcaga 1140

ggacgggacc ctgagatggg tggcaaacca agacgaaaaa acccccagga gggtctctat 1200

aatgagctgc agaaggataa gatggctgaa gcctattctg aaataggcat gaaaggagag 1260

cggagaaggg gaaaagggca cgacggtttg taccagggac tcagcactgc tacgaaggat 1320

acttatgacg ctctccacat gcaagccctg ccacctagg 1359

<210> 216

<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 216
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

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

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

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

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

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

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

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser
130 135 140

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

Val Ser Ser Leu Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
165 170 175

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Arg Leu Leu Ile Phe Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala
            180                 185                 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser
        195                 200                 205

Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp
    210                 215                 220

Thr Trp Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Phe Lys Arg
225                 230                 235                 240

Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val
                245                 250                 255

Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys
            260                 265                 270

Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
        275                 280                 285

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
    290                 295                 300

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
305                 310                 315                 320

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
                325                 330                 335

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
            340                 345                 350

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
        355                 360                 365

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
    370                 375                 380
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Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
385 390 395 400

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
405 410 415

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
420 425 430

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
435 440 445

Ala Leu Pro Pro Arg
450

<210> 217
<211> 1452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 217
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctcgtgga gtctggcggc ggcgtggtcc agcccggccg gtccctgcgc 120

ctgtcctgcg ccgccagcgg gtttactttt tcctcctacg gcatgcactg ggtgcgccag 180

gctcccggca agggcctcga gtgggtcgcc gtgatctcat acgatgggtc agacaaatac 240

tatgtcgatt ctgttaaagg gcggtttacc atttcaagag ataactctaa gaataggctg 300

tatttgcaga tgaacagcct gagggctgaa gataccgcag tgtactattg cgctagggag 360

cggtatagtg gccgcgatta ctggggacag ggtacactgg tgaccgtgag ctctgggggt 420

ggcggaagcg ggggtggcgg aagcggcgga gggggtagtg aaattgtgat gacccagtct 480

ccggctacac tttcagtctc ccctggggag agagctacac tgtcatgcag agcgtcccag 540

tccgtctctt ctctccttac ctggtatcag cagaagcccg gccaggctcc tcgactgctg 600

atcttcggtg cctccacaag ggcgaccggg attccagccc gcttctcagg ttctgggagc 660

ggaactggtt tcactttgac aatcagttca ctgcagtcag aggatttcgc cgtgtactac 720

tgccagcaat acgacacatg gccattcact ttcggacccg gtaccaaagt cgatttcaag 780

agagccgcgg ccatcgaggt tatgtaccca ccaccatatc tggacaatga aaaaagcaat 840

ggaaccatta tccatgtgaa gggtaaacac ctctgcccta gcccactttt ccctggccca 900

tcaaagccct tctgggtctt ggtggtcgtg gggggtgtgc tggcctgtta cagccttctg 960

gtgacggttg ctttcattat cttctgggtt agatccaaaa gaagccgcct gctccatagc 1020

gattacatga atatgactcc acgccgccct ggccccacaa ggaaacacta ccagccttac 1080

gcaccaccta gagatttcgc tgcctatcgg agcagggtga agttttccag atctgcagat 1140

gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg 1200

gaagagtatg acgttttgga caagcgcaga ggacgggacc ctgagatggg tggcaaacca 1260

agacgaaaaa acccccagga gggtctctat aatgagctgc agaaggataa gatggctgaa 1320

gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg 1380

taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440

ccacctaggt aa 1452

<210> 218
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 218
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
35 40 45

```
Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asp Lys Tyr
65                  70                  75                  80

Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
                85                  90                  95

Lys Asn Arg Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Glu Arg Tyr Ser Gly Arg Asp Tyr Trp
        115                 120                 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser
145                 150                 155                 160

Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                165                 170                 175

Arg Ala Ser Gln Ser Val Ser Ser Leu Leu Thr Trp Tyr Gln Gln Lys
            180                 185                 190

Pro Gly Gln Ala Pro Arg Leu Leu Ile Phe Gly Ala Ser Thr Arg Ala
        195                 200                 205

Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Gly Phe
    210                 215                 220

Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr
225                 230                 235                 240

Cys Gln Gln Tyr Asp Thr Trp Pro Phe Thr Phe Gly Pro Gly Thr Lys
                245                 250                 255

Val Asp Phe Lys Arg Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro
```

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            260                 265                 270

Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly
        275                 280                 285

Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe
    290                 295                 300

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
305                 310                 315                 320

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
                325                 330                 335

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
            340                 345                 350

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
        355                 360                 365

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
    370                 375                 380

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
385                 390                 395                 400

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
                405                 410                 415

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
            420                 425                 430

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
        435                 440                 445

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
    450                 455                 460

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
465                 470                 475                 480
```

Pro Pro Arg

<210> 219
<211> 1386
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 219
caggtgcagc tcgtggagtc tggcggcggc gtggtccagc ccggccggtc cctgcgcctg 60

tcctgcgccg ccagcgggtt tacttttcc tcctacggca tgcactgggt gcgccaggct 120

cccggcaagg gcctcgagtg ggtcgccgtg atctcatacg atgggtcaga caaatactat 180

gtcgattctg ttaaagggcg gtttaccatt tcaagagata actctaagaa taggctgtat 240

ttgcagatga acagcctgag ggctgaagat accgcagtgt actattgcgc tagggagcgg 300

tatagtggcc gcgattactg gggacagggt acactggtga ccgtgagctc tgggggtggc 360

ggaagcgggg gtggcggaag cggcggaggg ggtagtgaaa ttgtgatgac ccagtctccg 420

gctacacttt cagtctcccc tggggagaga gctacactgt catgcagagc gtcccagtcc 480

gtctcttctc tccttacctg gtatcagcag aagcccggcc aggctcctcg actgctgatc 540

ttcggtgcct ccacaagggc gaccgggatt ccagcccgct tctcaggttc tgggagcgga 600

actggtttca ctttgacaat cagttcactg cagtcagagg atttcgccgt gtactactgc 660

cagcaatacg acacatggcc attcactttc ggacccggta ccaaagtcga tttcaagaga 720

gccgcggcca tcgaggttat gtacccacca ccatatctgg acaatgaaaa aagcaatgga 780

accattatcc atgtgaaggg taaacacctc tgccctagcc cacttttccc tggcccatca 840

aagcccttct gggtcttggt ggtcgtgggg ggtgtgctgg cctgttacag ccttctggtg 900

acggttgctt tcattatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat 960

tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1020

ccacctagag atttcgctgc ctatcggagc agggtgaagt tttccagatc tgcagatgca 1080

ccagcgtatc agcagggcca gaaccaactg tataacgagc tcaacctggg acgcagggaa 1140

gagtatgacg ttttggacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga 1200

cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc 1260

tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac 1320

cagggactca gcactgctac gaaggatact tatgacgctc tccacatgca agccctgcca 1380

cctagg 1386

<210> 220
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 220
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

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

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

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

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

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

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

```
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser
    130                 135                 140

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

Val Ser Ser Leu Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
                165                 170                 175

Arg Leu Leu Ile Phe Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala
            180                 185                 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser
        195                 200                 205

Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp
    210                 215                 220

Thr Trp Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Phe Lys Arg
225                 230                 235                 240

Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu
                245                 250                 255

Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro
            260                 265                 270

Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val
        275                 280                 285

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
    290                 295                 300

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
305                 310                 315                 320

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
                325                 330                 335
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```
Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
            340                 345                 350

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
        355                 360                 365

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
    370                 375                 380

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
385                 390                 395                 400

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
                405                 410                 415

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
            420                 425                 430

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
        435                 440                 445

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
    450                 455                 460
```

<210> 221
<211> 1533
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 221
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agttggttga atcaggaggg ggtgtggtgc aacccggtcg gtcactgcgc 120

ctcagttgtg ctgcttccgg gtttactttc agctcatatg ggatgcactg ggtacggcag 180

gctccaggta aaggcttgga atgggtggcg gtgatcagct atgacggctc tgacaaatat 240

tatgtggact ccgtgaaagg cagattcacc atcagtcgag acaactcaaa gaatagactc 300

tacttgcaga tgaatagcct ccgggccgaa gatactgcag tctattattg cgcccgggag 360

cgctacagtg gaagagacta ttgggggcaa ggaactcttg tcacagtctc atctggcggc 420

ggcggcagcg gtgggggcgg atctggcggg ggcggcagcg aaatcgttat gactcagagt 480

cctgccacac tgagcgttag ccctggtgag agagcaacac ttagctgcag agctagtcag 540

agtgtttcca gtcttttgac atggtaccaa cagaagcccg gtcaagctcc acgactgctc 600

atcttcggtg catccacccg cgcaaccggg atacccgccc ggttttccgg ttctggaagt 660

ggcacaggat tcacgctcac catttcttct ctgcagtctg aagactttgc cgtgtattac 720

tgccagcagt acgatacctg gccctttacc tttggcccag gtactaaagt ggattttaaa 780

cgagctgctg cactttccaa tagtattatg tacttttcac attttgtgcc cgtgttcctg 840

cctgcgaagc ctacgacaac cccagcccct aggccgccca caccggcccc aactattgcc 900

tcccagccat tgtctctgag acccgaagct tgcagacctg ctgctggagg cgccgttcac 960

acccgaggat tggatttcgc atgtgacatt tacatctggg ccccttggc cggaacctgc 1020

ggtgtgctgc tgctgtcact cgtgattaca ctttactgca accaccgaaa cagatccaaa 1080

agaagccgcc tgctccatag cgattacatg aatatgactc cacgccgccc tggccccaca 1140

aggaaacact accagcctta cgcaccacct agagatttcg ctgcctatcg gagcagggtg 1200

aagttttcca gatctgcaga tgcaccagcg tatcagcagg gccagaacca actgtataac 1260

gagctcaacc tgggacgcag ggaagagtat gacgttttgg acaagcgcag aggacgggac 1320

cctgagatgg gtggcaaacc aagacgaaaa aacccccagg agggtctcta taatgagctg 1380

cagaaggata agatggctga agcctattct gaaataggca tgaaaggaga gcggagaagg 1440

ggaaaagggc acgacggttt gtaccaggga ctcagcactg ctacgaagga tacttatgac 1500

gctctccaca tgcaagccct gccacctagg taa 1533

<210> 222
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 222
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
            20   25   30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
        35   40   45

Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
    50   55   60

Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asp Lys Tyr
65   70   75   80

Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
                85   90   95

Lys Asn Arg Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100   105   110

Ala Val Tyr Tyr Cys Ala Arg Glu Arg Tyr Ser Gly Arg Asp Tyr Trp
        115   120   125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
    130   135   140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser
145   150   155   160

Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                165   170   175

Arg Ala Ser Gln Ser Val Ser Ser Leu Leu Thr Trp Tyr Gln Gln Lys
            180   185   190

Pro Gly Gln Ala Pro Arg Leu Leu Ile Phe Gly Ala Ser Thr Arg Ala

```
        195                 200                 205

Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Gly Phe
    210                 215                 220

Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr
225                 230                 235                 240

Cys Gln Gln Tyr Asp Thr Trp Pro Phe Thr Phe Gly Pro Gly Thr Lys
                245                 250                 255

Val Asp Phe Lys Arg Ala Ala Ala Leu Ser Asn Ser Ile Met Tyr Phe
            260                 265                 270

Ser His Phe Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro
        275                 280                 285

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
    290                 295                 300

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
305                 310                 315                 320

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
                325                 330                 335

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
            340                 345                 350

Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
        355                 360                 365

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
    370                 375                 380

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
385                 390                 395                 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
                405                 410                 415
```

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
420 425 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
435 440 445

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
450 455 460

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465 470 475 480

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
485 490 495

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505 510

<210> 223
<211> 1467
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 223
caggtgcagt tggttgaatc aggaggggt gtggtgcaac ccggtcggtc actgcgcctc 60

agttgtgctg cttccgggtt tactttcagc tcatatggga tgcactgggt acggcaggct 120

ccaggtaaag gcttggaatg ggtggcggtg atcagctatg acggctctga caaatattat 180

gtggactccg tgaaaggcag attcaccatc agtcgagaca actcaaagaa tagactctac 240

ttgcagatga atagcctccg ggccgaagat actgcagtct attattgcgc ccgggagcgc 300

tacagtggaa gagactattg ggggcaagga actcttgtca cagtctcatc tggcggcggc 360

ggcagcggtg ggggcggatc tggcgggggc ggcagcgaaa tcgttatgac tcagagtcct 420

gccacactga gcgttagccc tggtgagaga gcaacactta gctgcagagc tagtcagagt 480

gtttccagtc ttttgacatg gtaccaacag aagcccggtc aagctccacg actgctcatc 540

ttcggtgcat ccacccgcgc aaccgggata cccgcccggt tttccggttc tggaagtggc 600

acaggattca cgctcaccat ttcttctctg cagtctgaag actttgccgt gtattactgc 660

cagcagtacg atacctggcc ctttaccttt ggcccaggta ctaaagtgga ttttaaacga 720

gctgctgcac tttccaatag tattatgtac ttttcacatt ttgtgcccgt gttcctgcct 780

gcgaagccta cgacaacccc agcccctagg ccgcccacac cggccccaac tattgcctcc 840

cagccattgt ctctgagacc cgaagcttgc agacctgctg ctggaggcgc cgttcacacc 900

cgaggattgg atttcgcatg tgacatttac atctgggccc ctttggccgg aacctgcggt 960

gtgctgctgc tgtcactcgt gattacactt tactgcaacc accgaaacag atccaaaaga 1020

agccgcctgc tccatagcga ttacatgaat atgactccac gccgccctgg ccccacaagg 1080

aaacactacc agccttacgc accacctaga gatttcgctg cctatcggag cagggtgaag 1140

ttttccagat ctgcagatgc accagcgtat cagcagggcc agaaccaact gtataacgag 1200

ctcaacctgg gacgcaggga agagtatgac gttttggaca agcgcagagg acgggaccct 1260

gagatgggtg gcaaaccaag acgaaaaaac ccccaggagg gtctctataa tgagctgcag 1320

aaggataaga tggctgaagc ctattctgaa ataggcatga aaggagagcg gagaagggga 1380

aaagggcacg acggtttgta ccagggactc agcactgcta cgaaggatac ttatgacgct 1440

ctccacatgc aagccctgcc acctagg 1467

<210> 224
<211> 489
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 224
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

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

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

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

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

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

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

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser
    130                 135                 140

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

Val Ser Ser Leu Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
                165                 170                 175

Arg Leu Leu Ile Phe Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala
            180                 185                 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser
        195                 200                 205

Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp
    210                 215                 220

Thr Trp Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Phe Lys Arg
225                 230                 235                 240
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Ala Ala Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro
                245                 250                 255

Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro
            260                 265                 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
        275                 280                 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
    290                 295                 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305                 310                 315                 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
                325                 330                 335

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
            340                 345                 350

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
        355                 360                 365

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
    370                 375                 380

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
385                 390                 395                 400

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
                405                 410                 415

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
            420                 425                 430

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
        435                 440                 445

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
    450                 455                 460
```

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
465 470 475 480

Leu His Met Gln Ala Leu Pro Pro Arg
485

<210> 225
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 225
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggagattg tgatgaccca gtcccctgct accctgtccg tcagtccggg cgagagagcc 120

accttgtcat gccgggccag ccagtccgtc agcagtctcc tgacttggta tcagcaaaaa 180

ccagggcagg caccgcggct tttgattttt ggtgcaagca cacgcgccac tggcattcca 240

gctaggtttt ctggaagtgg atctgggaca ggcttcactc tgacaatcag tagcctgcag 300

agtgaggact ttgctgttta ctactgtcaa cagtacgaca cctggccatt cacattcggg 360

cccggcacca aggtcgactt caagaggggc ggtggaggtt caggtggtgg cgggtcaggc 420

ggcggtgggt ctcaggttca actggtggaa tcaggtggcg gcgttgtcca accggggcga 480

tcacttcgac tttcctgtgc tgcctcaggc tttacttttt catcctatgg gatgcactgg 540

gttcggcagg ctcccggaaa aggactcgag tgggttgcag tgatctctta cgatggctca 600

gacaagtatt atgtggactc agtcaagggg agattcacaa taagccgaga caactccaaa 660

aaccggcttt atctccagat gaacagcctt agagcggaag ataccgcggt atactactgt 720

gcccgcgaga ggtattccgg cagagactac tggggacagg gcacactggt caccgtgagt 780

tctgccgcag cgctcgataa cgaaaagagc aacggaacca ttatccacgt taagggcaag 840

cacctgtgcc ccagtcccct cttcccagga ccatctaaac ccttctgggt tctggtagta 900

gttggagggg tccttgcatg ttactccctt ttggtcaccg tcgccttcat tattttctgg 960

gtgagatcca aaagaagccg cctgctccat agcgattaca tgaatatgac tccacgccgc 1020

cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat 1080

cggagcaggg tgaagttttc cagatctgca gatgcaccag cgtatcagca gggccagaac 1140

caactgtata acgagctcaa cctgggacgc agggaagagt atgacgtttt ggacaagcgc 1200

agaggacggg accctgagat gggtggcaaa ccaagacgaa aaaaccccca ggagggtctc 1260

tataatgagc tgcagaagga taagatggct gaagcctatt ctgaaatagg catgaaagga 1320

gagcggagaa ggggaaaagg gcacgacggt ttgtaccagg gactcagcac tgctacgaag 1380

gatacttatg acgctctcca catgcaagcc ctgccaccta ggtaa 1425

<210> 226
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 226
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

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

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

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile
85 90 95

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

Asp Thr Trp Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Phe Lys
        115                 120                 125

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
145                 150                 155                 160

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
                165                 170                 175

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
            180                 185                 190

Ala Val Ile Ser Tyr Asp Gly Ser Asp Lys Tyr Tyr Val Asp Ser Val
        195                 200                 205

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr
    210                 215                 220

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
225                 230                 235                 240

Ala Arg Glu Arg Tyr Ser Gly Arg Asp Tyr Trp Gly Gln Gly Thr Leu
                245                 250                 255

Val Thr Val Ser Ser Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn Gly
            260                 265                 270

Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe
        275                 280                 285

Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val
    290                 295                 300

Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp
```

305 310 315 320

Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met
325 330 335

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
340 345 350

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg
355 360 365

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
370 375 380

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
385 390 395 400

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
405 410 415

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
420 425 430

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
435 440 445

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
450 455 460

Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470

<210> 227
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 227
gagattgtga tgacccagtc ccctgctacc ctgtccgtca gtccgggcga gagagccacc 60

ttgtcatgcc gggccagcca gtccgtcagc agtctcctga cttggtatca gcaaaaacca 120

gggcaggcac cgcggctttt gatttttggt gcaagcacac gcgccactgg cattccagct 180

aggttttctg gaagtggatc tgggacaggc ttcactctga caatcagtag cctgcagagt 240

gaggactttg ctgtttacta ctgtcaacag tacgacacct ggccattcac attcgggccc 300

ggcaccaagg tcgacttcaa gaggggcggt ggaggttcag gtggtggcgg gtcaggcggc 360

ggtgggtctc aggttcaact ggtggaatca ggtggcggcg ttgtccaacc ggggcgatca 420

cttcgacttt cctgtgctgc ctcaggcttt acttttcat cctatgggat gcactgggtt 480

cggcaggctc ccggaaaagg actcgagtgg gttgcagtga tctcttacga tggctcagac 540

aagtattatg tggactcagt caaggggaga ttcacaataa gccgagacaa ctccaaaaac 600

cggctttatc tccagatgaa cagccttaga gcggaagata ccgcggtata ctactgtgcc 660

cgcgagaggt attccggcag agactactgg ggacagggca cactggtcac cgtgagttct 720

gccgcagcgc tcgataacga aaagagcaac ggaaccatta tccacgttaa gggcaagcac 780

ctgtgcccca gtcccctctt cccaggacca tctaaaccct tctgggttct ggtagtagtt 840

ggaggggtcc ttgcatgtta ctccctttg gtcaccgtcg ccttcattat tttctgggtg 900

agatccaaaa gaagccgcct gctccatagc gattacatga atatgactcc acgccgccct 960

ggccccacaa ggaaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 1020

agcagggtga agttttccag atctgcagat gcaccagcgt atcagcaggg ccagaaccaa 1080

ctgtataacg agctcaacct gggacgcagg gaagagtatg acgttttgga caagcgcaga 1140

ggacgggacc ctgagatggg tggcaaacca agacgaaaaa acccccagga gggtctctat 1200

aatgagctgc agaaggataa gatggctgaa gcctattctg aaataggcat gaaaggagag 1260

cggagaaggg gaaaagggca cgacggtttg taccagggac tcagcactgc tacgaaggat 1320

acttatgacg ctctccacat gcaagccctg ccacctagg 1359

<210> 228
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 228
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Pro Gly Thr Lys Val Asp Phe Lys Arg Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val
115 120 125

Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser
130 135 140

Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly Met His Trp Val
145 150 155 160

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr
165 170 175

Asp Gly Ser Asp Lys Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr
180 185 190

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Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr Leu Gln Met Asn Ser
        195                 200                 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Arg Tyr
    210                 215                 220

Ser Gly Arg Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225                 230                 235                 240

Ala Ala Ala Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val
                245                 250                 255

Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys
            260                 265                 270

Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
        275                 280                 285

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
    290                 295                 300

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
305                 310                 315                 320

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
                325                 330                 335

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
            340                 345                 350

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
        355                 360                 365

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
    370                 375                 380

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
385                 390                 395                 400
```

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
405 410 415

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
420 425 430

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
435 440 445

Ala Leu Pro Pro Arg
450

<210> 229
<211> 1452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 229
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggagatcg tcatgacaca gagtccagct accctgagcg tgtcccctgg agagagagcc 120

accctgtcct gtagggctag tcagagtgtg tccagcctcc tcacctggta tcaacagaag 180

cctggtcaag ctccccggct gcttatcttc ggggccagca cgcgagccac aggcatcccg 240

gccagattct ctggctctgg cagtggcacc gggttcactc tcacgatctc atccctgcag 300

tcagaggatt tcgctgtgta ttactgtcag cagtacgata catggccctt caccttcggc 360

ccgggcacaa aagtagattt caagcgcggc ggcgggggta gtgggggcgg gggatcagga 420

ggagggggct cccaagtaca gctggttgag agcggcggcg gggtggttca gcccgggcgc 480

agcctcaggc tgagttgcgc agcatcagga ttcacattca gttcttatgg aatgcattgg 540

gtcagacagg ctcccgggaa gggccttgaa tgggtggcag tcattagcta cgacggaagc 600

gataagtact atgtggactc agttaaaggg agatttacta tcagccgcga caattccaaa 660

aacagattgt atttgcagat gaactccctc agggcggagg acactgctgt atattactgc 720

gcacgagaga gatactccgg ccgagactat tggggccaag gaacattggt aactgtgagc 780

tccgccgcag ctattgaggt catgtacccc ccaccttatc tcgataatga gaagagtaat 840

gggactataa ttcacgtaaa gggcaaacac ctgtgccctt ccccgctgtt tccaggtcca 900

agtaagccgt tctgggtcct ggttgtggtg ggaggggtgc tggcctgcta ttctctgttg 960

gttaccgtgg cctttatcat tttctgggtg agatccaaaa gaagccgcct gctccatagc 1020

gattacatga atatgactcc acgccgccct ggccccacaa ggaaacacta ccagccttac 1080

gcaccaccta gagatttcgc tgcctatcgg agcagggtga agttttccag atctgcagat 1140

gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg 1200

gaagagtatg acgttttgga caagcgcaga ggacgggacc ctgagatggg tggcaaacca 1260

agacgaaaaa acccccagga gggtctctat aatgagctgc agaaggataa gatggctgaa 1320

gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg 1380

taccagggac tcagcactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440

ccacctaggt aa 1452

<210> 230
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 230
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

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

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

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile
                85                  90                  95

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

Asp Thr Trp Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Phe Lys
        115                 120                 125

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
145                 150                 155                 160

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
                165                 170                 175

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
            180                 185                 190

Ala Val Ile Ser Tyr Asp Gly Ser Asp Lys Tyr Tyr Val Asp Ser Val
        195                 200                 205

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr
    210                 215                 220

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
225                 230                 235                 240

Ala Arg Glu Arg Tyr Ser Gly Arg Asp Tyr Trp Gly Gln Gly Thr Leu
                245                 250                 255

Val Thr Val Ser Ser Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro
            260                 265                 270

Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly
```

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        275                 280                 285

Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe
    290                 295                 300

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
305                 310                 315                 320

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
                325                 330                 335

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
            340                 345                 350

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
        355                 360                 365

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
    370                 375                 380

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
385                 390                 395                 400

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
                405                 410                 415

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
            420                 425                 430

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
        435                 440                 445

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
    450                 455                 460

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
465                 470                 475                 480

Pro Pro Arg
```

<210> 231
<211> 1386
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 231
gagatcgtca tgacacagag tccagctacc ctgagcgtgt cccctggaga gagagccacc 60

ctgtcctgta gggctagtca gagtgtgtcc agcctcctca cctggtatca acagaagcct 120

ggtcaagctc cccggctgct tatcttcggg gccagcacgc gagccacagg catcccggcc 180

agattctctg gctctggcag tggcaccggg ttcactctca cgatctcatc cctgcagtca 240

gaggatttcg ctgtgtatta ctgtcagcag tacgatacat ggcccttcac cttcggcccg 300

ggcacaaaag tagatttcaa gcgcggcggc gggggtagtg ggggcggggg atcaggagga 360

gggggctccc aagtacagct ggttgagagc ggcggcgggg tggttcagcc cgggcgcagc 420

ctcaggctga gttgcgcagc atcaggattc acattcagtt cttatggaat gcattgggtc 480

agacaggctc ccgggaaggg ccttgaatgg gtggcagtca ttagctacga cggaagcgat 540

aagtactatg tggactcagt taaagggaga tttactatca gccgcgacaa ttccaaaaac 600

agattgtatt tgcagatgaa ctccctcagg gcggaggaca ctgctgtata ttactgcgca 660

cgagagagat actccggccg agactattgg ggccaaggaa cattggtaac tgtgagctcc 720

gccgcagcta ttgaggtcat gtaccccca ccttatctcg ataatgagaa gagtaatggg 780

actataattc acgtaaaggg caaacacctg tgcccttccc cgctgtttcc aggtccaagt 840

aagccgttct gggtcctggt tgtggtggga ggggtgctgg cctgctattc tctgttggtt 900

accgtggcct ttatcatttt ctgggtgaga tccaaaagaa gccgcctgct ccatagcgat 960

tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1020

ccacctagag atttcgctgc ctatcggagc agggtgaagt tttccagatc tgcagatgca 1080

ccagcgtatc agcagggcca gaaccaactg tataacgagc tcaacctggg acgcagggaa 1140

gagtatgacg ttttggacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga 1200

cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc 1260

tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac 1320

cagggactca gcactgctac gaaggatact tatgacgctc tccacatgca agccctgcca 1380

cctagg 1386

<210> 232
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 232
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Pro Gly Thr Lys Val Asp Phe Lys Arg Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val
115 120 125

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Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser
    130                 135                 140

Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly Met His Trp Val
145                 150                 155                 160

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr
                165                 170                 175

Asp Gly Ser Asp Lys Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr
            180                 185                 190

Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr Leu Gln Met Asn Ser
        195                 200                 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Arg Tyr
    210                 215                 220

Ser Gly Arg Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225                 230                 235                 240

Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu
                245                 250                 255

Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro
            260                 265                 270

Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val
        275                 280                 285

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
    290                 295                 300

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
305                 310                 315                 320

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
                325                 330                 335

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
            340                 345                 350
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Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
        355                 360                 365

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
    370                 375                 380

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
385                 390                 395                 400

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
                405                 410                 415

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
            420                 425                 430

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
        435                 440                 445

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
    450                 455                 460
```

<210> 233
<211> 1533
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 233
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaaatag tgatgactca gtccccggcc accctcagcg tgtccccgg ggagcgagcg 120

accctgtcat gcagggcttc ccagagtgtc agctccctgc tcacttggta tcagcaaaag 180

ccggggcagg ctccccgcct cctcatcttc ggggcatcaa ctagggccac cggcattcct 240

gcaagatttt ccgggtctgg cagcggcacc ggcttcaccc ttaccattag ctctctgcag 300

tctgaggact tcgccgttta ctattgtcag cagtatgata cttggccctt taccttcggt 360

cccggaacta aggtggactt caagcgcggg gggggtggat ctggaggtgg tggctccggg 420

ggcggtggaa gccaggtcca gttggttgag agcggcggcg gagtggtgca gcccgggagg 480

tccttgcggc tgagctgtgc agcctccggt tttacttttt ctagctatgg aatgcattgg 540

gtaagacagg ctcccggaaa aggcctcgag tgggtggcgg tcattagcta tgatggatct 600

gataaatact atgtggactc agttaagggg cgcttcacaa tctcaagaga caatagcaaa 660

aatagactgt acctgcagat gaatagtctg cgcgccgagg acactgccgt gtactactgc 720

gcccgcgaga gatacagcgg acgggattac tggggccagg gtaccctcgt aacggtgtcc 780

tccgctgccg cccttagcaa cagcattatg tacttttctc atttcgtgcc agtctttctc 840

ccagcaaagc ccaccactac cccggccccc aggccgccta ctcctgcccc cactatcgcg 900

tctcagcctc tctccttgcg gcccgaggcc tgccggccag ccgcaggggg cgccgtacat 960

actcggggtt tggatttcgc ttgcgacata tatatttggg ccccctcgc cggcacatgt 1020

ggagtgctgc tcctgagtct cgttataacc ctctattgca accatagaaa cagatccaaa 1080

agaagccgcc tgctccatag cgattacatg aatatgactc cacgccgccc tggccccaca 1140

aggaaacact accagcctta cgcaccacct agagatttcg ctgcctatcg gagcagggtg 1200

aagttttcca gatctgcaga tgcaccagcg tatcagcagg gccagaacca actgtataac 1260

gagctcaacc tgggacgcag ggaagagtat gacgttttgg acaagcgcag aggacgggac 1320

cctgagatgg gtggcaaacc aagacgaaaa aacccccagg agggtctcta taatgagctg 1380

cagaaggata agatggctga agcctattct gaaataggca tgaaaggaga gcggagaagg 1440

ggaaaagggc acgacggttt gtaccaggga ctcagcactg ctacgaagga tacttatgac 1500

gctctccaca tgcaagccct gccacctagg taa 1533

<210> 234
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 234
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

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

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

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

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

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile
                85   90   95

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

Asp Thr Trp Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Phe Lys
        115   120   125

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130   135   140

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
145   150   155   160

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
                165   170   175

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
            180   185   190

Ala Val Ile Ser Tyr Asp Gly Ser Asp Lys Tyr Tyr Val Asp Ser Val
        195   200   205

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr

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    210                 215                 220

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
225                 230                 235                 240

Ala Arg Glu Arg Tyr Ser Gly Arg Asp Tyr Trp Gly Gln Gly Thr Leu
                245                 250                 255

Val Thr Val Ser Ser Ala Ala Ala Leu Ser Asn Ser Ile Met Tyr Phe
            260                 265                 270

Ser His Phe Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro
        275                 280                 285

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
    290                 295                 300

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
305                 310                 315                 320

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
                325                 330                 335

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
            340                 345                 350

Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
        355                 360                 365

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
    370                 375                 380

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
385                 390                 395                 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
                405                 410                 415

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            420                 425                 430
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Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
435 440 445

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
450 455 460

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
465 470 475 480

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
485 490 495

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505 510

<210> 235
<211> 1467
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> anti-CLL-1 CAR construct

<400> 235
gaaatagtga tgactcagtc cccggccacc ctcagcgtgt cccccgggga gcgagcgacc 60

ctgtcatgca gggcttccca gagtgtcagc tccctgctca cttggtatca gcaaaagccg 120

gggcaggctc cccgcctcct catcttcggg gcatcaacta gggccaccgg cattcctgca 180

agattttccg ggtctggcag cggcaccggc ttcaccctta ccattagctc tctgcagtct 240

gaggacttcg ccgtttacta ttgtcagcag tatgatactt ggcccтttac cttcggtccc 300

ggaactaagg tggacttcaa gcgcgggggg ggtggatctg gaggtggtgg ctccgggggc 360

ggtggaagcc aggtccagtt ggttgagagc ggcggcggag tggtgcagcc cgggaggtcc 420

ttgcggctga gctgtgcagc ctccggtttt acttttctа gctatggaat gcattgggta 480

agacaggctc ccggaaaagg cctcgagtgg gtggcggtca ttagctatga tggatctgat 540

aaatactatg tggactcagt taaggggcgc ttcacaatct caagagacaa tagcaaaaat 600

agactgtacc tgcagatgaa tagtctgcgc gccgaggaca ctgccgtgta ctactgcgcc 660

cgcgagagat acagcggacg ggattactgg ggccagggta ccctcgtaac ggtgtcctcc 720

gctgccgccc ttagcaacag cattatgtac ttttctcatt tcgtgccagt ctttctccca 780

gcaaagccca ccactacccc ggcccccagg ccgcctactc ctgcccccac tatcgcgtct 840

cagcctctct ccttgcggcc cgaggcctgc cggccagccg caggggcgc cgtacatact 900

cggggtttgg atttcgcttg cgacatatat atttgggccc ccctcgccgg cacatgtgga 960

gtgctgctcc tgagtctcgt tataaccctc tattgcaacc atagaaacag atccaaaaga 1020

agccgcctgc tccatagcga ttacatgaat atgactccac gccgccctgg ccccacaagg 1080

aaacactacc agccttacgc accacctaga gatttcgctg cctatcggag cagggtgaag 1140

ttttccagat ctgcagatgc accagcgtat cagcagggcc agaaccaact gtataacgag 1200

ctcaacctgg gacgcaggga agagtatgac gttttggaca agcgcagagg acgggaccct 1260

gagatgggtg gcaaaccaag acgaaaaaac ccccaggagg gtctctataa tgagctgcag 1320

aaggataaga tggctgaagc ctattctgaa ataggcatga aaggagagcg gagaagggga 1380

aaagggcacg acggtttgta ccagggactc agcactgcta cgaaggatac ttatgacgct 1440

ctccacatgc aagccctgcc acctagg 1467

<210> 236
<211> 489
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> anti-CLL-1 CAR construct

<400> 236
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Pro Gly Thr Lys Val Asp Phe Lys Arg Gly Gly Gly Gly
            100                 105                 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val
        115                 120                 125

Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser
    130                 135                 140

Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly Met His Trp Val
145                 150                 155                 160

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr
                165                 170                 175

Asp Gly Ser Asp Lys Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr
            180                 185                 190

Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr Leu Gln Met Asn Ser
        195                 200                 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Arg Tyr
    210                 215                 220

Ser Gly Arg Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
225                 230                 235                 240

Ala Ala Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro
                245                 250                 255
```

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Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro
            260                 265                 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
        275                 280                 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
    290                 295                 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305                 310                 315                 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
                325                 330                 335

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
            340                 345                 350

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
        355                 360                 365

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
    370                 375                 380

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
385                 390                 395                 400

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
                405                 410                 415

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
            420                 425                 430

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
        435                 440                 445

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
    450                 455                 460

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
465                 470                 475                 480
```

Leu His Met Gln Ala Leu Pro Pro Arg
485

<210> 237
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<223> scFv G4s linker

<400> 237
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 238
<211> 288
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> Description of Combined DNA/RNA Molecule: Synthetic polynucleotide

<220>
<223> CD8 extracellular

<400> 238
gctgcagcat tgagcaactc aataatgtat tttagtcact ttgtaccagt gttcttgccg 60

gctaagccta ctaccacacc cgctccacgg ccacctaccc cagctcctac catcgcttca 120

cagcctctgt ccctgcgccc agaggcttgc cgaccggccg caggggcgc tgttcatacc 180

agaggactgg atttcgcctg cgatatctat atctgggcac ccctggccgg aacctgcggc 240

gtactcctgc tgtccctggt catcacgctc tattgtaatc acaggaac 288

<210> 239
<211> 96
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> Description of Combined DNA/RNA Molecule: Synthetic
polypeptide

<220>
<223> CD8 extracellular

<400> 239
Ala Ala Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro
1 5 10 15

Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro
20 25 30

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
35 40 45

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
50 55 60

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
65 70 75 80

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
85 90 95

<210> 240
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> extracellular and intracellular domains

<400> 240
cttgataatg aaaagtcaaa cggaacaatc attcacgtga agggcaagca cctctgtccg 60

tcacccttgt tccctggtcc atccaagcca ttctgggtgt tggtcgtagt gggtggagtc 120

ctcgcttgtt actctctgct cgtcaccgtg gcttttataa tcttctgggt tagatccaaa 180

agaagccgcc tgctccatag cgattacatg aatatgactc cacgccgccc tggccccaca 240

aggaaacact accagcctta cgcaccacct agagatttcg ctgcctatcg gagc 294

<210> 241
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> extracellular and intracellular domains

<400> 241
Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys
1 5 10 15

His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp
20 25 30

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
35 40 45

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
50 55 60

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
65 70 75 80

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
85 90 95

Arg Ser

<210> 242
<211> 1482
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> 10E3_CHD_DNA

<400> 242
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtga ccctcaaaga gtctggaccc gtgctcgtaa aacctacgga gaccctgaca 120

ctcacctgca cagtctccgg cttcagcctc atcaatgcca ggatgggagt ttcctggatc 180

aggcaaccgc ccggaaaggc cctggaatgg ctcgcacata ttttcagtaa cgctgaaaaa 240

agctatcgga cttctctgaa aagtcggctc acgattagta aggacacatc caagagccaa 300

gtggtgctta cgatgactaa catggaccct gtggatactg caacctatta ctgtgctcga 360

atccctggtt atggcggaaa tggggactac cactactacg gtatggatgt ctggggccaa 420

gggaccacgg ttactgtttc aagcggaggg ggagggagtg ggggtggcgg atctggcgga 480

ggaggcagcg atatccagat gacgcagtcc cctagttcac tttccgcatc cctgggggat 540

cgggttacca ttacatgccg cgcgtcacag ggtatccgga atgatctggg atggtaccag 600

cagaagccgg gaaaggctcc taagcgcctc atctacgcca gctccaccct gcagagtgga 660

gtgccctccc ggttttcagg cagtggctcc ggtacggagt ttactcttac aattagcagc 720

ctgcagccag aagattttgc aacttactac tgtttgcagc ataataattt cccctggacc 780

tttggtcagg gcaccaaggt ggagatcaaa agagcagccg ccatcgaagt aatgtatccc 840

cccccgtacc ttgacaatga gaagtcaaat ggaaccatta tccatgttaa gggcaaacac 900

ctctgccctt ctccactgtt ccctggccct agtaagccgt tttgggtgct ggtggtagtc 960

ggtggggtgc tggcttgtta ctctcttctc gtgaccgtcg cctttataat cttttgggtc 1020

agatccaaaa gaagccgcct gctccatagc gattacatga atatgactcc acgccgccct 1080

ggccccacaa ggaaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 1140

agccgagtga aattttctag atcagctgat gctcccgcct atcagcaggg acagaatcaa 1200

ctttacaatg agctgaacct gggtcgcaga gaagagtacg acgttttgga caaacgccgg 1260

ggccgagatc ctgagatggg ggggaagccg agaaggaaga atcctcaaga aggcctgtac 1320

aacgagcttc aaaaagacaa aatggctgag gcgtactctg agatcggcat gaagggcgag 1380

cggagacgag gcaagggtca cgatggcttg tatcagggcc tgagtacagc cacaaaggac 1440

acctatgacg ccctccacat gcaggcactg cccccacgct ag 1482

<210> 243
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> 10E3_CHD_AA

<400> 243
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

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

Gly Lys Ala Leu Glu Trp Leu Ala His Ile Phe Ser Asn Ala Glu Lys
65 70 75 80

Ser Tyr Arg Thr Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr
85 90 95

Ser Lys Ser Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp
100 105 110

Thr Ala Thr Tyr Tyr Cys Ala Arg Ile Pro Gly Tyr Gly Gly Asn Gly
115 120 125

Asp Tyr His Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val
130 135 140

```
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145                 150                 155                 160

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

Ser Leu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile
            180                 185                 190

Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
        195                 200                 205

Arg Leu Ile Tyr Ala Ser Ser Thr Leu Gln Ser Gly Val Pro Ser Arg
    210                 215                 220

Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
225                 230                 235                 240

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Asn
                245                 250                 255

Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala
            260                 265                 270

Ala Ala Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys
        275                 280                 285

Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser
    290                 295                 300

Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val
305                 310                 315                 320

Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
                325                 330                 335

Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
            340                 345                 350

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
        355                 360                 365
```

```
Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys
    370                 375                 380

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
385                 390                 395                 400

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
                405                 410                 415

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
            420                 425                 430

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
        435                 440                 445

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
    450                 455                 460

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
465                 470                 475                 480

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490
```

<210> 244
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> 10E3_THD_DNA

<400> 244

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ccgcaagtta ctttgaagga gtctggacct gtactggtga agccaaccga gacactgaca      120

ctcacgtgta cagtgagtgg tttttccttg atcaacgcaa ggatgggcgt cagctggatc      180

aggcaacccc ctggcaaggc tctggaatgg ctcgctcaca tattcagcaa tgccgaaaaa      240
```

agctaccgga caagcctgaa atcccgcctg actatttcca aggacacttc taagtctcag 300

gtggtgctga ccatgaccaa catggacccg gtggacaccg ccacctatta ctgcgcaaga 360

atccctgggt atggtgggaa tggtgactac cattattatg ggatggatgt gtgggggcaa 420

ggcacaaccg taacggtctc aagcggtggg ggaggctcag ggggcggagg ctccggaggt 480

ggcggctccg acattcagat gacccaaagc ccgtccagcc tgtccgccag cctgggagat 540

agagtgacaa tcacgtgtag agcttcccaa gggataagaa atgatctcgg gtggtatcag 600

cagaagcccg gcaaagcccc caaaaggctt atatatgcta gtagtacact gcagtctgga 660

gttccttccc gattttcagg tagcggctcc ggtacagagt tcaccctcac gataagctca 720

ctccagcctg aggatttcgc aacgtactac tgcctccagc acaacaattt tccctggact 780

ttcggccagg gcaccaaggt ggagatcaag agggccgctg cccttgataa tgaaaagtca 840

aacggaacaa tcattcacgt gaagggcaag cacctctgtc cgtcaccctt gttccctggt 900

ccatccaagc cattctgggt gttggtcgta gtgggtggag tcctcgcttg ttactctctg 960

ctcgtcaccg tggcttttat aatcttctgg gttagatcca aaagaagccg cctgctccat 1020

agcgattaca tgaatatgac tccacgccgc cctggcccca caaggaaaca ctaccagcct 1080

tacgcaccac ctagagattt cgctgcctat cggagccgag tgaaattttc tagatcagct 1140

gatgctcccg cctatcagca gggacagaat caactttaca atgagctgaa cctgggtcgc 1200

agagaagagt acgacgtttt ggacaaacgc cggggccgag atcctgagat gggggggaag 1260

ccgagaagga agaatcctca agaaggcctg tacaacgagc ttcaaaaaga caaaatggct 1320

gaggcgtact ctgagatcgg catgaagggc gagcggagac gaggcaaggg tcacgatggc 1380

ttgtatcagg gcctgagtac agccacaaag gacacctatg acgccctcca catgcaggca 1440

ctgcccccac gctag 1455

<210> 245
<211> 484
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>

<223> 10E3_THD_AA

<400> 245

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

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

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

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

Gly Lys Ala Leu Glu Trp Leu Ala His Ile Phe Ser Asn Ala Glu Lys
65                  70                  75                  80

Ser Tyr Arg Thr Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr
                85                  90                  95

Ser Lys Ser Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp
            100                 105                 110

Thr Ala Thr Tyr Tyr Cys Ala Arg Ile Pro Gly Tyr Gly Gly Asn Gly
        115                 120                 125

Asp Tyr His Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val
    130                 135                 140

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145                 150                 155                 160

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

Ser Leu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile
            180                 185                 190

Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
        195                 200                 205
```

```
Arg Leu Ile Tyr Ala Ser Ser Thr Leu Gln Ser Gly Val Pro Ser Arg
    210                 215                 220

Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
225                 230                 235                 240

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Asn
                245                 250                 255

Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala
            260                 265                 270

Ala Ala Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys
        275                 280                 285

Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro
    290                 295                 300

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
305                 310                 315                 320

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
                325                 330                 335

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
            340                 345                 350

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
        355                 360                 365

Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
    370                 375                 380

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
385                 390                 395                 400

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
                405                 410                 415

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
```

420 425 430

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
435 440 445

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
450 455 460

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
465 470 475 480

Leu Pro Pro Arg

<210> 246
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> 8B5_CHD_DNA

<400> 246
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcagatcc agttggtgga atcaggggc ggtgtggtgc agccgggtag gagcctgaga 120

ctgtcatgcg tggcgtctgg cttcacattc aagaactacg gcatgcactg ggtgcgacag 180

gcccccggaa agggtttgga gtgggtcgcc gtgatctggt acgacggatc taatgagtat 240

tacggagatc ctgtgaaggg aaggttcacc atctcccgcg acaatagcaa aaatatgctc 300

tacctgcaaa tgaactcact cagggcggat gatacggcgg tctactattg cgctcgctca 360

gggattgctg tggccggcgc attcgattac tggggacagg gtaccctggt gacagtatca 420

agcggaggcg gcggctctgg cggcggcgga tctggcgggg ggggaagtga gattgtgttg 480

acacagtctc ccgataccct gtcactgtca cccggcgaga aggcaacgct gagttgcaga 540

gcaagccagt cagtctcctc ttcttttctg gcctggtatc agcaaaaacc aggtcaggca 600

ccatctctcc tgatttacgt tgccagcaga cgggcggctg gcattcccga caggttctct 660

ggaagcggat ctgggaccga ttttaccctg acaattagcc gcttggagcc cgaagacttt 720

ggtatgtttt actgccagca ctacggaagg acacctttca catttggccc gggcacgaaa 780

gtcgatataa aacgcgcagc cgccattgaa gtaatgtacc caccacctta tttggacaat 840

gaaaagtcca atggtaccat tattcacgtc aagggaaagc atctctgtcc aagccctctg 900

ttccccggcc cctccaaacc attctgggtg ctggtggtcg tcggcggagt tctggcctgc 960

tattctctgc tcgtgactgt tgcattcatc attttctggg tgagatccaa aagaagccgc 1020

ctgctccata gcgattacat gaatatgact ccacgccgcc ctggccccac aaggaaacac 1080

taccagcctt acgcaccacc tagagatttc gctgcctatc ggagccgagt gaaattttct 1140

agatcagctg atgctcccgc ctatcagcag ggacagaatc aactttacaa tgagctgaac 1200

ctgggtcgca gagaagagta cgacgttttg gacaaacgcc ggggccgaga tcctgagatg 1260

gggggggaagc cgagaaggaa gaatcctcaa gaaggcctgt acaacgagct tcaaaaagac 1320

aaaatggctg aggcgtactc tgagatcggc atgaagggcg agcggagacg aggcaagggt 1380

cacgatggct tgtatcaggg cctgagtaca gccacaaagg acacctatga cgccctccac 1440

atgcaggcac tgcccccacg ctag 1464

<210> 247
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> 8B5_CHD_AA

<400> 247
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Ile Gln Leu Val Glu Ser Gly Gly Gly Val
20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe
35 40 45

```
Thr Phe Lys Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
    50                  55                  60

Gly Leu Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr
65                  70                  75                  80

Tyr Gly Asp Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
                85                  90                  95

Lys Asn Met Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Ser Gly Ile Ala Val Ala Gly Ala Phe
        115                 120                 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu
145                 150                 155                 160

Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Lys Ala Thr
                165                 170                 175

Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Phe Leu Ala Trp
            180                 185                 190

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

Ser Arg Arg Ala Ala Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
    210                 215                 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
225                 230                 235                 240

Gly Met Phe Tyr Cys Gln His Tyr Gly Arg Thr Pro Phe Thr Phe Gly
                245                 250                 255

Pro Gly Thr Lys Val Asp Ile Lys Arg Ala Ala Ala Ile Glu Val Met
            260                 265                 270
```

```
Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile
        275                 280                 285

His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro
    290                 295                 300

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

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
                325                 330                 335

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
            340                 345                 350

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
        355                 360                 365

Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp
    370                 375                 380

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
385                 390                 395                 400

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
                405                 410                 415

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
            420                 425                 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
        435                 440                 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
    450                 455                 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465                 470                 475                 480
```

Met Gln Ala Leu Pro Pro Arg
485

<210> 248
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> 8B5_THD_DNA

<400> 248
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcagattc agctcgtgga gtcaggtggt ggcgtggttc agcccggacg gtccctgcga 120

ctctcttgtg tggcaagcgg atttaccttt aagaactatg gcatgcactg ggtgaggcag 180

gcccctggaa aaggactgga gtgggttgct gtgatctggt acgacgggtc caacgaatat 240

tatggcgatc ctgtgaaggg acggtttaca atctcacgcg ataactcaaa gaacatgctg 300

tacctgcaaa tgaactctct gcgcgctgat gacactgccg tgtattattg cgctcggagt 360

ggtatcgccg tcgcaggagc atttgattat tgggggcaag ggaccctcgt gacagtgagt 420

tccggagggg gaggttctgg tggaggcggc tctggtgggg gaggcagcga gatcgttctg 480

acccagtctc ctgacacact gtcactgtcc cctggtgaaa aggccacact gtcttgtaga 540

gcgtcccaga gcgtttccag ttccttcctt gcatggtatc aacaaaaacc cgggcaggct 600

ccaagcttgc tgatctacgt ggccagccgc cgggccgcag gcatccctga taggtttagc 660

ggttctggga gcgggacgga cttcaccttg acaatatcac ggctggaacc cgaagacttc 720

ggaatgtttt attgccagca ctacggaaga actccattca cctttggccc gggaacgaag 780

gtagacatca agagagcagc agccctcgac aacgagaaat ccaatggaac cattatccat 840

gtgaagggga aacatctctg cccttcacca ttgttccctg gacccagcaa gccttttttgg 900

gttctggtcg tggtgggggg cgtcctggct tgttactccc tcctcgttac agtcgccttc 960

ataatctttt gggttagatc caaaagaagc cgcctgctcc atagcgatta catgaatatg 1020

actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat 1080

ttcgctgcct atcggagccg agtgaaattt tctagatcag ctgatgctcc cgcctatcag 1140

cagggacaga atcaacttta caatgagctg aacctgggtc gcagagaaga gtacgacgtt 1200

ttggacaaac gccggggccg agatcctgag atgggggga agccgagaag gaagaatcct 1260

caagaaggcc tgtacaacga gcttcaaaaa gacaaaatgg ctgaggcgta ctctgagatc 1320

ggcatgaagg gcgagcggag acgaggcaag ggtcacgatg gcttgtatca gggcctgagt 1380

acagccacaa aggacaccta tgacgccctc cacatgcagg cactgccccc acgctag 1437

<210> 249
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> 8B5_THD_AA

<400> 249
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Ile Gln Leu Val Glu Ser Gly Gly Gly Val
20 25 30

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe
35 40 45

Thr Phe Lys Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Asn Glu Tyr
65 70 75 80

Tyr Gly Asp Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
85 90 95

Lys Asn Met Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Ser Gly Ile Ala Val Ala Gly Ala Phe

```
        115                 120                 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu
145                 150                 155                 160

Thr Gln Ser Pro Asp Thr Leu Ser Leu Ser Pro Gly Glu Lys Ala Thr
                165                 170                 175

Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Phe Leu Ala Trp
            180                 185                 190

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

Ser Arg Arg Ala Ala Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
    210                 215                 220

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
225                 230                 235                 240

Gly Met Phe Tyr Cys Gln His Tyr Gly Arg Thr Pro Phe Thr Phe Gly
                245                 250                 255

Pro Gly Thr Lys Val Asp Ile Lys Arg Ala Ala Ala Leu Asp Asn Glu
            260                 265                 270

Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro
        275                 280                 285

Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val
    290                 295                 300

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
305                 310                 315                 320

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
                325                 330                 335
```

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
340 345 350

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
355 360 365

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
370 375 380

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
385 390 395 400

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
405 410 415

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
420 425 430

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
435 440 445

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
450 455 460

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
465 470 475

<210> 250
<211> 9
<212> PRT
<213> Homo sapiens

<400> 250
Ile Glu Val Met Tyr Pro Pro Pro Tyr
1 5

<210> 251
<211> 112
<212> PRT
<213> Homo sapiens

<400> 251
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly

1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 252
<211> 6762
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 252
ctgacgcgcc ctgtagcggc gcattaagcg cggcgggtgt ggtggttacg cgcagcgtga 60

ccgctacact tgccagcgcc ctagcgcccg ctcctttcgc tttcttccct tcctttctcg 120

ccacgttcgc cggctttccc cgtcaagctc taaatcgggg gctcccttta gggttccgat 180

ttagtgcttt acggcacctc gaccccaaaa aacttgatta gggtgatggt tcacgtagtg 240

ggccatcgcc ctgatagacg gtttttcgcc ctttgacgtt ggagtccacg ttctttaata 300

gtggactctt gttccaaact ggaacaacac tcaaccctat ctcggtctat tcttttgatt 360

tataagggat tttgccgatt tcggcctatt ggttaaaaaa tgagctgatt taacaaaaat 420

ttaacgcgaa ttttaacaaa atattaacgc ttacaatttg ccattcgcca ttcaggctgc 480

gcaactgttg ggaagggcga tcggtgcggg cctcttcgct attacgccag ctggcgaaag 540

ggggatgtgc tgcaaggcga ttaagttggg taacgccagg gttttcccag tcacgacgtt 600

gtaaaacgac ggccagtgaa ttgtaatacg actcactata gggcgacccg gggatggcgc 660

gccagtaatc aattacgggg tcattagttc atagcccata tatggagttc cgcgttacat 720

aacttacggt aaatggcccg cctggctgac cgcccaacga cccccgccca ttgacgtcaa 780

taatgacgta tgttcccata gtaacgccaa tagggacttt ccattgacgt caatgggtgg 840

agtatttacg gtaaactgcc cacttggcag tacatcaagt gtatcatatg ccaagtacgc 900

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VH CDR2

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Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
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Gly

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Gly

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Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
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Gly

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Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
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<400> 268
Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
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Gly

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Met Asp Val

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