

SEQUENCE LISTING

<110> KITE PHARMA, INC.

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

<130> K-1031.02

<150> US 62/317,258

<151> 2016-04-01

<160> 251

<170> PatentIn version 3.5

<210> 1

<211> 220

<212> PRT

<213> Homo sapiens

<400> 1

Met Leu Arg Leu Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val
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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

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro

His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro
20 25 30

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<223> TM Domain

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ttctgggtgt tggtcgtagt gggaggagtc ctcgcttggt actctctgct cgtcaccgtg 60
gcttttataa tcttctgggt t 81

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Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
20 25

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<220>
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ggccccacaa ggaaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 120
agc 123

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<220>
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<400> 7

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 8

<211> 336

<212> DNA

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<220>

<223> CD3z Activation Domain

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agggtgaagt ttccagatc tgcagatgca ccagcgtatc agcagggcca gaaccaactg 60

tataacgagc tcaacctggg acgcagggaa gagtatgacg ttttggacaa gcgcagagga 120

cgggaccctg agatgggtgg caaaccaaga cgaaaaaacc cccaggaggg tctctataat 180

gagctgcaga aggataagat ggctgaagcc tattctgaaa taggcatgaa aggagagcgg 240

agaaggggaa aagggcacga cggttgtac cagggactca gcactgctac gaaggatact 300

tatgacgctc tccacatgca agccctgcc ctagg 336

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<211> 112

<212> PRT

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<223> CD3z Activation Domain

<400> 9

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

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<220>

<223> Signal (leader) Peptide

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atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccg

63

<210> 11

<211> 21

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<220>

<223> Signal (leader) Peptide

<400> 11

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
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His Ala Ala Arg Pro
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<211> 18

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<213> Artificial Sequence

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<223> Linker

<400> 12

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
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Lys Gly

<210> 13

<211> 7

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Gly Phe Thr Phe Ser Ser Tyr
1 5

<210> 14

<211> 6

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<213> Artificial Sequence

<220>

<223> VH CDR1

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Phe Thr Phe Ser Ser Tyr
1 5

<210> 15

<211> 7

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<213> Artificial Sequence

<220>

<223> VH CDR1

<400> 15

Gly Tyr Thr Phe Thr Ser Tyr
1 5

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<400> 16

Gly Gly Ser Ile Ser Ser Ser Ser Tyr
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<220>
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<400> 17

Gly Phe Thr Phe Ser Ser Tyr
1 5

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<211> 10
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Gly Phe Thr Phe Ser Ser Tyr Gly Met His
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<400> 19

Gly Gly Thr Phe Ser Ser Tyr

1 5

<210> 20
<211> 7
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<213> Artificial Sequence

<220>
<223> VH CDR1

<400> 20

Gly Phe Thr Phe Ser Ser Tyr
1 5

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<220>
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<400> 21

Ser Gly Ser Gly Gly Ser
1 5

<210> 22
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<220>
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<400> 22

Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 23
<211> 6
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<220>
<223> VH CDR2

<400> 23

Asn Pro Gly Gly Gly Ser
1 5

<210> 24
<211> 5
<212> PRT
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<220>
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<400> 24

Ser Tyr Ser Gly Ser
1 5

<210> 25
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<220>
<223> VH CDR2

<400> 25

Ser Ser Ser Ser Ser Thr
1 5

<210> 26
<211> 6
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<220>
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<400> 26

Ser Tyr Asp Gly Ser Asn
1 5

<210> 27
<211> 6
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<213> Artificial Sequence

<220>
<223> VH CDR2

<400> 27

Ile Pro Ile Phe Gly Thr
1 5

<210> 28
<211> 6
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<220>
<223> VH CDR2

<400> 28

Ser Tyr Asp Gly Ser Asn
1 5

<210> 29
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VH CDR3

<400> 29

Ala Glu Met Gly Ala Val Phe Asp Ile
1 5

<210> 30
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<220>
<223> VH CDR3

<400> 30

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

<210> 31
<211> 7
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<223> VH CDR3

<400> 31

Glu Ser Trp Pro Met Asp Val
1 5

<210> 32

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> VH CDR3

<400> 32

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

<210> 33

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<223> VH CDR3

<400> 33

Gly Ser Gln Glu His Leu Ile Phe Asp Tyr
1 5 10

<210> 34

<211> 13

<212> PRT

<213> Artificial Sequence

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<223> VH CDR3

<400> 34

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

<210> 35

<211> 17

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<223> VH CDR3

<400> 35

Thr Pro Glu Tyr Ser Ser Ser Ile Trp His Tyr Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> 36

<211> 14

<212> PRT

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<220>

<223> VH CDR3

<400> 36

Gly Pro Leu Gln Glu Pro Pro Tyr Asp Tyr Gly Met Asp Val
1 5 10

<210> 37

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> VL CDR1

<400> 37

Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Ala
1 5 10

<210> 38

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> VL CDR1

<400> 38

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1 5 10 15

<210> 39

<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> VL CDR1

<400> 39

Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
1 5 10

<210> 40
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<400> 40

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 41
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<212> PRT
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<220>
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<400> 41

Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Ala
1 5 10

<210> 42
<211> 11
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<220>
<223> VL CDR1

<400> 42

Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 43

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

<220>
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<400> 43

Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 44
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<212> PRT
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<400> 44

Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
1 5 10

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Asp Ala Ser Asn Arg Ala Thr
1 5

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<400> 46

Leu Gly Ser Asn Arg Ala Ser
1 5

<210> 47
<211> 7
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<400> 47

Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 48
<211> 7
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<400> 48

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 49
<211> 7
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<400> 49

Asp Ala Ser Asn Arg Ala Thr
1 5

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Gly Ala Ser Ser Leu Gln Ser
1 5

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<211> 7
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<400> 51

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 52
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<400> 52

Ser Ala Ser Thr Arg Ala Thr
1 5

<210> 53
<211> 9
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<220>
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<400> 53

Gln Gln Arg Ile Ser Trp Pro Phe Thr
1 5

<210> 54
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<400> 54

Met Gln Gly Leu Gly Leu Pro Leu Thr
1 5

<210> 55

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> VL CDR3

<400> 55

Gln Gln Tyr Ala Ala Tyr Pro Thr
1 5

<210> 56

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> VL CDR3

<400> 56

Gln Gln Arg His Val Trp Pro Pro Thr
1 5

<210> 57

<211> 9

<212> PRT

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<220>

<223> VL CDR3

<400> 57

Gln Gln Arg Phe Tyr Tyr Pro Trp Thr
1 5

<210> 58

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> VL CDR3

<400> 58

Gln Gln Ile Tyr Thr Phe Pro Phe Thr
1 5

<210> 59

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> VL CDR3

<400> 59

Gln Gln Phe Ala His Thr Pro Phe Thr
1 5

<210> 60

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> VL CDR3

<400> 60

Gln Gln His His Val Trp Pro Leu Thr
1 5

<210> 61

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> VH DNA

<400> 61

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tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggcgggtg actactgcgc aagagccgag 300

atgggagccg tattcgacat atggggtcag ggtacaatgg tcaccgtctc ctca 354

<210> 62
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> VH DNA

<400> 62
caggtgcagc tggaggagtc tgggggaggc gtggccagc ctgggaggct 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 actactgcgc cagagacggt 300
acttatctag gtggtctctg gtacttcgac ttatggggga gaggtacctt ggccaccgtc 360
tcctca 366

<210> 63
<211> 348
<212> DNA
<213> Artificial Sequence

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<223> VH DNA

<400> 63
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tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggaata atcaaccctg gtggtggtag cacaagctac 180
gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240
atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc cagagagagt 300
tggccaatgg acgtatgggg ccagggaaca actgtaccg tctcctca 348

<210> 64
<211> 366
<212> DNA
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<223> VH DNA

<400> 64
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acctgcactg tctctggtgg ctccatcagc agtagtagtt actactgggg ctggatccgc 120
cagcccccag ggaaggggct ggagtggatt gggagtatct cctatagtgg gagcacctac 180
tacaaccctg ccctcaagag tcgagtcacc atatccgtag acacgtccaa gaaccagttc 240
tcctgaagc tgagtctgt gaccgccga gacacggcgg tgtactactg cgccagaggc 300
aggggatatg caaccagctt agccttcgat atctggggtc aggggtacaat ggtcaccgtc 360
tcctca 366

<210> 65
<211> 357
<212> DNA
<213> Artificial Sequence

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<223> VH DNA

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tcctgtgcag cctctggatt caccttcagt agctatagca tgaactgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtttcaacc attagtagta gtagtagtac catatactac 180
gcagactctg tgaagggccg attcaccatc tccagagaca atgccaagaa ctactgtat 240
ctgcaaatga acagcctgag agctgaggac acggcggtgt actactgcgc cagaggttct 300
caggagcacc tgattttcga ttattgggga cagggtacat tggtcaccgt ctctca 357

<210> 66
<211> 366
<212> DNA
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<223> VH DNA

<400> 66
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ccaggcaagg ggctggagtg ggtggcagtt atatcgtatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggcgggtgt actactgcgc cagaactgac 300
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 tcctca 366

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 <223> VH DNA

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 tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120
 cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttgttac agcaaactac 180
 gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac acggcgggtgt actactgcgc cagaactcct 300
 gaatactcct ccagcatatg gcactattac tacggcatgg acgtatgggg ccagggaaca 360
 actgtcaccg tctcctca 378

<210> 68
 <211> 369
 <212> DNA
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<220>
 <223> VH DNA

<400> 68
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 tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atatcgtatg atggaagtaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgag agccgaggac acggcgggtgt actactgcgt caaggggccg 300
 ttgcaggagc cgccatacga ttatggaatg gacgtatggg gccagggaac aactgtcacc 360
 gtctcctca 369

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

<220>
<223> VL DNA

<400> 69
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ctctctcgca gggccagtca gagtgttagc aggtacttag cctggtacca acagaaacct 120
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180
aggttcagtg gcagtgggtc tgggacagac ttactctca ccatcagcag cctagagcct 240
gaagattttg cagtttatta ctgtcagcag agaattctct ggcctttcac tttggcgga 300
gggaccaagg ttgagatcaa a 321

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

<220>
<223> VL DNA

<400> 70
gatattgtga tgactcagtc tccactctcc ctgcccgtca cccttgaga gccggcctcc 60
atctctcgca ggtctagtca gagcctctg catagtaatg gatacaacta tttggattgg 120
tacctgcaga agccagggca gtctccacag ctctgatct atttgggttc taatcgggcc 180
tccgggggtc ctgacagggt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
agcagagtgg aggctgagga tgttgggggt tattactgca tgcagggact cggcctcct 300
ctcacttttg gcggagggac caaggttgag atcaaa 336

<210> 71
<211> 318
<212> DNA
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<220>
<223> VL DNA

<400> 71
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctctgca gggccagtca gagggttagc agcaacttag cctggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180
agggtcagtg gcagtgggtc tgggacagag ttactctca ccatcagcag cctgcagtct 240
gaagattttg cagttatta ctgtcagcag tacgccgct accctacttt tggcggaggg 300
accaaggttg agatcaaa 318

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<211> 321
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<400> 72
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ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180
agggtcagtg gcagtgggtc tgggacagac ttactctca ccatcagcag cctagagcct 240
gaagattttg cagttatta ctgtcagcag agacacgtct ggctctctac tttggcgga 300
gggaccaagg ttgatcaaa a 321

<210> 73
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<212> DNA
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<223> VL DNA

<400> 73
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctctgca gggccagtca gagggttagc aggtacttag cctggtacca acagaaacct 120
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180
agggtcagtg gcagtgggtc tgggacagac ttactctca ccatcagcag cctagagcct 240
gaagattttg cagttatta ctgtcagcag agattctact acccttggac tttggcgga 300
gggaccaagg ttgatcaaa a 321

<210> 74
<211> 321
<212> DNA
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<220>
<223> VL DNA

<400> 74
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atcacttgtc gggcgagtc gggattagc agctggtag cctggatca gcagaaacca 120
gggaaagccc ctaagctct gatctatgg gcatccagtt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttactctca ccatcagcag cctgcagcct 240
gaagatttg caactatta ctgtcagcag atatacacct tcccttcac tttggcgga 300
gggaccaagg ttgagatcaa a 321

<210> 75
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<212> DNA
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<220>
<223> VL DNA

<400> 75
gacatcgtga tgaccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
atcaactgca agtccagcca gagtgttta tacagctcca acaataagaa ctacttagct 120
tggtaccagc agaaaccagg acagcctcct aagctgctca ttactgggc atctaccgg 180
gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240
atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcagtt cgccacact 300
cctttcactt ttggcggagg gaccaaggtt gagatcaaa 339

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

<220>
<223> VL DNA

<400> 76
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctatagc gcatccacca gggccactgg tatcccagcc 180
aggttcagtg gcagtgggctc tgggacagag ttactctca 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> 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> 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> 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> 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> 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
 35 40 45

Ser Thr Ile 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> 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

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> 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> 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> 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> 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> 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> 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> 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> 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> 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> 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> VH CDR1

<400> 93

Gly Gly Ser Ile Ser Ser Tyr
1 5

<210> 94

<211> 9

<212> PRT

<213> Artificial Sequence

<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> VH CDR1

<400> 95

Gly Tyr Thr Leu Thr Glu Leu
1 5

<210> 96

<211> 7

<212> PRT

<213> Artificial Sequence

<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> VH CDR2

<400> 97

Tyr Tyr Ser Gly Ser
1 5

<210> 98

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> VH CDR2

<400> 98

His His Ser Gly Ser
1 5

<210> 99

<211> 6

<212> PRT

<213> Artificial Sequence

<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> VH CDR2

<400> 100

Ser Tyr Asp Gly Ser Asp
1 5

<210> 101

<211> 14

<212> PRT
<213> Artificial Sequence

<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> 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> 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> 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> 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> 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> 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> 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> VL CDR2

<400> 109

Asp Ala Ser Asn Leu Glu Thr
1 5

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

<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> VL CDR2

<400> 111

Gly Ala Ser Ser Leu Lys Ser
1 5

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

<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> 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> 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> 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> 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> VH DNA

<400> 117
caggtgcagc tgcaggaatc cggaccgggg ctggtgaagc ccagcgagac tctgagtctc 60
acgtgtacag ttctggagg tagcattagc tctactatt ggtcatggat aaggcagccc 120
cccgggaagg gattggaatg gatcggctat atttactaca gtgggagcac caattacaac 180
ccctcactga agtctagagt tacaatcagc gttgacacct caaagaatca gttcagtttg 240
aaattgtcta gcgtcacagc agctgataca gccgtctatt attgtgttc tctggtctat 300
tgcggtgggg attgttacag tggctttgac tattgggggc aggttactct ggttacagtt 360
tcttcc 366

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

<220>
<223> VH DNA

<400> 118
caggtacagc tgcaggaatc tgggcccggg ctgtcaagc caagtcagac actttctctt 60
acatgtaccg tgagcggcgg aagtataagc agtggaggct ttactggtc ttggatacgg 120
cagcaccag gcaaaggctt ggagtggatt ggatacttc atcattcagg atctacacac 180
tataatccat cccttaagtc ccgggtcacc attagcattg atacgtctaa gaatctgttc 240
agtctcaggc tgcctccgt cactgctgcc gacacagccg tgtactactg cgcctccttg 300
gtttactgcg gaggcgactg ttatagcggc ttgattatt gggggcaggg gaccctcgta 360
accgtgagct ct 372

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

<220>

<223> VH DNA

<400> 119

cagggtccaac tgggtgcagtc cggagccgaa gtcaagaaac cagggtgcctc cgftaaagtg 60

agttgcaaag tctctggata cactctgacc gagctctcta tgcactgggt ccggcaggcc 120

cccggcaagg gattggaatg gatgggcggg ttcgacctg aggacggaga gactatctac 180

gctcaaaaat tccaggacg agtgactgtg accgaagaca ctagtaccga cactgcctac 240

atggaacttt cctctctcg 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> VH DNA

<400> 120

cagggtccagt tggtcgaaag tggcgggtgt gtagtgcagc cgggccgcag ttgaggctt 60

tcctgtgcgg cttcaggctt tacttttcc agctatggaa tgcactgggt gcggcaggcc 120

cccggcaaag gacttgagtg ggtggccgtc atttctatg acggatcaga taagtactac 180

gtggacagcg tcaagggcag attcaccatc tctagggaca acagtaaaaa tagactctac 240

ctccagatga atagcctcag agctgaagac acggccgtct actattgtgc tcgggagcgg 300

tatagtggca gagactactg ggggcagggc acactcgta cagtgagtag c 351

<210> 121

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> VL DNA

<400> 121

gacatccagt tgacacagag cccgagttcc ttgtccgcct ccgtcgggga tagagtgtca 60

tttacctgtc aggctctca ggatattaat aactttctga attggtatca gcaaaagccc 120

ggaaaggcac ccaagctgtt gatttacgac gccagtaacc tggagacagg cgtgccctcc 180

cggtttagtg gtagcggaag cggtaggat ttaccttta ctatcagctc tctccaaccc 240
 gaagacattg caacctacta ttgtcaaca tatggaaacc tgccttttac atttggcggc 300
 ggcaccaagg tggagattaa gcgg 324

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

<220>
 <223> VL DNA

<400> 122
 gataccagc tcaactaaag cccctctagt ctctctgcct cagtggggga tcgggtcagt 60
 ttacttgtc aagcttcaca ggatatcaac aacttcctta attggtatca gcagaagcca 120
 ggaaaagcac ccaagctgct catctatgat gcctcaaatt tggagacggg tgttcccagt 180
 cgattctctg ggtcagggc cgggaccgac ttacgttta cgatctctc tctgcagccc 240
 gaagacatcg ccacatacta ttgtcaacag tacggcaact tgcctttcac atttgggggc 300
 gggactaagg ttgaaatcaa gagg 324

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

<220>
 <223> VL DNA

<400> 123
 gatattcaga tgactcaatc tccttctct ctgtccgctt ccgtgggcga tagagtgacc 60
 attacttga gggcgtccca gtcaatctcc agttatttga attggtatca gcagaagccc 120
 gggaaagcac ctaagctgtt gatcagcggg gcttctagcc tgaagagtgg ggtacattca 180
 cggttcagcg gaagcggaag cggaaccgat ttcacctga ctatcagcag cctgccacct 240
 gaggactttg caacttacta ctgccaacag tcatacagca ctccgatcac ttccggccag 300
 ggcacccggc tcgaaatcaa gcgc 324

<210> 124
 <211> 324
 <212> DNA

<213> Artificial Sequence

<220>

<223> VL DNA

<400> 124

gagattgtta tgaccagag tcctgcgacc ctctcagtca gccccgggga gcgcgcaact 60

ttgtcttga gagctagtca gtccgtgtcc tctcttctga catggtacca gcaaaagccc 120

gggcaggctc cgcgcccttt gatctttggg gcttcaaca gagccactgg gattcccgca 180

cgattctctg gctccgggag cggtagtggg ttaccctga cgattagcag tctccagagc 240

gaggacttcg ccgtatacta ctgccagcag tacgatacgt ggccattcac ttttgacca 300

gggactaaag tggattttaa gcgc 324

<210> 125

<211> 122

<212> PRT

<213> Artificial Sequence

<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 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> 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> 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> 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> 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> VL AA

<400> 130

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> 131
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> VL AA

<400> 131

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
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> 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> FS-21495CARDNAHxL

<400> 133
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccggagggtgc agctgttggga gtctggggga ggcttggtac agcctggggg gtcctgaga 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 catatgggggt cagggtacaa tggtcaccgt ctctcaggg 420
tctacatccg gctccgggaa gcccgaagt ggccaaggta gtacaaaggg ggaaattgtg 480
ttgacacagt ctccagccac cctgtctttg tctccagggg aaagagccac cctctcctgc 540
agggccagtc agagtgttag caggtactta gcctgtgacc aacagaaacc tggccaggct 600
cccaggctcc tcattatga tgcattcaac agggccactg gcatcccagc caggttcagt 660
ggcagtggtg ctgggacaga cttcactctc accatcagca gcctagagcc tgaagatttt 720
gcagtttatt actgtcagca gagaatctcc tggccttca cttttggcgg agggaccaag 780
gttgagatca aacgggccgc tgccttgat aatgaaaagt caaacggaac aatcattcac 840
gtgaagggca agcacctctg tccgtaccc ttgtccctg gtccatcaa gccattctgg 900
gtgttggtcg tagtgggtgg agtctctgct tgttactctc tgctcgtcac cgtggctttt 960
ataatcttct gggtagatc caaaagaagc cgctgctcc atagcgatta catgaatatg 1020
actccagcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat 1080
ttcgtgcct atcgagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag 1140

cagggccaga accaactgta taacgagctc aacctgggac gcaggaaga gtatgacgtt 1200
 ttggacaagc gcagaggacg ggaccctgag atgggtggca aaccaagacg aaaaaacccc 1260
 caggagggtc tctataatga gctgcagaag gataagatgg ctgaagccta ttctgaaata 1320
 ggcatgaaag gagagcggag aaggggaaaa gggcacgacg gttgtacca gggactcagc 1380
 actgctacga aggataactta tgacgtctc cacatgcaag ccctgccacc taggtaa 1437

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

<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
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> FS-21495CARDNALxH

<400> 135
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccggaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc 120
accctctctt gcagggccag tcagagtgtt agcaggtact tagcctggta ccaacagaaa 180
cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatcca 240
gccaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagcctagag 300
cctgaagatt ttgcagtta ttactgtcag cagagaatct cctggccttt cacttttggc 360
ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420

ggccaaggta gtacaaaggg ggaggtgcag ctgttgagct ctgggggagg cttggtacag 480
 cctgggggggt ccctgagact ctctgtgca gcctctggat tcacctttag cagctatgcc 540
 atgagctggg tccgccaggc tccagggaag gggctggagt gggcttcagc tattagtgtt 600
 agtgggtgta gcacatacta cgcagactcc gtgaagggcc gggtcaccat ctccagagac 660
 aattccaaga acacgtgtga tctgcaaata aacagcctga gagccgagga cacggcggtg 720
 tactactgcg caagagccga gatgggagcc gtattcgaca tatggggtca ggttacaatg 780
 gtcaccgtct cctcagccgc tgccttgat aatgaaaagt caaacggaac aatcattcac 840
 gtgaagggca agcacctctg tccgtcacc ttgtccctg gtccatcaa gccattctgg 900
 gtgttggtcg tagtgggtgg agtctctgct tgttactctc tgctcgtcac cgtggctttt 960
 ataattctct gggtagatc caaaagaagc cgctgctcc atagcgatta catgaatatg 1020
 actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagatat 1080
 ttcgctgctc atcggagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag 1140
 cagggccaga accaactgta taacagctc aacctgggac gcagggaaga gtatgacgtt 1200
 ttggacaagc gcagaggacg ggaccctgag atgggtggca aaccaagacg aaaaaacccc 1260
 caggagggtc tctataatga gctgcagaag gataagatgg ctgaagccta ttctgaaata 1320
 ggcatgaaag gagagcggag aaggggaaaa gggcacgacg gttgtacca gggactcagc 1380
 actgctacga aggatactta tgacgtctc cacatgcaag ccctgccacc taggtaa 1437

<210> 136

<211> 478

<212> PRT

<213> Artificial Sequence

<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

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 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

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

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> PC-21497CARDNAHxL

<400> 137
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccgcagggtgc agctgggtgga gtctggggga ggctgtgtcc agcctgggag gtcctgaga 120
ctctcctgtg cagcgtctgg attcaccttc agtagctatg gcatgcactg ggtccgccag 180
gctccaggca aggggctgga gtgggtggca gttatatcgt atgatggaag taataaatac 240
tatgcagact ccgtgaaggc ccgattcacc atctccagag acaattcaa gaacacgtg 300
tatctgcaaa tgaacagcct gagagccgag gacacggcgg tgtactactg cgccagagac 360
ggctactatc tagtggtct ctggtacttc gacttatggg ggagaggtac cttggtcacc 420
gtctctcag ggtctacatc cggctccggg aagcccggaa gtggcgaagg tagtaciaag 480
ggggatattg tgatgactca gtctccactc tcctgcccgc tcaccctgg agagccggcc 540
tccatctcct gcaggcttag tcagagcctc ctgcatagta atggatacaa ctatttgat 600
tggtacctgc agaagccagg gcagctcca cagctcctga tctatttggg ttctaactcg 660
gcctccgggg tcctgacag gttcagtggc agtgatcag gcacagattt tactgaaa 720
atcagcagag tggaggctga ggatgttggg gtttattact gcatgcaggg actcggcctc 780
cctctcactt ttggcggagg gaccaaggtt gagatcaaac gggccgctgc ccttgataat 840
gaaaagtcaa acggaacaat cattcacgtg aagggaagc acctctgtcc gtcaccctg 900
ttcctggtc catcaagcc attctgggtg ttggtcgtag tgggtggagt cctcgcttgt 960
tactctctgc tcgtaccgt ggctttata atctctggg ttagatcaa aagaagccgc 1020
ctgtccata gcgattacat gaatatgact ccacgccgcc ctggcccccac aaggaaacac 1080
taccagcctt acgcaccacc tagagatttc gctgcctatc ggagcagggt gaagttttcc 1140
agatctgcag atgcaccagc gtatcagcag ggccagaacc aactgtataa cgagctcaac 1200
ctgggacgca gggaagagta tgacgtttg gacaagcgca gaggacggga ccctgagatg 1260
gggtggcaaac caagacgaaa aaacccccag gaggtctct ataatgagct gcagaaggat 1320
aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1380

cacgacgggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1440

atgcaagccc tgccacctag gtaa 1464

<210> 138

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<223> PC-21497CARHxL

<400> 138

Met Ala Leu Pro Val Thr Ala 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

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> 139
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<223> PC-21497CARDNALxH

<400> 139
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ccggatattg tgatgactca gtctccactc tcctgcccgc tcacccttgg agagccggcc 120
tccatctcct gcaggtctag tcagagcctc ctgcatagta atggatacaa ctatttgat 180
tggtacctgc agaagccagg gcagtctcca cagctcctga tctatttggg ttctaactcg 240
gcctccgggg tcctgacag gttcagtggc agtggatcag gcacagattt tacactgaaa 300
atcagcagag tggaggctga ggatgttggg gtttattact gcatgcaggg actcggcctc 360
cctctcactt ttggcggagg gaccaaggtt gagatcaaac ggggggtctac atccggctcc 420
gggaagcccc 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 gacgggtactt atctaggtgg tctctgttac 780
 ttcgacttat gggggagagg taccttggtc accgtctcct cagccgctgc ccttgataat 840
 gaaaagtcaa acggaacaat cattcacgtg aagggaagc acctctgtcc gtcacccttg 900
 ttccctggtc catccaagcc attctgggtg ttggtcgtag tgggtggagt cctcgttgt 960
 tactctctgc tcgtaccgt ggcttttata atcttctggg ttgatccaa 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 gaggtctct ataatgagct gcagaaggat 1320
 aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1380
 cagcaggggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1440
 atgcaagccc tgccacctag gtaa 1464

<210> 140

<211> 487

<212> PRT

<213> Artificial Sequence

<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

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

<220>
 <223> AJ-21508CARDNAHxL

<400> 141
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 gtttctctgca aggcattctgg atacaccttc accagctact atatgcactg ggtgcgacag 180
 gcccttgac aagggcttga gtggatggga ataataacc ctggtggtgg tagcacaagc 240
 tacgcacaga agttccaggg cagagtcacc atgaccaggg acacgtccac gagcacagtc 300
 tacatggagc tgagcagcct gagatctgag gacacggcgg tgtactactg cgccagagag 360
 agttggccaa tggacgtatg gggccaggga acaactgtca ccgtctctc agggctctaca 420
 tccggctccg ggaagcccgg aagtggcgaa ggtagtaca aggggggaaat agtgatgacg 480
 cagtctccag ccacctgtc tgtgtctcca ggggaaagag ccacctctc ctgcagggcc 540
 agtcagagtg ttagcagcaa cttagcctgg taccagcaga aacctggcca ggctcccagg 600
 ctctcatct atggtgcatc caccagggcc actggtatcc cagccaggtt cagtggcagt 660
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 cgccctggcc ccacaaggaa aactaccag ccttacgcac cacctagaga tttcgtgcc 1080
 tatcggagca gggtaagt ttccagatct gcagatgcac cagcgtatca gcagggccag 1140
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ggagagcggga gaaggggaaa agggcacgac ggttgtacc agggactcag cactgctacg 1380

aaggatactt atgacgtctt ccacatgcaa gccctgccac ctaggtaa 1428

<210> 142

<211> 475

<212> PRT

<213> Artificial Sequence

<220>

<223> AJ-21508CARHxL

<400> 142

Met Ala Leu Pro Val Thr Ala 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> AJ-21508CARDNALxH

<400> 143

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accctctcct gcagggccag tcagagtgtt agcagcaact tagcctggta ccagcagaaa 180

cctggccagg ctcccaggct cctcatctat ggtgcatcca ccagggccac tggatccca 240

gccaggttca gtggcagtgg gtctgggaca gagttcactc tcaccatcag cagcctgcag 300

tctgaagatt ttgcagttta ttactgtcag cagtacgccg cctaccctac tttggcgga 360

gggaccaagg ttgagatcaa acgggggtct acatccggct ccgggaagcc cggaagtggc 420

gaaggtagta caaaggggca ggtgcagctg gtgcagtctg gggctgaggt gaagaagcct 480

ggggcctcag tgaaggttcc ctgaaggca tctggataca cttcaccag ctactatatg 540

cactgggtgc gacaggcccc tggacaaggg cttgagtgga tgggaataat caaccctgt 600

ggtgtagca caagctacgc acagaagttc cagggcagag tcacatgac caggacacg 660
 tccacgagca cagtctacat ggagctgagc agcctgagat ctgaggacac ggcggtgtac 720
 tactgcgcca gagagagttg gccaatggac gtatggggcc agggaacaac tgtcacccgc 780
 tcctcagccg ctgcccttga taatgaaaag tcaaacggaa caatcattca cgtgaagggc 840
 aagcacctct gtccgtcacc ctgttccct ggtecatcca agccattctg ggtgttggtc 900
 gtagtgggtg gagtctcgc ttgttactct ctgctcgtca ccgtggcttt tataatcttc 960
 tgggttagat ccaaaagaag ccgctgctc catagcgatt acatgaatat gactccacgc 1020
 cgccctggcc ccacaaggaa aactaccag ccttacgcac cacctagaga ttctgctgcc 1080
 tatcggagca gggatgaagt ttccagatct gcagatgcac cagcgtatca gcagggccag 1140
 aaccaactgt ataacgagct caacctggga cgcagggaag agtatgacgt ttggacaag 1200
 cgcagaggac gggaccctga gatgggtggc aaaccaagac gaaaaaaccc ccaggagggt 1260
 ctctataatg agctgcagaa ggataagatg gctgaagcct attctgaaat aggcataaaa 1320
 ggagagcgga gaaggggaaa agggcacgac ggtttgtacc agggactcag cactgctacg 1380
 aagatactt atgacgtct ccacatgcaa gcctgccac ctaggtaa 1428

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

<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

<210> 145

<211> 1449

<212> DNA

<213> Artificial Sequence

<220>

<223> NM-21517CARDNAHxL

<400> 145

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ctcacctgca ctgtctctgg tggctccatc agcagtagta gttactactg gggctggatc    180
cgccagcccc caggaagg gctggagtgg attgggagta tctcctatag tgggagcacc    240
tactacaacc cgtccctcaa gactcgagtc accatatccg tagacacgtc caagaaccag    300
ttctccctga agctgagttc tgtgaccgcc gcagacacgg cggtgtacta ctgcgccaga    360
ggcaggggat atgcaaccag cttagccttc gatatctggg gtcagggtac aatggtcacc    420
gtctctcag ggtctacatc cggctccggg aagcccggaa gtggcgaagg tagtacaag    480
ggggaaattg tgtgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc    540
accctctct gcagggccag tcagagtgtt agcagctact tagcctggtta ccaacagaaa    600
cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatcca    660
gccaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagcctagag    720
cctgaagatt ttgcagttta ttactgtcag cagagacacg tctggcctcc tacttttggc    780
ggagggacca aggttagat caaacgggcc gctgcccttg ataataaaaa gtcaaacgga    840
acaatcattc acgtgaaggg caagcacctc tgtccgtcac cttgttccc tggccatcc    900
aagccattct ggggtgttgt cgtagtgggt ggagtctctg cttgttactc tctgctcgtc    960
accgtggctt ttataatctt ctgggttaga tccaaaagaa gccgcctgct ccatagcgat   1020
tacatgaata tgactccacg ccgccttggc cccacaagga aacactacca gccttacgca   1080
ccacctagag atttcgtgc ctatcggagc aggtgaagt ttccagatc tgcagatgca   1140
ccagcgtatc agcagggcca gaaccaactg tataacgagc tcaacctggg acgcagggaa   1200
gagtatgacg ttttgacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga   1260
cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc   1320
tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggttgtac   1380
cagggactca gcactgctac gaaggatact tatgacgctc tccacatgca agccctgcca   1440
cctaggtaa                                     1449
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<210> 146

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

<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

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

<220>
<223> NM-21517CARDNALxH

<400> 147
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accctctcct gcagggccag tcagagtgtt agcagctact tagcctggta ccaacagaaa 180
cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatcca 240
gccaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagcctagag 300
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ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420
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ccttcggaga ccctgtccct cacctgcact gtctctggtg gctccatcag cagtagtagt 540
tactactggg gctggatccg ccagccccc ggggaaggggc tggagtggat tgggagtatc 600
tcctatagtg ggagcaccta ctacaaccg tcctcaaga gtcgagtcac catatccgta 660
gacacgtcca agaaccagtt ctccctgaag ctgagttctg tgaccgccgc agacacggcg 720

gtgtactact gcgccagagg caggggatat gcaaccagct tagccttcga tatctggggt 780
 caggggtacaa tggtcaccgt ctctcagcc gctgcccttg ataataaaaa gtcaaacgga 840
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 cctaggtaa 1449

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

<220>
 <223> NM-21517CARLxH

<400> 148

Met Ala Leu Pro Val Thr Ala 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

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> TS-21522CARDNAHxL

<400> 149

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gctccaggga aggggctgga gtgggttca accattagta gtagtagtag taccatatac    240
tacgcagact ctgtgaaggc ccgattcacc atctccagag acaatgcaa gaactcactg    300
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gtgttgacac agtctccagc caccctgtct ttgtctccag gggaaagagc caccctctcc    540
tgcagggccca gtcagagtgt tagcaggtag ttagcctggg accaacagaa acctggccag    600
gctcccaggc tctcatcta tgatgcatcc aacagggccca ctggcatccc agccagggtc    660
agtggcagtg ggtctgggac agacttact ctacatca gcagcctaga gcctgaagat    720
tttcagttt attactgtca gcagagattc tactaccctt ggacttttgg cggagggacc    780
aaggttgaga tcaaacgggc cgctgccctt gataatgaaa agtcaaacgg aacaatcatt    840
cacgtgaagg gcaagcacct ctgtccgtca cccttgttcc ctggtccatc caagccattc    900
tgggtgttgg tcgtagtggg tggagtctc gcttgttact ctctgctcgt caccgtggct    960
tttataatct tctgggftag atccaaaaga agccgcctgc tccatagcga ttacatgaat   1020
atgactccac gccgccttgg ccccaagg aaacactacc agccttacgc accacctaga   1080
gatttcgtg cctatcggag cagggtgaag tttccagat ctgcagatgc accagcgtat   1140
cagcagggcc agaaccaact gtataacgag ctcaacctgg gacgcaggga agagtatgac   1200
gttttgaca agcgagagg acgggacct gagatgggtg gcaaaccaag acgaaaaaac   1260
ccccaggagg gtctctataa tgagctgcag aaggataaga tggctgaagc ctattctgaa   1320
ataggcatga aaggagagcg gagaagggga aaagggcacg acggtttgta ccagggactc   1380
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<210> 150
<211> 479
<212> PRT
<213> Artificial Sequence

<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

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> 151

<211> 1440

<212> DNA

<213> Artificial Sequence

<220>

<223> TS-21522CARDNALxH

<400> 151

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accctctct gcagggccag tcagagtgtt agcaggtact tagcctggta ccaacagaaa 180

cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatcca 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

cctggggggg cctgagact ctctgtgca gcctctggat tcaccttcag tagctatagc 540

atgaactggg tccgccaggc tccagggaag gggctggagt gggtttcaac cattagtagt 600

agtagtagta ccatatacta cgcagactct gtgaagggcc gattcacat ctccagagac 660

aatccaaga actcactgta tctgcaaatg aacagcctga gagctgagga cacggcgggtg 720

tactactgcg ccagaggttc tcaggagcac ctgattttcg attattgggg acaggttaca 780

ttggtcaccg tctcctcagc cgctgccctt gataatgaaa agtcaaacgg aacaatcatt 840
 cagtggaagg gcaagcacct ctgtccgtca cccttgttcc ctggtccatc caagccattc 900
 tgggtgttgg tcgtagtggg tggagtctc gcttgttact ctctgctcgt caccgtggct 960
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 atgactccac gccgccttgg ccccaacaagg aaactactacc agccttacgc accacctaga 1080
 gatttcgtg cctatcggag caggggtgaag tttccagat ctgcagatgc accagcgtat 1140
 cagcagggcc agaaccaact gtataacgag ctcaacctgg gacgcaggga agagtatgac 1200
 gttttggaca agcgcagagg acgggaccct gagatgggtg gcaaaccaag acgaaaaaac 1260
 cccagaggag 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> 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> RY-21527CARDNAHxL

<400> 153

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ctctctgtg 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
 gtctctcag ggtctacatc cggtccggg aagcccggaa gtggcgaagg tagtaciaaag 480
 ggggacatcc agttgaccca gtctccatct tccgtgtctg catctgtagg agacagagtc 540
 accatcactt gtcgggcgag tcagggtatt agcagctggg tagcctggta tcagcagaaa 600
 ccagggaag ccctaagct cctgatctat ggtgcatcca gttgcaaag tggggtcca 660
 tcaaggtca gcggcagtgg atctgggaca gatttactc tcaccatcag cagcctgcag 720
 cctgaagatt ttgcaactta ttactgtcag cagatataca ccttcccttt cacttttggc 780
 ggagggacca aggttgagat caaacgggcc gctgcccttg ataataaaaa gtcaaacgga 840
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 aagccattct ggggtgttgt cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc 960
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 tacatgaata tgactccacg ccgccctggc cccacaagga aacactacca gccttacgca 1080
 ccacctagag atttcgtgc ctatcggagc aggggtgaagt ttccagatc tgcagatgca 1140
 ccagcgtatc agcagggccca gaaccaactg tataacgagc tcaacctggg acgcaggga 1200
 gagtatgacg ttttgacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga 1260
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 tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggttgtac 1380
 cagggactca gactgctac gaaggatact tatgacgctc tccacatgca agccctgcca 1440
 cctaggtaa 1449

<210> 154

<211> 482

<212> PRT

<213> Artificial Sequence

<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> RY-21527CARDNALxH

<400> 155
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accatcactt gtcgggcgag tcagggtatt agcagctggg tagcctggta tcagcagaaa 180
ccagggaag ccctaagct cctgatctat ggtgcatcca gtttgcaaag tggggtccca 240
tcaaggtca gcggcagtgg atctgggaca gatttactc tcaccatcag cagcctgcag 300
cctgaagatt ttgcaactta ttactgtcag cagatataca ccttccttt cacttttggc 360
ggagggacca aggttgagat caaacggggg tctacatccg gctccgggaa gcccggaagt 420
ggcgaaggta gtacaaagg gcaggtgcag ctggtggagt ctgggggagg cgtggtccag 480
cctgggagggt ccctgagact ctctgtgca gcgtctggat tcaccttcag tagctatggc 540
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gatggaagta ataaatacta tgcagactcc gtgaagggcc gattcaccat ctccagagac 660
aattccaaga acacgtgta tctgcaaagt aacagcctga gagccgagga cacggcggtg 720
tactactgcg ccagaactga cttctggagc ggatccctc caggcttaga ttactgggga 780
cagggtacat tggtcaccgt ctctcagcc gctgccctg ataataaaaa gtcaaacgga 840
acaatcattc acgtgaaggg caagcacctc tgtccgtcac cctgttccc tggatcatcc 900

aagccattct ggggtgttggc cgtagtgggt ggagtcctcg cttgttactc tctgctcgtc 960
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tacatgaata tgactccacg ccgcctggc cccacaagga aacactacca gccttacgca 1080
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gagtatgacg ttttgacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga 1260
cgaaaaaacc cccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc 1320
tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggttgtac 1380
cagggactca gcactgctac gaaggatact tatgacgctc tccacatgca agccctgcca 1440
cctaggtaa 1449

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

<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> PP-21528CARDNAHxL

<400> 157

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 gtctcctgca aggcttctgg aggcaccttc agcagctatg ctatcagctg ggtgcgacag 180
 gcccttgac aagggttga gtggatggga gggatcatcc ctatcttgg tacagcaaac 240
 tacgcacaga agttccaggg cagagtcacg attaccgcgg acgaatccac gagcacagcc 300
 tacatggagc tgagcagcct gagatctgag gacacggcgg tgtactactg cgccagaact 360
 cctgaatact cctccagcat atggcactat tactacggca tggacgtatg gggccaggga 420
 acaactgtca ccgtctctc aggggtctaca tccggctccg ggaagcccgg aagtggcgaa 480
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 ggcgagaggg ccaccatcaa ctgcaagtc agccagagtg tttatacag ctccaacaat 600
 aagaactact tagcttggtg ccagcagaaa ccaggacagc ctctaagct gctcatttac 660
 tgggcatcta cccgggaatc cggggtcctt gaccgattca gtggcagcgg gtctgggaca 720
 gatttactc tcaccatcag cagcctgcag gctgaagatg tggcagttta ttactgtcag 780
 cagttcgccc acactcctt cacttttggc ggagggacca aggttgagat caaacgggcc 840
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 tgtccgtcac cttgttccc tgggtccatcc aagccattct ggggtgttgg ctagtgggt 960
 ggagtcctcg ctgttactc tctgctcgtc accgtggctt ttataatctt ctgggttaga 1020
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 aggggtgaagt ttccagatc tgcatatgca ccagcgtatc agcagggccca gaaccaactg 1200
 tataacgagc tcaacctggg acgcaggga gagtatgacg ttttgacaa gcgcagagga 1260
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 gagctgcaga aggataagat ggctgaagcc tattctgaaa taggcatgaa aggagagcgg 1380
 agaaggggaa aagggcacga cgtttgtac cagggactca gcactgctac gaaggatact 1440
 tatgacgctc tccacatgca agccctgcc ctaggtaa 1479

<210> 158

<211> 492

<212> PRT

<213> Artificial Sequence

<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> PP-21528CARDNALxH

<400> 159

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accatcaact gcaagtccag ccagagtgtt ttatacagct ccaacaataa gaactactta 180
gcttgggtacc agcagaaacc aggacagcct cctaagctgc tcatttactg ggcatctacc 240
cgggaaatccg gggtcctga ccgattcagt ggcagcgggt ctgggacaga ttctactctc 300
accatcagca gcctgcaggc tgaagatgtg gcagtttatt actgtcagca gttcgccac 360
actcctttca ctttggcgg 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 tcacccctat ctttgggtaca gcaaactacg cacagaagtt ccagggcaga 660
gtcacgatta ccgcggacga atccacgagc acagcctaca tggagctgag cagcctgaga 720
tctgaggaca cggcgggtga ctactgcgcc agaactctg aatactctc cagcatatgg 780

cactattact acggcatgga cgtatggggc caggaacaa ctgtaccgt ctctcagcc 840
 gctgcccttg ataatgaaaa gtcaaacgga acaatcattc acgtgaaggg caagcacctc 900
 tgtccgtcac cctgttccc tggtcaccc aagccattct ggggtgtggg cgtagtgggt 960
 ggagtcctcg cttgttactc tctgctcgtc accgtggctt ttataatctt ctgggttaga 1020
 tccaaaagaa gccgcctgct ccatagcgat tacatgaata tgactccacg ccgccttggc 1080
 cccacaagga aacactacca gccttacgca ccacctagag atttcgctgc ctatcggagc 1140
 aggggtgaagt ttccagatc tgcagatgca ccagcgtatc agcagggcca gaaccaactg 1200
 tataacgagc tcaacctggg acgcagggaa gagtatgacg ttttgacaa gcgcagagga 1260
 cgggaccctg agatgggtgg caaaccaaga cgaaaaaacc cccaggaggg tctctataat 1320
 gagctgcaga aggataagat ggctgaagcc tattctgaaa taggcatgaa aggagagcgg 1380
 agaaggggaa aagggcacga cggttgtac cagggactca gcactgctac gaaggatact 1440
 tatgacgctc tccacatgca agccctgcc ctaggtaa 1479

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

<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 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> RD-21530CARDNAHxL

<400> 161

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ctctcctgtg cagcgtctgg attcaccttc agtagctatg gcatgcactg ggtccgccag    180
gctccaggca aggggctgga gtgggtggca gttatatcgt atgatggaag taataaatac    240
tatgcagact ccgtaaggga ccgattcacc atctccagag acaattcaa gaacacgctg    300
tatctgcaaa tgaacagcct gagagccgag gacacggcgg tgtactactg cgtcaagggg    360
ccgttgagg agccgccata cgattatgga atggacgtat ggggccaggg aacaactgtc    420
accgtctcct cagggtctac atccggctcc gggaagcccga gaagtggcga aggtagtaca    480
aagggggaaa tagtgatgac gcagtctcca gccaccctgt ctgtgtctcc aggggaaaga    540
gccaccctct cctgcagggc cagtcaaggt gttagcagca acttagcctg gtaccagcag    600
aaacctggcc aggtcccgag gctcctcatc tatagcgcat ccaccagggc cactggtatc    660
ccagccaggt tcagtggcag tgggtctggg acagagtcca ctctcccat cagcagcctg    720
cagtctgaag attttgagt ttattactgt cagcagcacc acgtctggcc tctcactttt    780
ggcggaggga ccaaggttga gatcaaacgg gccgctgccc ttgataatga aaagtcaaac    840
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tccaagccat tctgggtgtt ggtcgtagtg ggtggagtcc tcgcttgta ctctctgctc    960
gtcaccgtgg cttttataat ctctgggtt agatccaaaa gaagccgct gtcctatagc    1020
gattacatga atatgactcc acgccgcctt ggccccacaa ggaaacacta ccagccttac    1080
gcaccaccta gagatttcgc tgcctatcgg agcagggtga agtttccag atctgcagat    1140
gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg    1200
gaagagtatg acgttttga caagcgaga ggacgggacc ctgagatggg tggcaaacca    1260
agacgaaaaa acccccagga gggctctat aatgagctgc agaaggataa gatggctgaa    1320
gcctattctg aaataggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg    1380
taccagggac tcagactgc tacgaaggat acttatgacg ctctccat gcaagccctg    1440
ccacctaggt aa
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1452

<210> 162

<211> 483
<212> PRT
<213> Artificial Sequence

<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

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> RD-21530CARDNALxH

<400> 163
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ccggaaatag tgatgacgca gtctccagcc accctgtctg tgtctccagg ggaaagagcc 120
accctctcct gcagggccag tcagagtgtt agcagcaact tagcctggta ccagcagaaa 180
cctggccagg ctcccaggct cctcatctat agcgcattcca ccagggccac tggatatcca 240
gccagggtca 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 ctctgtgtga gcgtctggat tcaccttcag tagctatggc 540
atgcactggg tccgccaggc tccaggcaag gggctggagt ggggtggcagt tatatcgtat 600
gatggaagta ataaatacta tgcagactcc gtgaagggcc gattcacat ctccagagac 660
aattccaaga acacgtgtga tctgcaaattg aacagcctga gagccgagga cacggcggtg 720

tactactgcg tcaaggggcc gttgcaggag ccgccatacg attatggaat ggacgtatgg 780
ggccaggggaa caactgtcac cgtctcctca gccgctgccc ttgataatga aaagtcaaac 840
ggaacaatca ttcacgtgaa gggcaagcac ctctgtccgt cacccttggt ccctgggtcca 900
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gattacatga atatgactcc acgccgcctt ggccccacaa ggaaacacta ccagccttac 1080
gcaccaccta gagatttcgc tgcctatcgg agcagggtga agttttccag atctgcagat 1140
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gaagagtatg acgttttga caagcgaga ggacgggacc ctgagatggg tggcaaacca 1260
agacgaaaaa acccccagga gggctcttat aatgagctgc agaaggataa gatggctgaa 1320
gcctattctg aaatagcat gaaaggagag cggagaaggg gaaaagggca cgacggttg 1380
taccagggac tcagactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440
ccacctaggt aa 1452

<210> 164
<211> 483
<212> PRT
<213> Artificial Sequence

<220>
<223> RD-21530CARLxH

<400> 164

Met Ala Leu Pro Val Thr Ala 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

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

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> anti-CLL-1 CAR construct

<400> 165

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ccgcaggtcc aactgcaaga aagcggaccc ggactgggtga agccttctga gacacttagt   120
ctgacgtgca cggtcagtgg cggtccatc tcctcctatt attggtcatg gatacgacaa   180
ccccaggta agggcctgga atggattggc tatacttact attcaggaag cacgaactac   240
aatcccagcc tgaagtcccg agtgacaatt tcagtagata ccagtaaaaa ccagttcagt   300
cttaaactgt caagcgtgac agtgccgac accgctgtgt attactgctg ctactgggtg   360
tattgtggag gggattgtta tagcgggttc gattattggg gacagggaa cctggtgact   420
gtatcttccg gcggcggcgg ctcagggggg ggcggtagtg gcggtggggg ttccgatatt   480
caactgacac aatccccag ctactcagc gccagcgtgg gggacagggt tagctttacc   540
tgtcaagcct ctaggatat aaataacttt ctgaactggt atcaacagaa gcctgggaag   600
gcgcccaaac tcctgatcta tgatgcgtcc aacctggaaa ctggcgtgcc ttcacgttt   660
agcggctctg gcagtggtag agacttact ttaccatct cttacttca gccggaggac   720
atgccacat attactgtca acagtacga aactgccct ttacttttg aggcggcacc   780
aaagttgaaa taaaagggc 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 cccacaagg aaactactacc agccttacgc accactaga  1080
gatttcgtg cctatcggag cagggtgaag tttccagat ctgcagatgc accagcgtat  1140
cagcagggcc agaaccaact gtataacgag ctcaacctgg gacgcaggga agagtatgac  1200
gttttgaca agcgagagg acgggacct gagatgggtg gcaaaccaag acgaaaaaac  1260
ccccaggagg gtctctataa tgagctgcag aaggataaga tggctgaagc ctattctgaa  1320
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<210> 166
<211> 479
<212> PRT
<213> Artificial Sequence

<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
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

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> anti-CLL-1 CAR construct

<400> 167

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acgtgcacgg tcagtggcgg ctccatctcc tcctattatt ggtcatggat acgacaaccc 120

ccaggttaagg gcctggaatg gattggctat atctactatt caggaagcac gaactacaat 180

cccagcctga agtcccagat gacaattca gtagatacca gtaaaaacca gttcagtctt 240

aaactgtcaa gcgtgacagc tgccgacacc gctgtgtatt actgcgtctc actggtgtat 300

tgtggagggg attgttatag cgggttcgat tattggggac agggaaccct ggtgactgta 360

tcttccggcg gcggcggctc aggggggtggc ggtagtggcg gtgggggttc cgatattcaa 420

ctgacacaat cccccagctc actcagcgcc agcgtggggg acagggttag ctttacctgt 480

caagcctctc aggatataaa taactttctg aactgggtatc aacagaagcc tgggaaggcg 540

cccaaactcc tgatctatga tgcgtccaac ctggaaactg gcgtgccttc acgctttagc 600

ggctctggca gtggtacaga cttcactttt accatctctt cacttcagcc ggaggacatc 660

gccacatatt actgtcaaca gtacggaaac ttgcccttta ctttggagg cggcaccaaa 720

gttgaaatca aaagggccgc tgcctggat aacgaaaaga gcaatgggac tataatacat 780

gttaaaggaa aacacctgtg tccatctccc ctgttcctg gaccgtcaaa gccattttgg 840
 gtgctcgtgg ttgtcggtag cgttctcgcc tggtatagct tgctggtagc agtagccttc 900
 attatctttt gggtagagatc caaaagaagc cgcctgctcc atagcgatta catgaatatg 960
 actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat 1020
 ttgctgcct atcgagagcag 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 gttgtacca gggactcagc 1320
 actgctacga aggataacta tgacgctctc cacatgcaag ccctgccacc tagg 1374

<210> 168
 <211> 458
 <212> PRT
 <213> Artificial Sequence

<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 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

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> anti-CLL-1 CAR construct

<400> 169

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctgcagga atccggaccg gggctgggtga agcccagcga gactctgagt 120

ctcacgtgta cagtttctgg aggtagcatt agctcctact attggtcatg gataaggcag 180

ccccccggga agggattgga atggatcggc tatatttact acagtgggag caccaattac 240

aaccctcac tgaagtctag agttacaatc agcgttgaca cctcaaagaa tcagttcagt 300

ttgaaattgt ctacggtcac agcagctgat acagccgtct attattgtgt ttctctggtc 360
 tattgcgggtg gggattgtta cagtggcttt gactattggg ggcaggggtac tctggttaca 420
 gtttcttccg gggggggagg ctctgggggc ggaggctcag gtggtggagg cagcgacatc 480
 cagttgacac agagcccgag ttcttgtcc gcctccgtcg gggatagagt gtcatttacc 540
 tgtcaggcct ctcaggatat taataacttt ctgaattggt atcagcaaaa gcccggaag 600
 gcaccaagc tgttgattta cgacgccagt aacctggaga caggcgtgcc ctcccggttt 660
 agtggtagcg gaagcggtag ggattttacc ttactatca 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 gttcttgggc tcgtgggagg cgtgcttgct 960
 tgttattctc tgctcggtac cgtggcggtt atcatttttt gggtagatc caaaagaagc 1020
 cgctgctcc atagcgatta catgaatatg actccacgcc gccctggccc cacaaggaaa 1080
 cactaccagc cttacgcacc acctagagat ttctgtcct 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 gttgtacca gggactcagc actgctacga aggatactta tgacgtctc 1440
 cacatgcaag ccctgccacc taggtaa 1467

<210> 170

<211> 488

<212> PRT

<213> Artificial Sequence

<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
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser 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

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> anti-CLL-1 CAR construct

<400> 171
caggtgcagc tgcaggaatc cggaccgggg ctggtgaagc ccagcgagac tctgagtctc 60
acgtgtacag ttcttgagg tagcattagc tcctactatt ggtcatggat aaggcagccc 120
cccgggaagg gattggaatg gatcggctat atttactaca gtgggagcac caattacaac 180
ccctcactga agtctagagt tacaatcagc gttgacacct caaagaatca gttcagtttg 240
aaattgtcta gcgtcacagc agctgataca gccgtctatt attgtgttc tctggtctat 300
tgcggtgggg attgttacag tggcttgac tattgggggc aggttactct ggttacagtt 360
tcttcgggg ggggaggctc tgggggcgga ggctcagggt gtggaggcag cgacatccag 420
ttgacacaga gcccaggttc cttgtccgcc tccgtcgggg atagagtgtc atttacctgt 480
caggcctctc aggatattaa taactttctg aattggatc agcaaaagcc cggaaggca 540
cccaagctgt tgattacga cgccagtaac ctggagacag gcgtgccctc ccggttagt 600
ggtagcggaa gcggtacgga ttttacctt actatcagct ctctccaacc cgaagacatt 660
gcaacctact attgtcaaca atatggaaac ctgccttta 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 atttttggg ttagatccaa aagaagccgc 960
ctgctccata gcgattacat gaatatgact ccacgccgcc ctggcccccac 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 gaggggtctct ataatgagct gcagaaggat 1260
 aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1320
 cacgacgggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1380
 atgcaagccc tgccacctag g 1401

<210> 172
 <211> 467
 <212> PRT
 <213> Artificial Sequence

 <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 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 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> anti-CLL-1 CAR construct

<400> 173
atggcactcc ccgtaactgc tctgtgctg ccgttgcat tgctcctgca cgccgcacgc 60
ccgcaggtgc aattgcaaga gtccggcccc ggactcgta aaccagtgac gacgcttagc 120
ctgacctgta ccgtctcagg gggcagcatc tctcttatt actggagctg gatcaggcag 180
cctccaggaa aaggccttga atggattggg tacatctact actctggctc aacaaattat 240
aatccatccc tgaagtcccg cgtgactatc tctgtggaca ccagcaagaa tcagttttca 300
ctgaagttgt ctagtgttac cgcgccgcac accgccgtat actactgtgt gtctcttg 360

tactgtggcg gcgactgcta ttccgggttc gactactggg gccaagggac tctgtaacc 420
gtgtcctcag gcggcggcgg gtcaggagga ggccggcagtg gaggtggcgg ctccgacatc 480
cagctgacac aatcaccatc ttccctttca gttcagtcg gggacagagt gtccttcaca 540
tgccaggcca gccaggatat caataacttc ctgaactggg accaacagaa acccggaag 600
gctccaaagc tcctgatcta tgatgcttc aacctggaga ccggcgtgcc ctccaggttc 660
agtggttcag gatcaggcac tgactttacg ttcaccatat ccagtcttca gcccgaagac 720
attgcaacct attactgcca acaatacggg aaccttcctt ttacattcgg aggcggcacc 780
aaggtggaaa tcaaaagggc tgcagcattg agcaactcaa taatgtattt tagtcacttt 840
gtaccagtgt tcttgccggc taagcctact accacacccg ctccacggcc acctaccca 900
gctctacca tcgttcaca gcctctgtcc ctgcgccag aggcttgccg accggccgca 960
gggggcgctg ttcataccag aggactggat ttgcctgcg atatctatat ctgggcacc 1020
ctggccggaa cctgcggcgt actcctgctg tccttggtca tcacgtcta ttgtaatcac 1080
aggaacagat ccaaaagaag ccgcctgctc catagcgatt acatgaatat gactccacgc 1140
cgccctggcc ccacaaggaa aactaccag ccttacgcac cacctagaga ttcgctgcc 1200
tatcggagca gggagaagt ttccagatct gcagatgcac cagcgtatca gcaggccag 1260
aaccaactgt ataacgagct caacctggga cgcagggaag agtatgacgt ttggacaag 1320
cgcagaggac gggaccctga gatgggtggc aaaccaagac gaaaaaacc ccaggagggt 1380
ctctataatg agctgcagaa ggataagatg gctgaagcct attctgaaat aggcataaaa 1440
ggagagcgga gaaggggaaa agggcacgac ggtttgtacc agggactcag cactgctacg 1500
aaggatactt atgacgtct ccacatgcaa gcctgccac ctaggtaa 1548

<210> 174

<211> 515

<212> PRT

<213> Artificial Sequence

<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
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 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

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> 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 agtcccgct gactatctct gtggacacca gcaagaatca gtttctactg 240
aagttgtcta gtgtaccgc ggccgacacc gccgtatact actgtgtgtc tcttgtgtac 300
tgtggcggcg actgctattc cgggttcgac tactggggcc aagggaactct ggtaaccgtg 360
tcctcaggcg gcggcgggtc aggaggaggc ggcagtggag gtggcggctc cgacatccag 420
ctgacacaat caccatcttc ctttcagct tcagtcgggg acagagtgtc cttcacatgc 480
caggccagcc aggatatcaa taacttcctg aactggtacc aacagaaacc cggaaaggct 540
ccaaagctcc tgatctatga tgctccaac ctggagaccg gcgtgccctc caggttcagt 600
ggttcaggat caggcactga ctttacgttc accatatcca gtcttcagcc cgaagacatt 660
gcaacctatt actgccaaca atacgggaac ctcccttta cattcggagg cggcaccaag 720
gtggaaatca aaagggtgc agcattgagc aactcaataa tgtattttag tcactttgta 780
ccagtgttct tgccggctaa gcctactacc acaccgctc cacggccacc taccacagct 840

cctaccatcg cttcacagcc tctgtccctg cgcccagagg cttgccgacc ggccgcaggg 900
 ggcgctgttc ataccagagg actggatttc gctgcgata tctatatctg ggcacccctg 960
 gccggaacct gggcgctact cctgctgtcc ctggatcatca cgctctattg taatcacagg 1020
 aacagatcca aaagaagccg cctgtcccat agcgattaca tgaatatgac tccacgccgc 1080
 cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat 1140
 cggagcaggg tgaagtttcc cagatctgca gatgcaccag cgtatcagca gggccagaac 1200
 caactgtata acgagctcaa cctgggacgc agggaagagt atgacgtttt ggacaagcgc 1260
 agaggacggg accctgagat ggggtggcaaa ccaagacgaa aaaacccccca 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> 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 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

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> anti-CLL-1 CAR construct

<400> 177

atggcactcc ccgtaactgc tctgtctgtg ccgttggcat tgctcctgca cgccgcacgc 60
ccggatatcc agctcagca atccccctca agcttgagtg cctccgtggg cgaccgggtg 120
tccttcacat gtcaggcaag ccaagacata aataatttcc tgaattggta ccaacaaaaa 180
cccggcaagg ctcccaaact cctgatttat gatgcctcca atctggagac cggggtcct 240
tctagattca gcggaagtgg cagcggcaca gactttacat ttactatctc ttctctgcaa 300
ccagaggaca tcgccacata ctattgccag caatacggca atctgccctt caccttcgga 360
ggcggaacca aggtagaaat taaaaggggc ggtggaggct ccggaggggg gggctctggc 420
ggaggggggt cccaagtaca attgcaggag tcagggcctg gactcgtgaa gccttcagaa 480
actttgtcac tgacatgtac agtgtccggc ggaagcattt ccagttacta ttggtcctgg 540
attagacagc caccggcaa aggactggaa tggattggat atatctacta ctctggatct 600
acaaactata atcccagcct caaatccagg gtcactatta gtgtggatac atcaaagaat 660
cagttctcct tgaagctgag ctcagtcact gctgccgaca ccgcagtgtg ctattgtgtg 720
agcctgggtct actgcccggg agattgttac agcggtttcg attactgggg ccagggcacc 780
ctgggtaccg ttagttccgc ggctgtcttt gataacgaga agtccaacgg tacgattatc 840
cacgttaagg gtaagcacct ttgcctagc ccgctgttcc caggccccag taagcccttt 900
tgggtcctcg ttgtggtagg tggggctact gcctgtact ccctgctcgt cactgtcgca 960
ttcatcatct tctgggtcag atccaaaaga agccgctgc tccatagcga ttacatgaat 1020
atgactccac gccgccctgg cccacaagg aaactactacc agccttacgc accacctaga 1080
gatttcgtg cctatcggag cagggtgaag tttccagat ctgcagatgc accagcgtat 1140
cagcagggcc agaaccaact gtataacgag ctcaacctgg gacgcaggga agagtatgac 1200
gttttgaca agcgcagagg acgggaccct gagatgggtg gcaaaccaag acgaaaaaac 1260
cccaggagg 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> 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> anti-CLL-1 CAR construct

<400> 179

gatatccagc tcacgcaatc cccctcaagc ttgagtgcct ccgtgggcga ccgggtgtcc 60

ttcacatgtc aggcaagcca agacataaat aatttctga attggtacca acaaaaaccc 120

ggcaaggctc ccaaactcct gatttatgat gcctccaatc tggagaccgg ggtcccttct 180

agattcagcg gaagtggcag cggcacagac ttacattta ctatctcttc tctgcaacca 240

gaggacatcg ccacatacta ttgccagcaa tacggcaatc tgccttcac 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 agtactgtct gccgacaccg cagtgtacta ttgtgtgagc 660

ctgggtact gcggcggaga ttgtacagc ggtttcgatt actggggcca gggcaccctg 720

gttaccgtta gttccgcggc tgctcttgat aacgagaagt ccaacggtag gattatccac 780

gttaagggtg agcacctttg ccctagcccc ctgttccag gccccagtaa gcccttttgg 840

gtcctcgttg tggtaggtgg ggtactcgcc tgctactccc tgctcgtcac tgcgcattc 900

atcatcttct gggtcagatc caaaagaagc cgctgtctcc atagegatta catgaatatg 960

actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat 1020
 ttcgctgcct atcggagcag ggtgaagttt tccagatctg cagatgcacc agcgtatcag 1080
 cagggccaga accaactgta taacagctc aacctgggac gcagggaaga gtatgacgtt 1140
 ttggacaagc gcagaggacg ggaccctgag atgggtggca aaccaagacg aaaaaacccc 1200
 caggagggtc tctataatga gctgcagaag gataagatgg ctgaagccta ttctgaaata 1260
 ggcatgaaag gagagcggag aaggggaaaa gggcacgacg gttgtacca gggactcagc 1320
 actgctacga aggatactta tgacgtctc cacatgcaag ccctgccacc tagg 1374

<210> 180
 <211> 458
 <212> PRT
 <213> Artificial Sequence

<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 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> 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 cgggggtgcc 240
agcagggtta gcgggagcgg ttctggcacg gattttacgt tcaccatctc ctctctgcag 300
cccaggata tagctactta ttactgtcag cagtacggga atctgccatt tacttttggg 360
gggtggaacta aggtggaaat caaaaggggc ggcgggggaa gcgggggcgg gggctcaggt 420

ggcgaggga gccaggtgca actccaggaa agtggcccag gattggtgaa gccagcgag 480
 accctttccc ttactgtac tgtagcgga ggcagcataa gcagctacta ttgtctctgg 540
 atcagacagc caccagggaa agggcttgaa tggattggct acatttacta ttccgggtcc 600
 accaactaca acccatccct caagtcctgc gtgacaattt ccgtcgacac aagcaagaac 660
 cagttctccc tgaacttag tagcgtcact gctgcagata cagcagtgtg ctattgtgtc 720
 agccttgtct actgtggcgg cgactgtac agtggcttg attactgggg acagggcacg 780
 ctcgtgacag tgccagcgc tgcggctatc gaggtaatgt atccgccacc gtatctggac 840
 aacgagaagt ctaatgggac aatcattcac gtgaaggga agcacctgtg tccatcccc 900
 ctgtttccgg gtccagtaa acccttctgg gtgcttggtg tcgttggcgg ggtgctggcc 960
 tgctattccc tgctggtgac cgctcgcttt attatttct gggtagatc caaaagaagc 1020
 cgctgtctcc atagcgatta catgaatatg actccacgcc gccctggccc cacaagaaa 1080
 cactaccagc cttacgcacc acctagagat ttgctgcct atcggagcag ggtgaagttt 1140
 tccagatctg cagatgcacc agcgtatcag cagggccaga accaactgta taacgagctc 1200
 aacctgggac gcaggaaga gtatgacgtt ttggacaagc gcagaggacg ggaccctgag 1260
 atgggtggca aaccaagacg aaaaaacccc caggagggtc tctataatga gctgcagaag 1320
 gataagatgg ctgaagccta ttctgaaata ggcatgaaag gagagcggag aaggggaaaa 1380
 gggcacgacg gttgtacca gggactcagc actgctacga aggatactta tgacgtctc 1440
 cacatgcaag ccctgccacc taggtaa 1467

<210> 182

<211> 488

<212> PRT

<213> Artificial Sequence

<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> anti-CLL-1 CAR construct

<400> 183
gataccagc tgaccagtc tccatcctct ttgagtcct ccgtgggtga ccgcgtctct 60
ttcacttgcc aagccagcca agacatcaac aactttctga attggtacca gcagaaacca 120
ggcaaagcac caaagctcct catctacgac gcctccaacc tggaaccgg ggtgccagc 180
aggtttagcg ggagcgggtc tggcacggat ttacgttca ccatctctc tctgcagccc 240
gaggatatag ctactatta ctgtcagcag tacgggaatc tgccatttac ttttgggggt 300
ggaactaagg tggaatcaa aaggggcggc gggggaagcg ggggcggggg ctgaggtggc 360
ggaggagacc aggtgcaact ccaggaaagt ggcccaggat tgggaagcc cagcgagacc 420
cttccctta ctgtactgt tagcggaggc agcataagca gctactattg gtcctggatc 480
agacagccac cagggaagg gctgaatgg attggtaca ttactattc cgggtccacc 540
aactacaacc catcctcaa gtccgcgtg acaatttccg tcgacacaag caagaaccag 600
tttccctga aacttagtag cgctactgct gcagatacag cagtgtacta ttgtgcagc 660
ctgtctact gtggcggcga ctgtacagt ggcttgatt actggggaca gggcacgctc 720
gtgacagtgt ccagcgtgc ggctatcgag gtaatgtatc cgccaccgta tctggacaac 780
gagaagtcta atgggacaat cattcacgtg aaggggaagc acctgtgtcc atccccctg 840
ttccgggtc ccagtaaacc ctctgggtg ctgttgtcg ttggcgggt gctggcctgc 900
tattccctgc tggtgaccgt cgcgtttatt atttctggg ttagatcaa aagaagccgc 960
ctgtccata gcgattacat gaatatgact ccacgccgc ctggcccccac aaggaaacac 1020
taccagcctt acgcaccacc tagagatttc gctgcctatc ggagcagggt gaagtttcc 1080
agatctgcag atgcaccagc gtatcagcag ggccagaacc aactgtataa cgagctcaac 1140
ctgggacgca gggaagagta tgacgtttg gacaagcgca gaggacggga ccctgagatg 1200

ggtggcaaac caagacgaaa aaacccccag gagggctctct ataagtagct gcagaaggat 1260
 aagatggctg aagcctattc tgaaataggc atgaaaggag agcggagaag gggaaaaggg 1320
 cagcaggggtt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1380
 atgcaagccc tgccacctag g 1401

<210> 184
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<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> anti-CLL-1 CAR construct

<400> 185
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccggacattc aattgaccca gtcccctagc agtctctcag caagtgtggg agatagggtg 120
tcattcacct gtcaggcttc acaggacatc aacaacttc tcaattggta tcagcagaag 180
ccagggaagg caccaaagct gctcatatat gacgcttcaa acctgaaac cggagtacct 240
agccgcttca gcggaagcgg atcagggact gacttcaact ttaccatctc ttactgcag 300
cccgaagaca tcgccacata ctactgccag cagtacggaa acttgccctt tacatttggg 360
ggcggcacca aagtggagat taagcgaggg ggaggcggct caggaggcgg tggctccgga 420
ggcgggggtt cccagggtcca gctccaggaa tccggcccag gtctgggtta gcccaagtga 480
actttgtccc tcacgtgtac tgtgagcggg ggttcaatct cctcatacta ttggtcttgg 540

atacggcaac ctcttgaaa gggcctcgag tggatcggct atatctacta tagtggctcc 600
 actaattaca acccttcct caagtccaga gtcaccattt ccgtggacac atctaagaac 660
 cagttcagtc tgaagttgtc cagcgttaca gccgcagaca cagccgttta ttactgtgtg 720
 tctctgttt actgcggggg agactgttat agcggcttcg attactgggg ccagggcacc 780
 ttggtcacag tctctccgc ggccgccctc tctaacagta ttatgtactt ttctcathtt 840
 gtaccctgt tcttccgc taagccaact actaccccg cccacggcc gcctaccct 900
 gcaccacaa tagccagtca gccttgagc ctgagacctg aggctgtcg gccggctgct 960
 gggggtgcag tgcacacacg aggtcttgat ttgcttgcg acatatacat ctgggccct 1020
 ctggccggga cctgtggggg gctgctctg agcttggtca tcacgtcta ttgcaacct 1080
 cgcaacagat ccaaaagaag ccgcctgctc catagcgatt acatgaatat gactccacgc 1140
 cgccctggcc ccacaaggaa acactaccag cttacgcac cacctagaga ttctgctgcc 1200
 tatcgagca ggggtgaagt ttccagatct gcagatgcac cagcgtatca gcaggccag 1260
 aaccaactgt ataacgagct caacctggga cgcagggaag agtatgacgt ttggacaag 1320
 cgcagaggac gggaccctga gatgggtggc aaaccaagac gaaaaaacc ccaggagggt 1380
 ctctataatg agctgcagaa ggataagatg gctgaagcct attctgaaat aggcatgaaa 1440
 ggagagcgga gaaggggaaa agggcacgac ggtttgtacc agggactcag cactgctacg 1500
 aaggatactt atgacgtct ccacatgcaa gccctgccac ctaggtaa 1548

<210> 186

<211> 515

<212> PRT

<213> Artificial Sequence

<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> anti-CLL-1 CAR construct

<400> 187
gacattcaat tgaccagtc cctagcagt ctctcagcaa gtgtgggaga tagggtgtca 60
ttcacctgtc aggcttcaca ggacatcaac aacttctca attggtatca gcagaagcca 120
gggaaggcac caaagctgct catatatgac gttcaaacc ttgaaaccgg agtacctagc 180
cgcttcagcg gaagcggatc agggactgac ttcacttta ccatctcttc actgcagccc 240
gaagacatcg ccacatacta ctgccagcag tacggaaact tgccttttac atttgggggc 300
ggcaccaaag tggagattaa gcgaggggga ggcggctcag gaggcggtgg ctccggaggc 360
gggggttccc aggtccagct ccaggaatcc ggcccaggtc tggtaagcc cagtgaaact 420
ttgtccctca cgtgtactgt gagcgggtgt tcaatctct cactactattg gtcttgata 480
cggcaacctc ctggaagggt cctcgagtgg atcggctata tctactatag tggctccact 540
aattacaacc ctccctcaa gtccagagtc accatttccg tggacacatc taagaaccag 600
ttcagtctga agttgtccag cggtacagcc gcagacacag ccgtttatta ctgtgtgtct 660
ctgttttact gcgggggaga ctgttatagc ggcttcgatt actggggcca gggcaccttg 720
gtcacagtct ctcccgggc cgcctctct aacagtatta tgtacttttc tcattttgta 780
cccgtgttcc ttccgctaa gccaactact accccggccc cacggccgcc taccctgca 840
cccacaatag ccagtcagcc tttagcctg agacctgagg ctgtcggcc ggctgctggg 900
gggtgcagtgc acacacgagg tcttgatttt gcttgcgaca tatacatctg ggcccctctg 960
gccgggacct gtgggggtgt gttctgagc 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 aggggaagagt atgacgtttt ggacaagcgc 1260
agaggacggg accctgagat ggggtggcaaa 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> 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

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> anti-CLL-1 CAR construct

<400> 189
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccgcaggtac agctgcagga atctgggccc ggacttgta agccaagtca gacactttct 120

cttacatgta ccgtgagcgg cggaagtata agcagtggag gcttttactg gtcttgata 180
 cggcagcacc caggcaaagg ctggagtggt attgataca ttcattcagg aggatctaca 240
 cactataatc catcccttaa gtcccggtgc accattagca ttgatacgtc taagaatctg 300
 ttcagttcca ggctgtctc cgctactgct gccgacacag ccgtgtacta ctgcgcctcc 360
 ttggtttact gcggaggcga ctgttatagc ggctttgatt attgggggca ggggaccctc 420
 gtaaccgtga gctctggagg ggggtgggagc gggggaggag gttcaggggg gggcggctcc 480
 gatatacagc tcaactaaag cccctctagt ctctctgcct cagtggggga tcgggtcagt 540
 ttacttgc aagcttcaca ggatatcaac aacttcctta attggtatca gcagaagcca 600
 ggaaaagcac ccaagctgct catctatgat gcctcaaatt tggagacggg tgttccagt 660
 cgattctctg ggctcagggtc cgggaccgac ttacgttta cgatctctc tctgcagccc 720
 gaagacatcg ccacatacta ttgtcaacag tacggcaact tgcctttcac atttgggggc 780
 gggactaagg ttgaaatcaa gagggccgct gactggaca atgagaagtc caacggcacc 840
 atcatccacg tgaagggcaa gcacctgtgc ctagtctc tgttccagg cccatccaaa 900
 ccttttggg ttctgtgtgt ggtcgggggg gtgtggcct gctattctt gctggtcacg 960
 gtggccttca taattttctg ggtagatcc aaaagaagcc gcctgtcca tagcgattac 1020
 atgaatatga ctccacgccg ccctggcccc acaaggaaac actaccagcc ttacgcacca 1080
 cctagagatt tcgctgccta tcggagcagg gtgaagttt ccagatctgc agatgcacca 1140
 gcgtatcagc agggccagaa ccaactgtat aacgagctca acctgggacg cagggaagag 1200
 tatgacgttt tggacaagcg cagaggacgg gacctgaga tgggtggcaa accaagacga 1260
 aaaaaccccc aggagggtct ctataatgag ctgcagaagg ataagatggc tgaagcctat 1320
 tctgaaatag gcatgaaagg agagcggaga aggggaaaag ggcacgacgg ttgtaccag 1380
 ggactcagca ctgctacgaa ggatacttat gacgtctcc acatgcaagc cctgccacct 1440
 aggtaa 1446

<210> 190

<211> 481

<212> PRT

<213> Artificial Sequence

<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
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

<210> 191
<211> 1380
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-CLL-1 CAR construct

<400> 191
caggtacagc tgcaggaatc tgggcccgga cttgtcaagc caagtcagac actttctctt 60
acatgtaccg tgagcggcgg aagtataagc agtggaggct ttactggtc ttgatacgg 120
cagcaccag gcaaaggctt ggagtggatt ggatacattc atcattcagg atctacacac 180
tataatccat cccttaagtc ccgggtcacc attagcattg atacgtctaa gaatctgttc 240
agtctcaggc tgtctccgt cactgtgcc gacacagccg tgtactactg cgctccttg 300
gtttactgcg gaggcgactg ttatagcggc ttgattatt gggggcaggg gaccctcgta 360
accgtgagct ctggaggggg tgggagcggg ggaggagggt cagggggggg cggtccgat 420
atccagctca ctcaaagccc ctctagtctc tctgcctcag tgggggatcg ggtagtttt 480
acttgtcaag cttcacagga tatcaacaac ttccttaatt ggtatcagca gaagccagga 540
aaagcaccca agctgctcat ctatgatgcc tcaaatttgg agacgggtgt tcccagtcga 600
ttctctgggt cagggtccgg gaccgacttt acgtttacga tctctctct gcagcccga 660
gacatcgcca catactattg tcaacagtac ggcaacttgc cttcacatt tgggggcggg 720
actaagggtg aaatcaagag ggccgtgca ctggacaatg agaagtcaa cggcaccatc 780
atccacgtga agggcaagca cctgtgccct agtcctctgt tcccaggccc atccaaacct 840
tttgggttc ttgtgtggt cgggggggtg ctggcctgct attctctgct ggtcacggtg 900

gccttcataa tttctgggt tagatccaaa agaagccgcc tgctccatag cgattacatg 960
aatatgactc cacgccgccc tggccccaca aggaacact 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 agggctctta taatgagctg cagaaggata agatggctga agcctattct 1260
gaaataggca tgaaaggaga gcggagaagg ggaaaagggc acgacggtt gtaccagga 1320
ctcagcactg ctacgaagga tacttatgac gctctccaca tgcaagccct gccacctagg 1380

<210> 192
<211> 460
<212> PRT
<213> Artificial Sequence

<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

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> anti-CLL-1 CAR construct

<400> 193

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctgcagga aagcgggtccg ggacttgtca agccgtccca aacgctgagt 120

ctgacgtgta ctgtctctgg tggctctatt tcttccgggg gcttttattg gtcttgatc 180

agacaacacc ctggcaaagg gctggagtgg ataggggtata ttcaccactc tgggtccact 240

cactacaacc catcattgaa atccagagtg actatctcaa tcgacacatc caagaacctt 300

ttcagcctga ggttgatc agttaccgcc gctgacaccg cggtgtatta ttgcgcctct 360

ctcgtgtact gcggtggcga ttgttatagt ggctttgact actgggggca ggggacattg 420

gttaccgttt caagtggagg cggtaggtct ggcgggggcg gtagcggagg tggggggagc 480
 gacatacagc ttacgcagag cccctccagc ctttcagcct ccgtggggga taggggtgcc 540
 ttacctgcc aggcttcca ggacataaac aacttctca attggtatca gcaaaagccc 600
 gggaaagcac caaagctgct catctacgat gccagcaacc tggaaaccgg agtgccgtct 660
 cgcttctctg gaagtggcag tgggaccgat ttcacttta caatctcaag ttgcagcca 720
 gaagacattg caacatacta ctgtcaacag tacggcaatc tcccctttac atttgggggg 780
 ggaactaaag tggagattaa gcgcgtgca gccattgaag ttatgtatcc gccccgtat 840
 ctggataacg agaaatctaa tggtagcata atacatgtga aggggaagca cctctgtcca 900
 tcaccgtgt tccccggccc tcaaaacct ttctgggtac tcgtgtcgt gggtaggatt 960
 ctggcctgct atagtctgct ggtgaccgtg gcgtttatca tcttctgggt aagatccaaa 1020
 agaagccgcc tgctccatag cgattacatg aatatgactc cagccgccc tggccccaca 1080
 aggaaacct accagccta cgcaccacct agagatttcg ctgcctatcg gagcagggtg 1140
 aagttttcca gatctgcaga tgcaccagcg tatcagcagg gccagaacca actgtataac 1200
 gagtcaacc tgggacgcag ggaagagtat gacgttttg acaagcgag aggacgggac 1260
 cctgagatgg gtggcaaacc aagacgaaa aacccccagg agggctctta taatgagctg 1320
 cagaaggata agatggctga agcctattct gaaataggca tgaaaggaga gcggagaagg 1380
 ggaaaagggc acgacggtt gtaccaggga ctgagcactg ctacgaagga tacttatgac 1440
 gctctccaca tgcaagccct gccacctagg taa 1473

<210> 194
 <211> 490
 <212> PRT
 <213> Artificial Sequence

<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

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> anti-CLL-1 CAR construct

<400> 195
cagggtgcagc tgcaggaaag cgggtccggga ctgtcaagc cgtcccaaac gctgagtctg 60
acgtgtactg tctctggtgg ctctatttct tccgggggct ttattggtc ttgatcaga 120
caacacctg gcaaagggt ggagtggata gggtatattc accactctgg gtccactcac 180
tacaacctat cattgaaatc cagagtgact atctcaatcg acacatcaa gaacctttc 240
agcctgaggt tgcatacagt taccgccgt gacaccgcg tgtattattg cgctctctc 300
gtgtactgcg gtggcgattg ttatagtggc ttgactact gggggcaggg gacattggtt 360
accgtttcaa gtggaggcgg tgggtctggc gggggcggtg gcggagggtg ggggagcgac 420
atacagctta cgcagagccc ctccagcctt tcagcctccg tgggggatag ggtgtccttt 480
acctgccagg ctccagga cataaacaac ttctcaatt ggtatcagca aaagcccggg 540
aaagcaccaa agctgctcat ctacgatgcc agcaacctgg aaaccggagt gccgtctcg 600
ttctctggaa gtggcagtgg gaccgatttc acttttaca tctcaagtt gcagccagaa 660
gacattgcaa catactactg tcaacagtac ggcaatctcc cctttacatt tgggggggga 720
actaaagtgg agattaagcg cgctgcagcc attgaagta tgtatccgcc cccgtatctg 780
gataacgaga aatctaattg taccataata catgtgaagg ggaagcacct ctgtccatca 840
ccgtgttcc ccggcccttc aaaaccttc tgggtactcg ttgtcgtggg tggagtctg 900
gcctgtata gtctgtggt gaccgtggcg ttatcatct tctgggtaag atccaaaaga 960
agccgcctgc tcatagcga ttacatgaat atgactccac gccgcctgg cccacaagg 1020
aaactacc agcctacgc accacctaga gatttcgctg cctatcgag cagggtgaag 1080
tttccagat ctgcagatgc accagcgtat cagcagggcc agaaccaact gtataacgag 1140
ctaacctgg gacgcaggga agagtatgac gttttggaca agcgagagg 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> 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> anti-CLL-1 CAR construct

<400> 197
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccgcaggtgc agttgcagga aagcgggcct ggccttgtga aaccaagcca gacactgagc 120
ctgacatgca ctgtgtccgg cgggtccata tcttcggggg gttttattg gtcttgata 180
cgccagcatc ccgggaaagg acttgaatgg attggatata tccaccattc cggaagcacc 240
cactacaatc caagccttaa atcccgggtg acaatctcca tcgacacctc aaagaatctt 300
tttccctgc ggttgtcttc agtaactgcc gccgataccg ctgtgtacta ctgtgccagc 360
ctcgtctatt gcggcggaga ttgtattct ggggttcgatt attgggggtca 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 ttaccttta cgattccag tctgcagcca 720
 gaggatatag caactatta ctgtcagcag tatggcaacc tcccttttac cttcgggtgt 780
 ggcacaaagg tcgagattaa aagagccgca gcgttgcca actccataat gtattttct 840
 cattttgtgc ccgttttct gctgcaaaa cctaccacca cccccgccc acgaccacct 900
 actccagccc ccaccatgc ctcccagccc ctacgcctga ggccagaggc ttgtcgcct 960
 gctgcggggg gcgctgtcca taccagagga ctgcactcg cctgcgatat ttatatatgg 1020
 gccccctcg ccggcacctg cggagtcttg ctctgagcc 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 cacgacgggt tgtaccaggg actcagcact 1500
 gctacgaagg atacttatga cgctctccac atgcaagccc tgccacctag gtaa 1554

<210> 198

<211> 517

<212> PRT

<213> Artificial Sequence

<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> 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 gccttaaate cgggtgaca atctccatcg acacctcaaa gaatctttt 240

tcctgcggt tgtcttcagt aactgccgc gataccgctg tgtactactg tgccagcctc 300

gtctattgcg gcggagattg ttattctggg ttcgattatt ggggtcaagg cacactggta 360

actgtcagca gcggaggcgg cggttccggg ggcgggggca gtggaggggg cggatctgac 420

attcagctta cgcagtcccc atcttcactt agcgccagcg ttggcgatcg ggtagcttc 480

acgtgtcaag caagtcagga tatcaacaac tttcttaact ggtaccagca gaagccaggc 540

aaggcaccca agttgctgat ttacgatgct tctaacctcg agacgggagt gcctagccgc 600

ttctccggga gcggcagcgg cacagacttt acctttacga ttccagtct gcagccagag 660

gatatagcaa cttattactg tcagcagtat ggcaacctcc cttttacctt cggtggtggc 720

acaaaggctg agattaaaag agccgcagcg ttgtcaaact ccataatgta tttttctcat 780

tttgtcccc tctttctgcc tgccaaacct accaccaccc ccgccccacg accacctact 840

ccagccccca ccatgcctc ccagcccctc agcctgaggc cagaggcttg tcgccctgct 900

gcggggggcg ctgtccatac cagaggactc gacttcgcct gcgatattta tatatgggcc 960

cccctcgccg gcacctgcgg agtcttgctc ctgagccttg tgatcacgct ttattgtaac 1020
 catcggaata gatccaaaag aagccgcctg ctccatagcg attacatgaa tatgactcca 1080
 cgccgccttg gccccacaag gaaacactac cagccttacg caccacctag agatttcgct 1140
 gcctatcgga gcagggtgaa gttttccaga tctgcagatg caccagcgta tcagcagggc 1200
 cagaaccaac tgtataacga gctcaacctg ggacgcaggg aagagtatga cgttttggac 1260
 aagcgcagag gacgggaccc tgagatgggt ggcaaacc aa gacgaaaaa ccccaggag 1320
 ggtctctata atgagctgca gaaggataag atggctgaag cctattctga aataggcatg 1380
 aaaggagagc ggagaagggg aaaagggcac gacggttgt accagggact cagcactgct 1440
 acgaaggata cttatgacgc tctccatg caagccctgc cacctagg 1488

<210> 200
 <211> 496
 <212> PRT
 <213> Artificial Sequence

<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> anti-CLL-1 CAR construct

<400> 201

atggcactcc ccgtaactgc tctgtgctg ccgttgcat tgctcctgca cgccgcacgc 60

ccgcaggctcc aactgggtgca gtccggagcc gaagtcaaga aaccaggtgc ctccgttaaa 120

gtgagttgca aagtctctgg atacactctg accgagctct ctatgcactg ggtccggcag 180
 gcccccgga agggattgga atggatgggc gggttcgac ctgaggacgg agagactatc 240
 tacgtcaaaa aattccaggg acgagtactg gtgaccgaag acactagtag cgacactgcc 300
 tacatggaac ttctctctct gcgacagaa gataccgcag tgtactactg tgctactgaa 360
 tctaggggca ttggatggcc ctacttcgat tactgggggc agggaaactct ggtgactgtc 420
 tccagcggtg gaggtggcag cgggtggggc ggaagcgggg ggggcggctc tgatattcag 480
 atgactcaat ctcttcttc tctgtccgt tccgtgggcg atagagtac cattacttgt 540
 agggcgctcc agtcaatctc cagttatttg aattggatc agcagaagcc cgggaaagca 600
 cctaagctgt tgatcagcgg ggcttctagc ctgaagagt gggtaccttc acggttcagc 660
 ggaagcggaa gcggaaccga ttccacctg actatcagca gcctgccacc tgaggacttt 720
 gcaacttact actccaaca gtcatacagc actccgatca ctttcggcca gggcacccgg 780
 ctcgaaatca agcgcgctgc tgctttggac aatgagaagt caaacggcac catcatacat 840
 gttaaaggta aacatctgtg tcctccccg ctgttccccg gcccttcaa accgttctgg 900
 gttctggtagg tggtcggagg cgtactcgtc tgctatagtc tgctggtaac tgcgccttc 960
 atcatctttt gggtagatc caaagaagc cgctgtctc atagcgatta catgaatatg 1020
 actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat 1080
 ttgctgcct atcgagcag 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 gttgtacca gggactcagc 1380
 actgctacga aggatactta tgacgtctc cacatgcaag cctgccacc taggtaa 1437

<210> 202

<211> 478

<212> PRT

<213> Artificial Sequence

<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> anti-CLL-1 CAR construct

<400> 203

caggtccaac tggcgagtc cggagccgaa gtcaagaaac caggtgcctc cgtaaagtg 60

agttgcaaag tctctggata cactctgacc gagctctcta tgcactgggt ccggcaggcc 120

cccggcaagg gattggaatg gatgggcggg ttgatcctg aggacggaga gactatctac 180

gctcaaaaat tccaggagc agtgactgtg accgaagaca ctagtaccga cactgcctac 240

atggaacttt cctctctcg atcagaagat accgcagtgt actactgtgc tactgaatct 300

aggggcattg gatggcccta ctctgattac tggggtcagg gaactctggt gactgtctcc 360

agcgggtggag gtggcagcgg tgggtggcga agcggggggg gcggctctga tattcagatg 420

actcaatctc cttctctct gtccgcttc gtgggcgata gagtgaccat tactttagg 480

gcgtccagt caatctccag ttatttgaat tggatcagc agaagcccgg gaaagcacct 540

aagctgttga tcagcggggc tttagcctg aagagtgggg taccttcacg gttcagcga 600

agcgggaagcg gaaccgattt caccctgact atcagcagcc tgccacctga ggactttgca 660

acttactact gccaacagtc atacagcact ccgatcatt tcggccaggg caccggctc 720

gaaatcaagc gcgctgctgc ttggacaat gagaagtcaa acggcaccat catacatgtt 780

aaaggtaaac atctgtgtcc ctccccgctg ttccccggcc ctccaaacc gttctgggtt 840

ctgggtgggtg tcggaggcgt actcgcttgc tatagtctgc tggtaactgt cgccttcac 900

atcttttggg tgagatcaa aagaagccg ctgctcata gcgattacat gaatatgact 960

ccacgccgcc ctggcccccac 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 cacgacgggt tgtaccaggg actcagcact 1320
gctacgaagg atacttatga cgctctccac atgcaagccc tgccacctag g 1371

<210> 204
<211> 457
<212> PRT
<213> Artificial Sequence

<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 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

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

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> 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

tacgccaga agttccaggg ccgggtcacc gtaacagaag acacctcaac tgacaccgct 300

tacatggagc tgagttcact gcgggtccgag gacacggccg tgtattattg tgccaccgag 360

agccgcggaa tcgcatggcc ttacttcgac tactggggac agggtagact tgttacagta 420

tcatccgggg gtggcggctc tgggtggggc ggctccggag ggggtggatc agatatcaa 480

atgactcaaa gtccaagttc cctgtctgcc tcagtcggag atagagtcac cataacctgc 540

agggcaagtc agtccatctc ctctatctg aactgggtacc 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 atgggacat cattcatgtg aagggttaagc acctttgcc tagccactg 900
 tttctggcc cgagtaaacc ctttgggta cttgtggtcg tcggcggcgt gctggcctgc 960
 tactcactcc tggttaccgt cgcattcatc atcttttggg tgagatcaa 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 gaggggtctct ataatgagct gcagaaggat 1320
 aagatggctg aagcctattc tgaatatggc atgaaaggag agcggagaag gggaaaaggg 1380
 cagcaggggt tgtaccaggg actcagcact gctacgaagg atacttatga cgctctccac 1440
 atgcaagccc tgccacctag gtaa 1464

<210> 206

<211> 487

<212> PRT

<213> Artificial Sequence

<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

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
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> anti-CLL-1 CAR construct

<400> 207

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cagggtgcagc ttgtgcagag cggggccgag gtgaagaagc ccggggccag cgtcaaagtg    60
tcctgtaagg tcagcgggta caccctcacc gagctgagca tgcactgggt acggcaggct    120
cccggcaaag gtcttgagtg gatgggtgga ttgatccag aagatggaga gactatctac    180
gccagaagt tccagggccg gggtaccgta acagaagaca cctcaactga caccgcttac    240
atggagctga gttcactgcg gtccgaggac acggccgtgt attattgtgc caccgagagc    300
cgcggaatcg gatggcctta cttcgactac tggggacagg gtacacttgt tacagtatca    360
tccgggggtg gcggtcttgg tgggggcggc tccggagggg gtggatcaga tatccaaatg    420
actcaaagtc caagttccct gtctgcctca gtcggagata gagtaccat aacctgcagg    480
gcaagtcagt ccattctctc ctatctgaac tggtagcaac agaaacctgg aaaggcgctt    540
aagctcctga tctccggagc ctcattcttg aaatccgggtg tccatctcg cttagtggtc    600
tctggaagcg gtacagattt tactttgacc attagcagcc tcccaccgga agactttgct    660
acatattact gccagcagtc ttactcaacc ccaatcacct tcgggcaagg caccagactc    720
gaaataaaaa gagcagctgc tatcgagggt atgtaccac cgccgtactt ggataacgaa    780
aaaagcaatg ggaccatcat tcatgtgaag ggtaagcacc ttgccctag cccactgttt    840
cctggcccga gtaaaccctt ttgggtactt gtggtcgtcg gcggcgtgct ggctgtctac    900
tactcctgg ttaccgtgc attcatcatc ttttgggtga gatccaaaag aagccgcctg    960
ctccatagcg attacatgaa tatgactcca cgccgccctg gcccacaag 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 cccccaggag ggtctctata atgagctgca gaaggataag   1260
atggctgaag cctattctga aataggcatg aaaggagagc ggagaagggg aaaagggcac   1320
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gacggtttgt accagggact cagcactgct acgaaggata cttatgacgc tctccacatg 1380

caagccctgc cacctagg 1398

<210> 208

<211> 466

<212> PRT

<213> Artificial Sequence

<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 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

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

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> anti-CLL-1 CAR construct

<400> 209

atggcactcc ccgtaactgc tctgctgctg ccgttgcat 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 aactagcac tgacacagcg 300

tacatggagc tgagttctct gagaagtga gacacagccg ttactactg cgctaccgag 360

tccagaggta ttggctggcc atacttcgac tattggggtc agggcaccct gggtacagtg 420

agttcaggag gcgggggctc tggggggggc ggttcggag gggggggctc agatatacag 480

atgacgcaga gtccatcaag tctctcagcc agcgtgggag atcgcgtgac tattacttgc 540

cgcgccagcc agagtattag ctctatctg aattggtacc agcaaaagcc cggaaggcc 600

cctaagcttc tgatttctgg cgctctctt tgaagtcag gtgtgccaag cagatttagc 660

gggtctggaa gtggcactga ctttacctt actatctcca gcctgcccc agaggatttt 720
 gccacatatt actgtcagca aagctactct actccaatca ctttcggcca gggcacaaga 780
 ttggagatta agagggtgc cgcactttca aattccatca tgtatttcag ccattttgtg 840
 cctgttttc ttccggccaa acctacaacc actcccgccc cagccccacc tactcccgcc 900
 cctaccattg cctcccagcc tctgtctctt agacctgagg cttgtagacc tgctgccggc 960
 ggagccgtgc aactcgcgg tctggacttc gcctgcgaca tctatatctg ggcccctctg 1020
 gccggcacct gggcggttct ctttctctca ctgtaatca cactctattg caatcacagg 1080
 aacagatcca aaagaagccg cctgtccat agcgattaca tgaatatgac tccacgccgc 1140
 cctggcccca caaggaaaca ctaccagcct tacgcaccac cttagagattt cgctgcctat 1200
 cggagcaggg tgaagtttc cagatctgca gatgcaccag cgtatcagca gggccagaac 1260
 caactgtata acgagctcaa cctgggacgc agggaagagt atgacgtttt ggacaagcgc 1320
 agaggacggg acctgagat ggggtggcaaa 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> 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

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> anti-CLL-1 CAR construct

<400> 211
caggtgcagt tggtgcaaag cggcgcagaa gtaagaaac ctggggcgctc agttaaggctg 60
tcttgcaaag tatctggcta taccctcact gagctgtcca tgcattgggt aaggcaggct 120
cctggaaagg ggctcgaatg gatgggagga ttgaccctg aagacggaga gaccatctac 180
gccagaaat tccagggtag agtaacagtg actgaggaca ctagcactga cacagcgta 240
atggagctga gttctctgag aagtgaggac acagccgttt actactgcgc taccgagtcc 300
agaggtattg gctggccata cttcgactat tggggtcagg gcacctgggt tacagtgagt 360
tcaggaggcg ggggctctgg ggggggcggg tccggagggg ggggctcaga tatacagatg 420
acgcagagtc catcaagtct ctacgccagc gtgggagatc gcgtgactat tacttgccgc 480
gccagccaga gtattagctc ctatctgaat tggtagcagc aaaagcccgg gaaggcccct 540
aagcttctga tttctggcg ctcctctttg aagtcagggt tgccaagcag atttagcggg 600
tctggaagtg gcactgactt tacacttact atctccagcc tgccccaga ggattttgcc 660
acatattact gtcagcaaag ctactctact ccaatcactt tcggccaggg cacaagattg 720
gagattaaga gggctgccgc actttcaaat tccatcatgt attcagcca tttgtgcct 780
gtttttcttc cgccaaacc tacaaccact cccgcccac gccacctac tcccgccct 840
accattgcct cccagcctct gtctcttaga cctgaggctt gtagacctgc tgccggcgga 900
gccgtgcaca ctgcgggtct ggacttcgcc tgcgacatct atatctgggc ccctctggcc 960
ggcacctgcg gcgttctcct tctctcactc gtaatcacac tctattgcaa tcacaggaac 1020
agatcaaaa gaagccgcct gtcctatagc gattacatga atatgactcc acgccgcct 1080
ggccccacaa ggaaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 1140

agcagggtga agttttccag atctgcagat gcaccagcgt atcagcaggg ccagaaccaa 1200
 ctgtataacg agctcaacct gggacgcagg gaagagtatg acgttttgga caagcgaga 1260
 ggacgggacc ctgagatggg tggcaaacca agacgaaaaa acccccagga gggctcttat 1320
 aatgagctgc agaaggataa gatggctgaa gcctattctg aaataggcat gaaaggagag 1380
 cggagaaggg gaaaagggca cgacggtttg taccaggacgac tcagcactgc tacgaaggat 1440
 acttatgacg ctctccacat gcaagccctg ccacctagg 1479

<210> 212
 <211> 493
 <212> PRT
 <213> Artificial Sequence

<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

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> anti-CLL-1 CAR construct

<400> 213

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtcc agttggtcga aagtggcggg ggtgtagtgc agccgggccg cagtttgagg 120

cttcctgtg cggttcagg ctttactttt tccagctatg gaatgcactg ggtgcggcag 180

gccccgggca aaggacttga gtgggtggcc gtcatttctt atgacggatc agataagtac 240

tacgtggaca gcgtaaggg cagattcacc atctctaggg acaacagtaa aaatagactc 300
 tacctccaga tgaatagcct cagagctgaa gacacggccg tctactattg tgctcgggag 360
 cggtatagtg gcagagacta ctgggggcag ggacactcg ttacagttag tagcggcgga 420
 ggagggagtg ggggcggtgg ctccggtgga ggaggttctg agattgttat gaccagagt 480
 cctgcgaccc tctcagtcag ccccggggag cgcgcaactt tgtcttcag agctagtcag 540
 tccgtgtcct ctctctgac atggtaccag caaaagcccg ggcaggctcc gcgcctttg 600
 atctttgggg ctcaacaag agccactggg attcccgac gattctctgg ctccgggagc 660
 ggtactggtt tcacctgac gattagcagt ctccagagcg aggacttcgc cgtatactac 720
 tgccagcagt acgatacgtg gccattcact ttggaccag ggactaaagt ggattttaag 780
 cgcgccgccc ctctcgataa cgaaaagtca aatggcacca taatccacgt caaaggcaag 840
 cacctgtgcc ctccccgct ctccccgga ccagtaaac cattttgggt gctggtgtt 900
 gtggggggcg tgctggcctg ctatagcctt ttggtcactg tagccttcat tatttttgg 960
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 cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat 1080
 cggagcaggg tgaagtttc cagatctgca gatgcaccag cgtatcagca gggccagaac 1140
 caactgtata acgagctcaa cctgggacgc aggggaagagt atgacgtttt ggacaagcgc 1200
 agaggacggg accctgagat ggggtggcaaa 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> 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> anti-CLL-1 CAR construct

<400> 215
cagggtccagt tggtcgaaag tggcgggtggt gtagtgcagc cgggccgcag ttgaggcct 60
tcctgtgcgg cttcaggcct 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 acactcgta cagtgagtag cggcggagga 360
gggagtgggg gcggtggctc cggaggagga ggttctgaga ttgttatgac ccagagtcct 420
gcgaccctct cagtcagccc cggggagcgc gcaactttgt cttgcagagc tagtcagtcc 480
gtgtcctctc ttctgacatg gtaccagcaa aagcccgggc aggctccgcg cctttgatc 540
tttgggctt caacaagagc cactgggatt ccgcacgat tctctggctc cgggagcgg 600
actggttca ccctgacgat tagcagtctc cagagcgagg acttcgccgt atactactgc 660
cagcagtacg atacgtggcc attcactttt ggaccaggga ctaaagtgga tttaagcgc 720
gccgccgctc tcgataacga aaagtcaat ggcaccataa tccacgtcaa aggcaagcac 780
ctgtgccctt ccccgtctt ccccgaccc agtaaaccat ttgggtgct ggtgtgtg 840
gggggcgtgc tggcctgcta tagcctttg gtcactgtag ccttcattat ttttgggtc 900
agatccaaaa gaagccgcct gctccatagc gattacatga atatgactcc acgccgcct 960
ggccccacaa ggaaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 1020
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ctgtataacg agctcaacct gggacgcagg gaagagtatg acgttttga caagcgaga 1140
ggacgggacc ctgagatggg tggcaaacca agacgaaaaa acccccagga ggtctctat 1200

aatgagctgc agaaggataa gatggctgaa gcctattctg aaataggcat gaaaggagag 1260
 cggagaaggg gaaaaggga cgacggttg taccaggga tcagcactgc tacgaaggat 1320
 acttatgacg ctctccacat gcaagccctg ccacctagg 1359

<210> 216
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<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

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

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> anti-CLL-1 CAR construct

<400> 217

atggcactcc ccgtaactgc tctgtgtctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtgc agctcgtgga gtctggcggc ggcgtgggcc agcccgccg gtcctgcgc 120

ctgtcctgcg ccgccagcgg gtttactttt tctctctacg gcatgcactg ggtgcgccag 180

gctcccgga agggcctcga gtgggtcgcc gtgatctcat acgatgggtc agacaaatac 240

tatgtcgatt ctgttaaagg gcggtttacc attcaagag ataactctaa gaataggctg 300

tatttgcaga tgaacagcct gagggctgaa gataccgcag tgtactattg cgctagggag 360

cggtatagtg gccgcgatta ctggggacag ggtacactgg tgaccgtgag ctctgggggt 420

ggcggaagcg ggggtggcgg aagcggcgga gggggtagt aaattgtgat gaccagttct 480

ccggctacac tttagtctc ccttggggag agagctacac tgatcatgcag agcgtcccag 540

tccgtctctt ctctccttac ctggtatcag cagaagcccc gccaggctcc tcgactgctg 600

atcttcggtg cctccacaag ggcgaccggg attccagccc gcttctcagg ttctgggagc 660

ggaactgggt tcactttgac aatcagttca ctgcagtcag aggatttcgc cgtgtactac 720

tgccagcaat acgacacatg gccattcact ttcggacccg gtaccaaagt cgatttcaag 780
 agagccgcgg ccatcgaggt tatgtacca ccaccatac tggacaatga aaaaagcaat 840
 ggaaccatta tccatgtgaa gggtaaacac ctctgcccta gccactttt ccctggccca 900
 tcaaagccct tctgggtctt ggtggctgtg ggggggtgtg tggcctgtta cagccttctg 960
 gtgacgggtg ctttcattat ctctgggtt agatccaaaa gaagccgcct gctccatagc 1020
 gattacatga atatgactcc acgccgcctt ggccccacaa ggaaacacta ccagccttac 1080
 gcaccaccta gagatttcgc tgcctatcgg agcagggtga agttttccag atctgcagat 1140
 gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg 1200
 gaagagtatg acgttttga caagcgaga ggacgggacc ctgagatggg tggcaaacca 1260
 agacgaaaaa acccccagga gggctcttat aatgagctgc agaaggataa gatggctgaa 1320
 gcctattctg aaatagcat gaaaggagag cggagaaggg gaaaaggga cgacggttg 1380
 taccaggac tcagactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440
 ccacctaggt aa 1452

<210> 218
 <211> 483
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-CLL-1 CAR construct

<400> 218

Met Ala Leu Pro Val Thr Ala 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 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
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> anti-CLL-1 CAR construct

<400> 219

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cagggtgcagc tcgtggagtc tggcggcggc gtggtccagc ccggccggtc cctgcgcctg    60
tcctgcgccg ccagcggggt tactttttcc tctacggca tgcactgggt gcgccaggct    120
cccggcaagg gcctcgagtg ggtcgccgtg atctcatagc atgggtcaga caaatactat    180
gtcgattctg ttaaagggcg gtttaccatt tcaagagata actctaagaa taggctgtat    240
ttgcagatga acagcctgag ggctgaagat accgcagtgt actattgcgc tagggagcgg    300
tatagtggcc gcgattactg gggacagggt aacttggtga ccgtgagctc tgggggtggc    360
ggaagcgggg gtggcggaag cggcggaggg ggtagtga aa ttgtgatgac ccagtctccg    420
gctacacttt cagtctcccc tggggagaga gctacactgt catgcagagc gtcccagtcc    480
gtctcttctc tccttacctg gtatcagcag aagcccggcc aggctcctcg actgctgac    540
ttcgggtgct ccacaagggc gaccgggatt ccagcccgt tctcagggtc tgggagcggg    600
actggttca ctttgacaat cagttcactg cagtcagagg atttcgccgt gtactactgc    660
cagcaatacg acacatggcc attcacttc ggacccggta ccaaagtcga ttcaagaga    720
gccgcggcca tcgaggttat gtaccacca ccatactgg acaatgaaa aagcaatgga    780
accattatcc atgtgaaggg taaacacctc tgcctagcc cacttttccc tggcccatca    840
aagcccttct gggcttgggt ggtcgtgggg ggtgtgctgg cctgttacag ctttctggtg    900
acggttgctt tcattatctt ctgggttaga tcaaaaagaa gccgcctgct ccatagcgat    960
tacatgaata tgactccagc ccgcctggc ccacaagga aacactacca gccttacgca   1020
ccacctagag atttcgtgc ctatcggagc aggtgaagt ttccagatc tgcagatgca   1080
ccagcgtatc agcaggggcca gaaccaactg tataacgagc tcaacctggg acgcagggaa   1140
gagtatgacg ttttgacaa gcgcagagga cgggaccctg agatgggtgg caaaccaaga   1200
cgaaaaaacc ccagggaggg tctctataat gagctgcaga aggataagat ggctgaagcc   1260
tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggtttgtac   1320
cagggactca gcaactgtac gaaggatact tatgacgctc tccacatgca agccctgcca   1380
cctagg
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1386

<210> 220
<211> 462
<212> PRT
<213> Artificial Sequence

<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 Ser 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

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> anti-CLL-1 CAR construct

<400> 221
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccgcagggtgc agttgggtga atcaggaggg ggtgtggtgc aaccgggtcg gtcactgcgc 120
ctcagttgtg ctgcttccgg gtttactttc agctcatatg ggatgcactg ggtacggcag 180
gctccaggta aaggcttga atgggtggcg gtgatcagct atgacggctc tgacaaatat 240
tatgtggact ccgtgaaagg cagattcacc atcagtcgag acaactcaa gaatagactc 300
tactgcaga tgaatagcct ccgggccgaa gatactgcag tctattattg cgccgggag 360
cgctacagtg gaagagacta ttggggggcaa ggaactcttg tcacagtctc atctggcggc 420
ggcggcagcg gtggggggcg atctggcggg ggcggcagcg aaatcggtat gactcagagt 480
cctgccacac tgagcgtag ccctggtgag agagcaacac ttagctgcag agctagtcag 540
agtgtttcca gtcttttgac atggtaccaa cagaagccc gtcaagctcc acgactgctc 600
atcttcggtg catccaccg cgcaaccggg atacccgcc gggtttccgg ttctggaagt 660
ggcacaggat tcacgctcac cattttctct ctgcagtctg aagactttgc cgtgtattac 720
tgccagcagt acgatacctg gccctttacc ttggcccag gtactaaagt ggattttaaa 780
cgagctgctg cactttccaa tagtattatg tacttttcac atttgtgcc cgtgttctg 840
cctgcgaagc ctacgacaac ccagcccct aggccgccca caccggcccc aactattgcc 900

tccagccat tgtctctgag acccgaagct tgcagacctg ctgctggagg cgccgttcac 960
 acccgaggat tggatttcgc atgtgacatt tacatctggg cccctttggc cggaacctgc 1020
 ggtgtgctgc tgctgtcact cgtgattaca ctttactgca accaccgaaa cagatccaaa 1080
 agaagccgcc tgctccatag cgattacatg aatatgactc cacgccgcc tggccccaca 1140
 aggaaacact accagcctta cgcaccacct agagatttcg ctgcctatcg gagcagggtg 1200
 aagttttcca gatctgcaga tgcaccagcg tatcagcagg gccagaacca actgtataac 1260
 gagctcaacc tgggacgcag ggaagagtat gacgttttgg acaagcgag aggacgggac 1320
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 cagaaggata agatggctga agcctattct gaaataggca tgaaaggaga gcggagaagg 1440
 ggaaaagggc acgacggttt gtaccaggga ctgagcactg ctacgaagga tacttatgac 1500
 gctctccaca tgcaagccct gccacctagg taa 1533

<210> 222
 <211> 510
 <212> PRT
 <213> Artificial Sequence

<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 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> anti-CLL-1 CAR construct

<400> 223

cagggtgcagt tgggtgaatc aggaggggggt gtggtgcaac ccggtcggtc actgcgcctc 60
agttgtgctg cttccgggtt tactttcagc tcatatggga tgcactgggt acggcaggct 120
ccaggtaaag gcttggaatg ggtggcgggtg 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
ggcagcgggtg ggggcggatc tggcgggggc ggcagcgaag tcgttatgac tcagagtcct 420
gccacactga gcgttagccc tggtagaga gcaacactta gctgcagagc tagtcagagt 480
gtttccagtc tttgacatg gtaccaacag aagcccggtc aagctccacg actgctcatc 540
ttcgggtgat ccacccgcgc aaccgggata cccgcccggt tttccgggtc tggaagtggc 600
acaggattca cgctcacatc ttctctctg cagtctgaag actttgccgt gtattactgc 660
cagcagtagc atacctggcc ctttacctt ggcccaggta ctaaagtga tttaaacga 720
gctgctgcac ttccaatag tattatgtac tttcacatt ttgtgccgt gttctgcct 780
gcgaagccta cgacaacccc agcccctagg ccgccacac cggccccaac tattgcctcc 840
cagccattgt ctctgagacc cgaagcttc agacctgctg ctggaggcgc cgttcacacc 900
cgaggattgg atttcgatg tgacatttac atctggggcc ctttgccgg aacctgcggt 960
gtgctgctgc tgtactcgt gattacactt tactgcaacc accgaaacag atccaaaaga 1020
agccgcctgc tccatagcga ttacatgaat atgactccac gccgccctgg cccacaagg 1080
aaacactacc agccttacgc accacctaga gatttcgctg cctatcgag cagggtgaag 1140
ttttccagat ctgcagatgc accagcgtat cagcagggcc agaaccaact gtataacgag 1200
ctcaacctgg gacgcaggga agagtatgac gttttggaca agcgcagagg acgggaccct 1260
gagatgggtg gcaaaccaag acgaaaaaac cccaggagg gtctctataa tgagctgcag 1320
aaggataaga tggctgaagc ctattctgaa ataggcatga aaggagagcg gagaaggga 1380
aaagggcacg acggtttgta ccagggactc agcactgcta cgaaggatac ttatgacgt 1440
ctccacatgc aagccctgcc acctagg 1467

<210> 224
<211> 489
<212> PRT
<213> Artificial Sequence

<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 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 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> anti-CLL-1 CAR construct

<400> 225

atggcactcc ccgtaactgc tctgctgctg ccgttgccat tgctcctgca cgccgcacgc 60
ccggagattg tgatgacca gtccctgct accctgtccg tcagtccggg cgagagagcc 120
acctgtcat gccgggccag ccagtccgtc agcagtctcc tgacttggtg tcagcaaaaa 180
ccagggcagg caccgcggct ttgattttt ggtgcaagca cacgcgccac tggcattcca 240
gctaggtttt ctggaagtgg atctgggaca ggcttcactc tgacaatcag tagcctgcag 300
agtgaggact ttgctgttta ctactgtcaa cagtacgaca cctggccatt cacattcggg 360
cccggcacca aggtcgactt caagaggggc ggtggagggt cagggtggtg cgggtcaggc 420
ggcgggtgggt ctcagggtca actggtggaa tcagggtggcg gcgttggtcca accggggcga 480
tcacttcgac ttctctgtgc tgcctcaggc ttacttttt catcctatgg gatgcactgg 540
gttcggcagg ctcccgaaa aggactcgag tgggttcag tgatcttta cgatggctca 600
gacaagtatt atgtggactc agtcaagggg agattcacia 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 ccagtcacct ctccacagga ccatctaaac ccttctgggt tctggtagta 900
gttgaggggg tccttgcagt ttactccctt ttgtcaccg tcgccttcatt tttttctgg 960
gtgagatcca aaagaagccg cctgctccat agcgattaca tgaatatgac tccacgccgc 1020
cctggcccca caaggaaaca ctaccagcct tacgcaccac ctagagattt cgctgcctat 1080
cggagcaggg tgaagtttcc cagatctgca gatgcaccag cgtatcagca gggccagaac 1140
caactgtata acgagctcaa cctgggacgc aggggaagagt atgacgtttt ggacaagcgc 1200
agaggacggg accctgagat ggggtggcaaa ccaagacgaa aaaaccccca ggagggtctc 1260
tataatgagc tgcagaagga taagatggct gaagcctatt ctgaaatagg catgaaagga 1320
gagcggagaa ggggaaaagg gcacgacggt ttgtaccagg gactcagcac tgctacgaag 1380
gatacttatg acgtctcca catgcaagcc ctgccaccta ggtaa 1425

<210> 226
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CLL-1 CAR construct

<400> 226

Met Ala Leu Pro Val Thr Ala 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
 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> anti-CLL-1 CAR construct

<400> 227

gagattgtga tgaccagtc cctgctacc ctgtccgtca gtccgggcga gagagccacc 60
ttgtcatgcc gggccagcca gtccgtcagc agtctcctga cttggtatca gcaaaaacca 120
gggcaggcac cgcggctttt gatatttgggt gcaagcacac gcgccactgg cattccagct 180
aggttttctg gaagtggatc tgggacaggc ttcactctga caatcagtag cctgcagagt 240
gaggactttg ctgtttacta ctgtcaacag tacgacacct ggccattcac attcgggccc 300
ggcaccaagg tcgacttcaa gaggggcggg ggaggttcag gtggtggcgg gtcaggcggc 360
ggtgggtctc aggttcaact ggtggaatca ggtggcggcg ttgtccaacc ggggcgatca 420
cttcgacttt cctgtgctgc ctgaggcttt acttttcat cctatgggat gcactgggtt 480
cggcaggctc ccgaaaagg 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
ctgtgcccc agtcccctctt cccaggacca tctaaacct tctgggttct ggtagtagtt 840
ggaggggtcc ttgcatgtta ctcccctttg gtcaccgtcg ccttcattat ttctgggtg 900
agatccaaaa gaagccgcct gtcctatagc gattacatga atatgactcc acgccgcct 960
ggccccacaa ggaaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 1020
agcagggtga agttttccag atctgcagat gcaccagcgt atcagcaggg ccagaaccaa 1080
ctgtataacg agctcaacct gggacgcagg gaagagtatg acgttttga caagcgaga 1140
ggacgggacc ctgagatggg tggcaaacca agacgaaaaa acccccagga gggctcttat 1200
aatgagctgc agaaggataa gatggctgaa gcctattctg aaataggcat gaaaggagag 1260
cggagaaggg gaaaagggca cgacggttg taccagggac tcagcactgc tacgaaggat 1320
acttatgacg ctctccacat gcaagccctg ccacctagg 1359

<210> 228

<211> 453

<212> PRT

<213> Artificial Sequence

<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

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> anti-CLL-1 CAR construct

<400> 229
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60
ccggagatcg tcatgacaca gaggccagct accctgagcg tgtcccctgg agagagagcc 120
accctgtcct gtagggctag tcagagtgtg tccagcctcc tcacctgga tcaacagaag 180
cctggtaag cccccggct gcttatcttc ggggccagca cgcgagccac aggcattccc 240
gccagattct ctggctctgg cagtggcacc ggggtcactc tcacgatctc atccctgcag 300
tcagaggatt tcgctgtgta ttactgtcag cagtacgata catggccctt caccttcggc 360
ccgggcacaa aagtagattt caagcgcggc ggcgggggta gtgggggcgg gggatcagga 420
ggagggggct cccaagtaca gctggtgag agcggcgcg ggggtggtca gcccgggcgc 480
agcctcaggc tgagttgcgc agcatcagga ttcacattca gttcttatgg aatgcattgg 540
gtcagacagg ctccgggaa gggccttgaa tgggtggcag tcattagcta cgacggaagc 600
gataagtact atgtggactc agttaaagg agatttacta tcagccgca caattcaaa 660
aacagattgt attgcagat gaactccctc agggcgagg aactgctgt atattactgc 720
gcacgagaga gatactccg ccgagactat tggggccaag gaacattggt aactgtgagc 780
tccgccgag ctattgagg catgtacccc ccaccttacc tcgataatga gaagagtaat 840
gggactataa ttcacgtaaa gggcaaacac ctgtgccctt ccccgctgt tccaggtcca 900
agtaagccgt tctgggtcct ggttgtgtg ggaggggtgc tggcctgcta ttctctgtg 960
gttaccgtgg cttttatcat ttctgggtg agatccaaaa gaagccgcct gtcctatagc 1020
gattacatga atatgactcc acgccgcct ggccccacaa ggaaacacta ccagccttac 1080

gcaccaccta gagatttcgc tgcctatcgg agcagggtga agttttccag atctgcagat 1140
gcaccagcgt atcagcaggg ccagaaccaa ctgtataacg agctcaacct gggacgcagg 1200
gaagagtatg acgttttggga caagcgcaga ggacgggacc ctgagatggg tggcaaacca 1260
agacgaaaaa acccccagga gggctcttat aatgagctgc agaaggataa gatggctgaa 1320
gcctattctg aaatagggcat gaaaggagag cggagaaggg gaaaagggca cgacggtttg 1380
taccagggac tcagactgc tacgaaggat acttatgacg ctctccacat gcaagccctg 1440
ccacctaggt aa 1452

<210> 230
<211> 483
<212> PRT
<213> Artificial Sequence

<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

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
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> anti-CLL-1 CAR construct

<400> 231

gagatcgtca tgacacagag tccagctacc ctgagcgtgt ccctggaga gagagccacc 60

ctgtcctgta gggctagtca gagtgtgtcc agcctctca cctggatatca acagaagcct 120

ggtcaagctc cccggctgct tatcttcggg gccagcacgc gagccacagg catcccggcc 180

agattctctg gctctggcag tggcaccggg ttcacttca cgatctcatc cctgcagtca 240

gaggatttcg ctgtgtatta ctgtcagcag tacgatacat ggcccttcac ctctggcccg 300
ggcacaaaag tagatttcaa gcgcggcggc gggggtagtg ggggcggggg atcaggagga 360
gggggctccc aagtacagct ggttgagagc ggccggcggg tggttcagcc cgggcgcagc 420
ctcaggctga gttgcgcagc atcaggattc acattcagtt cttatggaat gcattgggtc 480
agacaggctc ccgggaaggg ccttgaatgg gtggcagtca ttagctacga cggaagcgat 540
aagtactatg tggactcagt taaagggaga ttactatca gccgcgacaa ttcaaaaac 600
agattgtatt tgcagatgaa ctccctcagg gcggaggaca ctgctgtata ttactgcgca 660
cgagagagat actccggccg agactattgg ggccaaggaa cattggtaac tgtgagctcc 720
gccgcagcta ttgaggctat gtacccccca ccttatctcg ataatgagaa gagtaatggg 780
actataattc acgtaaaggg caaacacctg tgccctccc cgctgttcc aggtccaagt 840
aagccgttct gggctctggt tgtggtggga ggggtgctgg cctgctattc tctgttggt 900
accgtggcct ttatcatttt ctgggtgaga tcaaaaagaa gccgcctgct ccatagcgat 960
tacatgaata tgactccacg ccgcctggc ccacaagga aacactacca gccttacgca 1020
ccacctagag atttcgtgc ctatcggagc aggggtgaagt ttccagatc tgcagatgca 1080
ccagcgtatc agcagggcca gaaccaactg tataacgagc tcaacctggg acgcagggaa 1140
gagtatgacg ttttgacaa gcgcagagga cgggacctg agatgggtgg caaaccaaga 1200
cgaaaaaacc ccaggaggg tctctataat gagctgcaga aggataagat ggctgaagcc 1260
tattctgaaa taggcatgaa aggagagcgg agaaggggaa aagggcacga cggttgtac 1320
cagggactca gcactgctac gaaggatact tatgacgctc tccacatgca agccctgcca 1380
cctagg 1386

<210> 232

<211> 462

<212> PRT

<213> Artificial Sequence

<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

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

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> anti-CLL-1 CAR construct

<400> 233
atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccggaaatag tgatgactca gtccccggcc accctcagcg tgtcccccg ggagcgagcg 120

accctgtcat gcagggcttc ccagagtgtc agctccctgc tacttggtg tcagcaaaag 180

ccggggcagg ctccccgct cctcatcttc ggggcatcaa ctagggccac cggcattcct 240

gcaagatttt ccgggtctgg cagcggcacc ggcttcaccc ttaccattag ctctctgcag 300

tctgaggact tcgccgttta ctattgtcag cagtatgata ctggccctt taccttcggt 360

cccggaacta aggtggactt caagcgcggg ggggggtggat ctggaggtgg tggctccggg 420

ggcgggtgaa gccaggtcca gttggttgag agcggcggcg gagtgggtgca gcccgggagg 480

tccttgccgc tgagctgtgc agcctccggt ttacttttt ctagctatgg aatgcattgg 540

gtaagacagg ctcccgaaa aggctcagag tgggtggcgg tcattagcta tgatggatct 600

gataaatact atgtggactc agttaagggg cgcttcacaa tctcaagaga caatagcaaa 660

aatagactgt acctgcagat gaatagtctg cgcgccgagg aactgccgt gtactactgc 720

gcccgcgaga gatacagcg acgggattac tggggccagg gtaccctcgt aacggtgtcc 780

tccgtgccg cccttagcaa cagcattatg tacttttctc atttcgtgcc agtctttctc 840

ccagcaaagc ccaccactac cccggcccc aggccgccta ctctgcccc cactatcgcg 900

tctcagcctc tctccttgcg gcccgaggcc tgccggccag ccgcaggggg cgccgtacat 960

actcgggggt tggatttcgc ttgcgacata tatatttggg cccccctgc cggcacatgt 1020

ggagtgtctg tctgagtct cgttataacc ctctattgca accatagaaa cagatccaaa 1080

agaagccgcc tgctccatag cgattacatg aatatgactc cagccgccc tggccccaca 1140

aggaaacact accagcctta cgcaccacct agagatttcg ctgcctatcg gagcagggtg 1200

aagttttcca gatctgcaga tgcaccagcg tatcagcagg gccagaacca actgtataac 1260

gagctcaacc tgggacgcag ggaagagtat gacgttttgg acaagcgag aggacgggac 1320

cctgagatgg gtggcaaacc aagacgaaaa aacccccagg agggctctcta taatgagctg 1380
 cagaaggata agatggctga agcctattct gaaataggca tgaaaggaga gcggagaagg 1440
 ggaaaagggc acgacgggtt gtaccaggga ctacgactg ctacgaagga tacttatgac 1500
 gctctccaca tgcaagccct gccacctagg taa 1533

<210> 234
 <211> 510
 <212> PRT
 <213> Artificial Sequence

<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
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

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> 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 ggccctttac ctccggtccc 300
ggaactaagg tggacttcaa gcgcgggggg ggtggatctg gaggtggtgg ctccgggggc 360
ggtggaagcc aggtccagtt ggttgagagc ggcggcggag tggcgcagcc cgggaggtcc 420
ttgcggctga gctgtgcagc ctccggtttt actttttcta gctatggaat gcattgggta 480
agacaggctc ccgaaaaagg cctcgagtgg gtggcggta ttagctatga tggatctgat 540
aaatactatg tggactcagt taaggggcgc ttcacaatct caagagacaa tagcaaaaat 600
agactgtacc tgcagatgaa tagtctgcgc gccgaggaca ctgccgtgta ctactgcgc 660
cgcgagagat acagcggacg ggattactgg ggccagggta ccctcgtaac ggtgtcctcc 720
gctgccgccc ttagcaacag cattatgtac ttttctcatt tcgtgccagt ctttctcca 780
gcaaagccca ccactacccc ggccccagg ccgcctactc ctgccccac tatcgcgtct 840
cagcctctct ctttgcggcc cgaggcctgc cggccagccg cagggggcgc cgtacatact 900
cggggtttgg atttcgcttg cgacatatat atttgggcc ccctcgccgg cacatgtgga 960
gtgctgctcc tgagtctcgt tataaccctc tattgcaacc atagaaacag atccaaaaga 1020
agccgcctgc tccatagcga ttacatgaat atgactccac gccgcctgg cccacaagg 1080
aaacactacc agccttacgc accacctaga gatttcgctg cctatcgag cagggtgaag 1140
tttccagat ctgcagatgc accagcgtat cagcagggcc agaaccaact gtataacgag 1200
ctcaacctgg gacgcaggga agagtatgac gttttggaca agcgcagagg acgggaccct 1260
gagatgggtg gcaaaccaag acgaaaaaac cccaggagg 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> 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

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

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> 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> CD8 extracellular & transmembrane domain

<400> 238
gctgcagcat tgagcaactc aataatgtat ttagtcact ttgtaccagt gttcttgccg 60
gctaagccta ctaccacacc cgctccacgg ccacctaccc cagctcctac catcgcttca 120
cagcctctgt ccttgcgccc agaggcttgc cgaccggccg cagggggcgc tgttcatacc 180
agaggactgg atttcgcctg cgatatctat atctgggcac ccctggccgg aacctgcggc 240
gtactctgctg tgtccctggg catcacgctc tattgtaatc acaggaac 288

<210> 239
<211> 96
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8 extracellular & transmembrane Domain

<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> extracellular and intracellular domains

<400> 240

cttgataatg aaaagtcaaa cggaacaatc attcacgtga agggcaagca cctctgtccg 60

tcacccttgt tcctgggtcc atccaagcca ttctgggtgt tggctgtagt ggggtggagtc 120

ctcgcttggt actctctgct cgtcaccgtg gcttttataa tcttctgggt tagatccaaa 180

agaagccgcc tgctccatag cgattacatg aatatgactc cagccgccc tggccccaca 240

aggaaacact accagcctta cgcaccacct agagatttcg ctgcctatcg gagc 294

<210> 241

<211> 98

<212> PRT

<213> Artificial Sequence

<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> 10E3_CHD_DNA

<400> 242

atggcactcc ccgtaactgc tctgctgctg ccgttggcat tgctcctgca cgccgcacgc 60

ccgcaggtga ccctcaaaga gtctggaccc gtgctcgtaa aacctacgga gaccctgaca 120

ctcacctgca cagtctccgg ctcagcctc atcaatgcca ggatgggagt ttctggatc 180

aggcaaccgc ccggaaaggc cctggaatgg ctgcacata tttcagtaa cgctgaaaaa 240

agctatcgga ctctctgaa aatcgggctc acgattagta aggacacatc caagagccaa 300

gtgggtgctta cgatgactaa catggaccct gtggatactg caacctatta ctgtgctcga 360

atccctgggt atggcggaaa tggggactac cactactacg gtatggatgt ctggggccaa 420

gggaccacgg ttactgtttc aagcggaggg ggagggagtg ggggtggcgg atctggcggg 480

ggaggcagcg atatccagat gacgcagtc cctagttcac ttccgcac cctgggggat 540

cgggttacca ttacatgccg cgcgtcacag ggtatccgga atgatctggg atggtaggag 600
 cagaagccgg gaaaggctcc taagcgctc atctacgcca gctccaccct gcagagtggg 660
 gtgccctccc gggtttcagg cagtggctcc ggtacggagt ttactcttac aattagcagc 720
 ctgcagccag aagattttgc aacttactac tgtttgcagc ataataattt cccctggacc 780
 ttgggtcagg gcaccaaggt ggagatcaaa agagcagccg ccatcgaagt aatgtatccc 840
 cccccgtacc ttgacaatga gaagtcaaat ggaaccatta tccatgttaa gggcaaacac 900
 ctctgccctt ctccactgtt ccttggcctt agtaagccgt ttgggtgct ggtggtagtc 960
 ggtggggtgc tggtttgta ctctcttctc gtgaccgtcg cttttataat cttttgggtc 1020
 agatccaaaa gaagccgcct gctccatagc gattacatga atatgactcc acgccgcctt 1080
 ggccccacaa ggaaacacta ccagccttac gcaccaccta gagatttcgc tgcctatcgg 1140
 agccgagtga aattttctag atcagctgat gctccgcct atcagcaggg acagaatcaa 1200
 ctttacaatg agctgaacct gggtcgcaga gaagagtacg acgttttga caaacgccgg 1260
 ggccgagatc ctgagatggg ggggaagccg agaaggaaga atcctcaaga aggcctgtac 1320
 aacgagcttc aaaaagacaa aatggctgag gcgtactctg agatcggcat gaagggcgag 1380
 cggagacgag gcaagggta cgtggcttg tatcagggcc tgagtacagc cacaaggac 1440
 acctatgacg cctccacat gcaggcactg cccccacgct ag 1482

<210> 243
 <211> 493
 <212> PRT
 <213> Artificial Sequence

<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> 10E3_THD_DNA

<400> 244
atggcactcc cgttaactgc tctgtgtcg ccgttggcat tgctcctgca cgccgcacgc 60
ccgcaagtta ctttgaagga gtctggacct gtactggtga agccaaccga gacactgaca 120
ctcacgtgta cagtgaagg ttttccttg atcaacgcaa ggatgggctg cagctggatc 180
aggcaacccc ctggcaaggc tctggaatgg ctgcctcaca tattcagcaa tgccgaaaaa 240
agctaccgga caagcctgaa atcccgcctg actatttcca aggacacttc taagtctcag 300
gtggtgctga ccatgaccaa catggaccgc gtggacaccg ccacctatta ctgcgcaaga 360
atccctgggt atggtgggaa tgggtactac cattattatg ggatggatgt gtgggggcaa 420
ggcacaaccg taacggtctc aagcgggtgg ggaggctcag ggggcggagg ctccggaggt 480
ggcgggtccg acattcagat gacccaaagc ccgtccagcc tgtccgccag cctgggagat 540
agagtgacaa tcacgtgtag agcttcccaa gggataagaa atgatctcgg gtggtatcag 600
cagaagcccc gcaaagcccc caaaaggctt atatatgcta gtagtacact gcagtctgga 660
gttccttccc gattttcagg tagcggctcc ggtacagagt tcacctcac gataagctca 720
ctccagcctg aggatttgc aacgtactac tgcctccagc acaacaattt tcctggact 780
ttcggccagg gcaccaaggt ggagatcaag agggccgctg cccttgataa tgaaaagtca 840
aacggaacaa tcattcacgt gaagggaag cacctctgtc cgtcacctt gtccctggt 900
ccatccaagc cattctgggt gttggtcgta gtgggtggag tcctcgctg ttactctctg 960
ctcgtcaccg tggttttat aatcttctgg gttagatcca aaagaagccg cctgctccat 1020
agcgattaca tgaatatgac tccacgccgc cctggcccca caaggaaaca ctaccagcct 1080
tacgaccac ctagagattt cgctgcctat cggagccgag tgaaatttc tagatcagct 1140
gatgctccc cctatcagca gggacagaat caacttaca atgagctgaa cctgggtcgc 1200
agagaagagt acgacgtttt ggacaaacgc cggggccgag atcctgagat gggggggaag 1260
ccgagaagga agaatcctca agaaggcctg tacaacgagc ttcaaaaaga caaatggct 1320

gaggcgtact ctgagatcgg catgaagggc gagcggagac gaggcaaggg tcacgatggc 1380

ttgtatcagg gcctgagtac agccacaaag gacacctatg acgccctcca catgcaggca 1440

ctgccccac gctag 1455

<210> 245

<211> 484

<212> PRT

<213> Artificial Sequence

<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> 8B5_CHD_DNA

<400> 246

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ctgtcatgcg tggcgtctgg cttcacattc aagaactacg gcatgcactg ggtgacacag 180

gcccccgaa agggtttggg gtgggtcgcc gtgatctggt acgacggatc taatgagtat 240

tacggagatc ctgtgaaggg aaggttcacc atctcccgcg acaatagcaa aaatagtctc 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 gattgcaga 540
 gcaagccagt cagtctctc ttctttctg gcctggatc agcaaaaacc aggtcaggca 600
 ccatctctcc tgatttacct tgccagcaga cgggcggctg gcattcccga caggttctct 660
 ggaagcggat ctgggaccga tttaccctg acaattagcc gcttgagacc cgaagacttt 720
 ggtatgtttt actgccagca ctacggaagg acaccttca catttggccc gggcacgaaa 780
 gtcgatataa aacgcgcagc cgccattgaa gtaatgtacc caccacctta ttggacaat 840
 gaaaagtcca atggtacctat tattcacgtc aagggaagc atctctgtcc aagccctctg 900
 ttccccggcc cctccaaacc attctgggtg ctggtggctg tcggcggagt tctggcctgc 960
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 ctgctccata gcgattacat gaatatgact ccacgccgcc ctggccccac aaggaaacac 1080
 taccagcctt acgcaccacc tagagatttc gctgcctatc ggagccgagt gaaattttct 1140
 agatcagctg atgctccgc ctatcagcag ggacagaatc aactttacaa tgagctgaac 1200
 ctgggtcgca gagaagagta cgacgttttg gacaaacgcc ggggccgaga tcctgagatg 1260
 ggggggaagc cgagaaggaa gaatcctcaa gaaggcctgt acaacgagct taaaaagac 1320
 aaaatggctg aggcgtactc tgagatcggc atgaaggcg agcggagacg aggcaagggt 1380
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 atgcaggcac tgccccacg ctag 1464

<210> 247
 <211> 487
 <212> PRT
 <213> Artificial Sequence

<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> 8B5_THD_DNA

<400> 248
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ctctcttggt tggcaagcgg atttacctt aagaactatg gcatgcactg ggtgaggcag 180
gcccctggaa aaggactgga gtgggttgct gtgatctggt acgacgggtc caacgaatat 240
tatggcgatc ctgtgaaggg acggtttaca atctcacgcg ataactcaa gaacatgctg 300
tacctgcaaa tgaactctct gcgcgctgat gacactgccg tgtattattg cgctcggagt 360
ggtatcgccg tcgcaggagc atttgattat tgggggcaag ggaccctctg gacagtgagt 420
tccggagggg gaggttctgg tggaggcggc tctgtgggg gaggcagcga gatcgttctg 480
accagcttc ctgacacact gtcactgtcc cctggtgaaa aggccacact gtctttaga 540
gcgtcccaga gcgtttccag ttcttcctt gcatggtatc aaaaaaac cgggcaggct 600
ccaagcttc tgatctacgt ggccagccgc cggccgcag gcatccctga taggtttagc 660
ggttctggga gcgggacgga cttcacctg acaatatcac ggctggaacc cgaagacttc 720
ggaatgtttt attgccagca ctacggaaga actccattca ctttggccc gggaacgaag 780
gtagacatca agagagcagc agccctcgac aacagaaaat ccaatggaac cattatccat 840
gtgaagggga aacatctctg ccctcacca ttgtccctg gaccagcaa gccttttgg 900
gttctggtcg tggtaggggg cgctctggct tgttactccc tctcgttac agtcgccttc 960
ataatctttt gggttagatc caaaagaagc gcctgctcc atagcgatta catgaatatg 1020
actccacgcc gccctggccc cacaaggaaa cactaccagc cttacgcacc acctagagat 1080
ttcgtgcct atcgagaccg agtgaaattt tctagatcag ctgatgctcc cgctatcag 1140
caggacaga atcaacttta caatgagctg aacctgggtc gcagagaaga gtacgacgtt 1200
ttgacaaaac gccggggccg agatcctgag atggggggga agccgagaag gaagaatcct 1260

caagaaggcc tgtacaacga gcttcaaaaa gacaaaatgg ctgaggcgta ctctgagatc 1320

ggcatgaagg gcgagcggag acgaggcaag ggtcacgatg gcttgatca gggcctgagt 1380

acagccacaa aggacaccta tgacgccctc cacatgcagg cactgcccc acgctag 1437

<210> 249

<211> 478

<212> PRT

<213> Artificial Sequence

<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