

305072_1.txt
SEQUENCE LISTING

<110> Noile-Immune Biotech Inc.

<120> Chimera antigen receptor

<130> PC25381

<150> JP2017-061461

<151> 2017-03-27

<160> 68

<170> PatentIn version 3.5

<210> 1

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> VH region of anti-GM2 antibody for VL15VH

<400> 1

gaagtgcagc tggatgcagtc cggagccgag gtgaaaaagc ctggcgcctc cgtcaaggtg 60

agctgcaagg ccagcggcta tacattcacc gactataaca tggactgggt gaagcagagc 120

cccggccagg gactggagt gatgggctac atctaccca ataacggcgg caccggctac 180

aaccagaagt tcaagtcaa ggtgaccatc accgtggaca ccagcaccag caccgcctac 240

atggaactgc acagcctcag aagcgaagac accgctgtgt actactgcgc cacctacggc 300

cactactacg gctacatgtt cgcctactgg ggacagggca ccctggtgac cgtcagcagc 360

<210> 2

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> VH region of anti-GM2 antibody

<400> 2

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr

20

25

30

Asn Met Asp Trp Val Lys Gln Ser Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

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

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

Ala Thr Tyr Gly His Tyr Tyr Gly Tyr Met Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 3
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> VL region of anti-GM2 antibody for VL15VH

<400> 3
gacatccagc tgaccagtc ccctagcagc ctgtccgcta gccccggaga cagagtgacc 60
atcacctgtt ccgccagctc cagcgtgagc tacatgcact gggtccagca gaagcccggc 120
aaggcccca agctgtggat ctacagcacc agcaacctgg cttccggcgt gcctgccaga 180
ttttccggct ccggcagcgg cacaagctac tccctgacca tcagcagact gcagcccgaa 240
gacatcgcca cctactactg tcagcagagg agcagctacc cctacacctt cggcggcggc 300
accaaggtgg agatcaag 318

<210> 4
<211> 106
<212> PRT

<213> Artificial Sequence

<220>

<223> VL region of anti-GM2 antibody

<400> 4

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

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

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

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

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

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

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

<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Linker 15 for VL15VH

<400> 5

ggcggcggcg gaagcggagg cggcggcagc ggcggaggcg gaagc

45

<210> 6

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker 15

<400> 6

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 7

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Linker 25 for VL25VH

<400> 7

agctccgctg acgacgctaa gaaggacgct gccaagaagg acgacgcaa gaaggatgac 60

gccaaaaaag acggc 75

<210> 8

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker 25

<400> 8

Ser Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala
 1 5 10 15

Lys Lys Asp Asp Ala Lys Lys Asp Gly
 20 25

<210> 9

<211> 723

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-GM2scFv (VL15VH)

<400> 9

gacatccagc tgaccagtc ccctagcagc ctgtccgcta gccccggaga cagagtgacc 60

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atcacctgtt ccgccagctc cagcgtgagc tacatgcact ggttccagca gaagcccggc      120
aaggcccca agctgtggat ctacagcacc agcaacctgg cttccggcgt gcctgccaga      180
ttttccggct ccggcagcgg cacaagctac tccctgacca tcagcagact gcagcccga      240
gacatcgcca cctactactg tcagcagagg agcagctacc cctacacctt cggcggcggc      300
accaaggtgg agatcaaggg cggcggcgga agcggaggcg gcggcagcgg cggaggcgga      360
agcgaagtgc agctgggtgca gtccggagcc gaggtgaaaa agcctggcgc ctccgtcaag      420
gtgagctgca aggccagcgg ctatacattc accgactata acatggactg ggtgaagcag      480
agccccggcc agggactgga gtggatgggc tacatctacc ccaataacgg cggcaccggc      540
tacaaccaga agttcaagtc caaggtgacc atcacctggg acaccagcac cagcaccgcc      600
tacatggaac tgcacagcct cagaagcgaa gacaccgctg tgtactactg cgccacctac      660
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agc                                                                    723

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<210> 10
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-GM2scFv (VL15VH)

<400> 10

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

```

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

```

```

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

```

```

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

```

```

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Leu Gln Pro Glu

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65

70

80

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

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln Ser
115 120 125

Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
130 135 140

Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Met Asp Trp Val Lys Gln
145 150 155 160

Ser Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Tyr Pro Asn Asn
165 170 175

Gly Gly Thr Gly Tyr Asn Gln Lys Phe Lys Ser Lys Val Thr Ile Thr
180 185 190

Val Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu Leu His Ser Leu Arg
195 200 205

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Thr Tyr Gly His Tyr Tyr
210 215 220

Gly Tyr Met Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
225 230 235 240

Ser

<210> 11
<211> 753
<212> DNA
<213> Artificial Sequence

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<220>

<223> anti-GM2scFv (VL25VH)

<400> 11

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gatatccaac tgaccagtc cccttcagc ctgagcgctt cccccggaga cagggtgaca      60
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aagggcccca agctgtggat ctactccaca agcaacctgg cctccggcgt gcctgccaga     180
tttagcggaa gcggcagcgg cacatcctac agcctgacca tctccaggct gcagcccagag    240
gacatcgcca catactactg ccagcagagg tccagctacc cttacacatt cggaggcggc     300
accaaggtgg agatcaagag ctccgctgac gacgctaaga aggacgctgc caagaaggac     360
gacgccaaga aggatgacgc caaaaaagac ggcgaagtcc agctggtgca gagcggcgct     420
gaggtgaaga agcctggcgc cagcgtcaag gtgagctgta aggcctccgg ctacaccttc     480
accgactaca acatggattg ggtgaagcag agccccggac agggcctgga gtggatgggc     540
tacatctacc ccaacaacgg cggcaccggc tacaaccaga aattcaagtc caaggtgacc     600
atcaccgtgg acaccagcac atccaccgcc tacatggaac tgcacagcct gaggtccgag     660
gacacagccg tgtactactg cgctacctac ggccactact acggctacat gttcgcttac     720
tggggacagg gcaccctggt gaccgtgagc tcc                                     753

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<210> 12

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-GM2scFv (VL25VH)

<400> 12

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

```

```

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

```

```

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

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

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

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

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

Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala Lys Lys Asp Asp Ala Lys
115 120 125

Lys Asp Gly Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
130 135 140

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

Thr Asp Tyr Asn Met Asp Trp Val Lys Gln Ser Pro Gly Gln Gly Leu
165 170 175

Glu Trp Met Gly Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Gly Tyr Asn
180 185 190

Gln Lys Phe Lys Ser Lys Val Thr Ile Thr Val Asp Thr Ser Thr Ser
195 200 205

Thr Ala Tyr Met Glu Leu His Ser Leu Arg Ser Glu Asp Thr Ala Val
210 215 220

Tyr Tyr Cys Ala Thr Tyr Gly His Tyr Tyr Gly Tyr Met Phe Ala Tyr
225 230 235 240

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
245 250

305072_1.txt

<210> 13
 <211> 723
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-GM2scFv (VH15VL)

<400> 13
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 agctgtaagg cctccggcta caccttcacc gactacaaca tggactgggt caagcagagc 120
 cctggccagg gcctggagt gatgggctat atctaccca acaacggcgg caccggctac 180
 aaccagaagt tcaagagcaa ggtcaccatc accgtggaca cctccacctc cacagcctac 240
 atggagctgc acagcctgag gagcgaggat accgccgtgt actactgcgc tacctacggc 300
 cattactacg gatacatgtt cgcctactgg ggccagggaa ccctggtcac cgtgtcctcc 360
 ggaggaggag gaagcggagg cggcggctcc ggcgaggcg gatccgacat ccagctgaca 420
 caatccccca gcagcctgag cgctagcccc ggcgataggg tgacaattac ctgcagcgcc 480
 tccagctccg tgtcctacat gcactggttt cagcaaaagc ccggcaaggc ccctaagctg 540
 tggatctaca gcaccagcaa cctggccagc ggagtgcctg ccagatttag cggcagcggc 600
 agcggcacca gctacagcct gaccatcagc agactgcagc ccgaggatat cgccacctac 660
 tactgccagc agaggagctc ctaccctac acattcggcg gcggaaccaa ggtggagatc 720
 aag 723

<210> 14
 <211> 241
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-GM2scFv (VH15VL)

<400> 14

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr

20

25

30

Asn Met Asp Trp Val Lys Gln Ser Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

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

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

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

Ala Thr Tyr Gly His Tyr Tyr Gly Tyr Met Phe Ala Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser
 130 135 140

Ser Leu Ser Ala Ser Pro Gly Asp Arg Val Thr Ile Thr Cys Ser Ala
 145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Lys
 165 170 175

Ala Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val
 180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
 195 200 205

Ile Ser Arg Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln
 210 215 220

Arg Ser Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile

225

230

240

Lys

<210> 15
<211> 753
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-GM2scFv (VH25VL)

<400> 15
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agctgcaaag ccagcggcta taccttcacc gactacaaca tggactgggt gaagcagagc 120
cccggccaag gcctcgagtg gatgggatac atctaccca acaacggcgg caccggctac 180
aaccagaagt tcaagagcaa ggtgaccatc accgtggaca catccacaag caccgcctat 240
atggagctcc acagcctgag gagcaggagc accgccgtgt actactgcgc cacctacggc 300
cactactacg gctatatgtt cgcctactgg ggccagggca ccctgggtgac agtgtcctcc 360
tccagcgccg atgatgcaa gaaggatgcc gccaaaaagg acgacgctaa gaaggatgac 420
gccaagaagg acggcgatat ccagctgaca cagagcccta gctccctgag cgctagccct 480
ggcgacagag tgaccatcac ctgcagcgcc agctccagcg tgagctacat gcaactggttc 540
cagcagaaac ccggcaaggc cccaagctg tggatctaca gcaccagcaa tctggctagc 600
ggcgtgcctg ccaggttttag cggatccggc agcggcacct cctactccct gacaatctcc 660
agactgcagc ccgaggacat cgccacctac tactgccaac agaggtcctc ctaccctac 720
accttcggcg gcggcaccaa agtggagatc aag 753

<210> 16
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-GM2scFv (VH25VL)

<400> 16

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

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

Asn Met Asp Trp Val Lys Gln Ser Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

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

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

Ala Thr Tyr Gly His Tyr Tyr Gly Tyr Met Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ser Ser Ala Asp Asp Ala Lys Lys
115 120 125

Asp Ala Ala Lys Lys Asp Asp Ala Lys Lys Asp Asp Ala Lys Lys Asp
130 135 140

Gly Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Pro
145 150 155 160

Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
165 170 175

Met His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile
180 185 190

Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
195 200 205

305072_1.txt

Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Leu Gln Pro
 210 215 220

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Tyr
 225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 245 250

<210> 17
 <211> 165
 <212> DNA
 <213> Homo sapiens

<400> 17
 ttcgtgccgg tcttcctgcc agcgaagccc accacgacgc cagcgccgcg accaccaaca 60
 ccggcgccca ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg 120
 gcggggggcg cagtgcacac gagggggctg gacttcgcct gtgat 165

<210> 18
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 18

Phe Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro
 1 5 10 15

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
 20 25 30

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
 35 40 45

Gly Leu Asp Phe Ala Cys Asp
 50 55

<210> 19
 <211> 63
 <212> DNA

<213> Homo sapiens

<400> 19

atctacatct gggcgccctt ggccgggact tgtggggtcc ttctcctgtc actggttatc 60

acc 63

<210> 20

<211> 21

<212> PRT

<213> Homo sapiens

<400> 20

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15

Ser Leu Val Ile Thr
20

<210> 21

<211> 21

<212> DNA

<213> Homo sapiens

<400> 21

ctttactgca accacaggaa c 21

<210> 22

<211> 7

<212> PRT

<213> Homo sapiens

<400> 22

Leu Tyr Cys Asn His Arg Asn
1 5

<210> 23

<211> 123

<212> DNA

<213> Homo sapiens

<400> 23

aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc ccgccgcccc 60

gggcccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 120

tcc

123

<210> 24
 <211> 41
 <212> PRT
 <213> Homo sapiens

<400> 24

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> 25
 <211> 138
 <212> DNA
 <213> Homo sapiens

<400> 25
 cgtttctctg ttgttaaacg gggcagaaag aagctcctgt atatattcaa acaaccattt 60
 atgagaccag taaaactac tcaagaggaa gatggctgta gctgccgatt tccagaagaa 120
 gaagaaggag gatgtgaa 138

<210> 26
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 26

Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
 1 5 10 15

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
 20 25 30

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu

35

40

45

<210> 27
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 27
 ctgagagtga agttcagcag gagcgcagac gccccgcgt accagcaggg ccagaaccag 60
 ctctataacg agctcaatct aggacgaaga gaggagtacg atgttttgga caagagacgt 120
 ggccgggacc ctgagatggg gggaaagccg agaaggaaga accctcagga aggcctgtac 180
 aatgaactgc agaaagataa gatggcggag gcctacagtg agattgggat gaaaggcgag 240
 cgccggaggg gcaaggggca cgatggcctt taccagggtc tcagtacagc caccaaggac 300
 acctacgacg cccttcacat gcaggccctg cccctcgc 339

<210> 28
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 28

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
 1 5 10 15

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
 20 25 30

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

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

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

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
 85 90 95

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Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
 100 105 110

Arg

<210> 29
 <211> 849
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD8 (hinge)_CD8 (transmembrane)_CD28 (signaling)_4-1BB
 (signaling)_CD3z (signaling)

<400> 29
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 ccggcgccca ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg 120
 gcggggggcg cagtgcacac gagggggctg gacttcgcct gtgatattcta catctgggagc 180
 cccttgggcg ggacttgtgg ggtccttctc ctgtcactgg ttatcacctt ttactgcaac 240
 cacaggaaca ggagtaagag gagcaggctc ctgcacagtg actacatgaa catgactccc 300
 cgccgccccg ggcccacccg caagcattac cagccctatg cccaccacg cgacttcgca 360
 gcctatcgct cccgtttctc tgttggttaa cggggcagaa agaagctcct gtatatattc 420
 aaacaacat ttatgagacc agtacaact actcaagagg aagatggctg tagctgccga 480
 tttccagaag aagaagaagg aggatgtgaa ctgagagtga agttcagcag gagcgagac 540
 gccccgcgt accagcaggg ccagaaccag ctctataacg agctcaatct aggacgaaga 600
 gaggagtacg atgttttgga caagagacgt ggccgggacc ctgagatggg gggaaagccg 660
 agaaggaaga accctcagga aggcctgtac aatgaactgc agaaagataa gatggcggag 720
 gcctacagtg agattgggat gaaaggcgag cgccggaggg gcaaggggca cgatggcctt 780
 taccagggtc tcagtacagc caccaaggac acctacgacg cccttcacat gcaggccctg 840
 cccctcgc 849

<210> 30
 <211> 283

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<212> PRT

<213> Artificial Sequence

<220>

<223> CD8 (hinge)_CD8 (transmembrane)_CD28 (signaling)_4-1BB
(signaling)_CD3z (signaling)

<400> 30

Phe Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro
1 5 10 15

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
20 25 30

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
35 40 45

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
50 55 60

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

His Arg Asn Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
85 90 95

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
100 105 110

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Phe Ser Val
115 120 125

Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe
130 135 140

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

Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser
165 170 175

305072_1.txt

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
180 185 190

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
195 200 205

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
210 215 220

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
225 230 235 240

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
245 250 255

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
260 265 270

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
275 280

<210> 31
<211> 86
<212> DNA
<213> Artificial Sequence

<220>
<223> EcoRI_F2A-NsiI

<400> 31
gaattcggaa gcggagtgaacacagactttg aattttgacc ttctcaagtt ggcgggagac 60
gtggagtcca accctggacc atgcat 86

<210> 32
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> EcoRI_F2A-NsiI

<400> 32

305072_1.txt

Glu Phe Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys
1 5 10 15

Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Cys
20 25

<210> 33
<211> 909
<212> DNA
<213> Artificial Sequence

<220>
<223> IL7_F2A_CCL19_SalI

<400> 33
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ctaattggtca gcatcgatca attattggac agcatgaaag aaattggttag caattgcctg 180
aataatgaat ttaacttttt taaaagacat atctgtgatg ctaataagga aggtatgttt 240
ttattccgtg ctgctcgcaa gttgaggcaa tttcttaaaa tgaatagcac tgggtgatttt 300
gatctccact tattaataagt ttcagaaggc acaacaatac tgttgaactg cactggccag 360
gttaaaggaa gaaaaccagc tggcctgggt gaagcccaac caacaaagag tttggaagaa 420
aataaatctt taaaggaaca gaaaaaactg aatgacttgt gtttcctaaa gagactatta 480
caagagataa aaacttggtg gaataaaatt ttgatgggca ctaaagaaca cggaagcgga 540
gtgaaacaga ctttgaattt tgaccttctc aagttggcgg gagacgtgga gtccaaccct 600
ggacctatgg ccctgctact ggccctcagc ctgctggttc tctggacttc cccagcccca 660
actctgagtg gcaccaatga tgctgaagac tgctgcctgt ctgtgacca gaaaccatc 720
cctgggtaca tcgtgaggaa cttccactac cttctcatca aggatggctg cagggtgcct 780
gctgtagtgt tcaccacact gaggggccgc cagctctgtg caccaccaga ccagccctgg 840
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taagtcgac 909

<210> 34

305072_1.txt

<211> 300
<212> PRT
<213> Artificial Sequence

<220>

<223> IL7_F2A_CCL19_SalI

<400> 34

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Leu Pro Pro Leu Ile
1 5 10 15

Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Glu Gly Lys
20 25 30

Asp Gly Lys Gln Tyr Glu Ser Val Leu Met Val Ser Ile Asp Gln Leu
35 40 45

Leu Asp Ser Met Lys Glu Ile Gly Ser Asn Cys Leu Asn Asn Glu Phe
50 55 60

Asn Phe Phe Lys Arg His Ile Cys Asp Ala Asn Lys Glu Gly Met Phe
65 70 75 80

Leu Phe Arg Ala Ala Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ser
85 90 95

Thr Gly Asp Phe Asp Leu His Leu Leu Lys Val Ser Glu Gly Thr Thr
100 105 110

Ile Leu Leu Asn Cys Thr Gly Gln Val Lys Gly Arg Lys Pro Ala Ala
115 120 125

Leu Gly Glu Ala Gln Pro Thr Lys Ser Leu Glu Glu Asn Lys Ser Leu
130 135 140

Lys Glu Gln Lys Lys Leu Asn Asp Leu Cys Phe Leu Lys Arg Leu Leu
145 150 155 160

Gln Glu Ile Lys Thr Cys Trp Asn Lys Ile Leu Met Gly Thr Lys Glu
165 170 175

305072_1.txt

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

Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Met Ala Leu Leu Leu Ala
195 200 205

Leu Ser Leu Leu Val Leu Trp Thr Ser Pro Ala Pro Thr Leu Ser Gly
210 215 220

Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser Val Thr Gln Lys Pro Ile
225 230 235 240

Pro Gly Tyr Ile Val Arg Asn Phe His Tyr Leu Leu Ile Lys Asp Gly
245 250 255

Cys Arg Val Pro Ala Val Val Phe Thr Thr Leu Arg Gly Arg Gln Leu
260 265 270

Cys Ala Pro Pro Asp Gln Pro Trp Val Glu Arg Ile Ile Gln Arg Leu
275 280 285

Gln Arg Thr Ser Ala Lys Met Lys Arg Arg Ser Ser
290 295 300

<210> 35
<211> 2112
<212> DNA
<213> Artificial Sequence

<220>
<223> IL7_F2A_CCL19_HSVtK_SalI

<400> 35
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cccgtaggcca gctccgactg tgacatcgaa ggaaaggatg gcaagcagta cgaaagcgtg 120
ctgatggtga gcatcgatca gctcctggat tccatgaagg aaatcggctc caactgcctc 180
aacaatgagt tcaacttttt taagaggcat atctgcgacg ccaacaagga gggcatgttt 240
ctgttcaggg ccgccaggaa gctgagacag ttcttcaaga tgaatagcac cggcgacttc 300

305072_1.txt

gacctccatc tgctgaaggt gtccgaggga accaccatcc tgctgaactg caccggccaa	360
gtgaagggaa gaaaacctgc tgccctgggc gaggctcagc ctaccaagag cctcgaggag	420
aacaaaagcc tgaaggagca gaagaagctg aacgacctgt gcttcctcaa gaggctcctg	480
caggagatta agacctgttg gaacaagatc ctgatgggca caaaggagca cggatccggc	540
gtgaagcaga ccctgaactt tgacctgctc aaactggccg gcgacgtcga gtccaatcct	600
ggacctatgg ctctgctgct cgccctgagc ctgctcgtcc tctggacctc ccctgctcct	660
accctgagcg gcaccaatga cgctgaagac tgctgcctgt ccgtgacca gaagcctatc	720
cccggatata tcgtgaggaa ttttcattac ctctgatca aggacggctg tagagtgtcc	780
gccgtcgtgt tcacaacact cagaggcagg cagctgtgtg cccccccga ccagccttgg	840
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ggcagcggag tgaagcagac actgaatttc gacctgctca agctggccgg cgatgtggag	960
agcaaccctg gacctatggc ttcctacccc ggacatcagc acgcttccgc cttcgaccag	1020
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gaggccaccg aggtgaggcc cgagcagaaa atgcccaccc tgctgagagt gtatatgtat	1140
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cccacactgc ctggcacaaa tatcgtgctc ggcgccctgc ctgaggacag gcacatcgat	1620
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agggaagact ggggccaact gagcggcaca gctgtgcctc ctcaaggcgc tgagccccag	1800
agcaacgctg gaccagacc tcacatcggc gataccctgt tcaccctgtt tagagcccct	1860

305072_1.txt

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 gccaagagac tcaggagcat gcacgtcttc attctggact acgaccagtc ccccgctggc 1980
 tgcagagatg ccctgctcca gctgacctcc ggcatgggtgc agaccacgt gaccaccct 2040
 ggaagcatcc ccacaatctg cgacctggcc aggacctttg ccagagaaat gggagaagcc 2100
 aactgagtcg ac 2112

<210> 36
 <211> 701
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL7_F2A_CCL19_HSVtK_SalI

<400> 36

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Leu Pro Pro Leu Ile
 1 5 10 15

Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Glu Gly Lys
 20 25 30

Asp Gly Lys Gln Tyr Glu Ser Val Leu Met Val Ser Ile Asp Gln Leu
 35 40 45

Leu Asp Ser Met Lys Glu Ile Gly Ser Asn Cys Leu Asn Asn Glu Phe
 50 55 60

Asn Phe Phe Lys Arg His Ile Cys Asp Ala Asn Lys Glu Gly Met Phe
 65 70 75 80

Leu Phe Arg Ala Ala Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ser
 85 90 95

Thr Gly Asp Phe Asp Leu His Leu Leu Lys Val Ser Glu Gly Thr Thr
 100 105 110

Ile Leu Leu Asn Cys Thr Gly Gln Val Lys Gly Arg Lys Pro Ala Ala
 115 120 125

305072_1.txt

Leu Gly Glu Ala Gln Pro Thr Lys Ser Leu Glu Glu Asn Lys Ser Leu
130 135 140

Lys Glu Gln Lys Lys Leu Asn Asp Leu Cys Phe Leu Lys Arg Leu Leu
145 150 155 160

Gln Glu Ile Lys Thr Cys Trp Asn Lys Ile Leu Met Gly Thr Lys Glu
165 170 175

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

Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Met Ala Leu Leu Leu Ala
195 200 205

Leu Ser Leu Leu Val Leu Trp Thr Ser Pro Ala Pro Thr Leu Ser Gly
210 215 220

Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser Val Thr Gln Lys Pro Ile
225 230 235 240

Pro Gly Tyr Ile Val Arg Asn Phe His Tyr Leu Leu Ile Lys Asp Gly
245 250 255

Cys Arg Val Pro Ala Val Val Phe Thr Thr Leu Arg Gly Arg Gln Leu
260 265 270

Cys Ala Pro Pro Asp Gln Pro Trp Val Glu Arg Ile Ile Gln Arg Leu
275 280 285

Gln Arg Thr Ser Ala Lys Met Lys Arg Arg Ser Ser Gly Ser Gly Val
290 295 300

Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu
305 310 315 320

Ser Asn Pro Gly Pro Met Ala Ser Tyr Pro Gly His Gln His Ala Ser
325 330 335

305072_1.txt

Ala Phe Asp Gln Ala Ala Arg Ser Arg Gly His Ser Asn Arg Arg Thr
340 345 350

Ala Leu Arg Pro Arg Arg Gln Gln Glu Ala Thr Glu Val Arg Pro Glu
355 360 365

Gln Lys Met Pro Thr Leu Leu Arg Val Tyr Ile Asp Gly Pro His Gly
370 375 380

Met Gly Lys Thr Thr Thr Thr Gln Leu Leu Val Ala Leu Gly Ser Arg
385 390 395 400

Asp Asp Ile Val Tyr Val Pro Glu Pro Met Thr Tyr Trp Arg Val Leu
405 410 415

Gly Ala Ser Glu Thr Ile Ala Asn Ile Tyr Thr Thr Gln His Arg Leu
420 425 430

Asp Gln Gly Glu Ile Ser Ala Gly Asp Ala Ala Val Val Met Thr Ser
435 440 445

Ala Gln Ile Thr Met Gly Met Pro Tyr Ala Val Thr Asp Ala Val Leu
450 455 460

Ala Pro His Ile Gly Gly Glu Ala Gly Ser Ser His Ala Pro Pro Pro
465 470 475 480

Ala Leu Thr Leu Ile Phe Asp Arg His Pro Ile Ala Ala Leu Leu Cys
485 490 495

Tyr Pro Ala Ala Arg Tyr Leu Met Gly Ser Met Thr Pro Gln Ala Val
500 505 510

Leu Ala Phe Val Ala Leu Ile Pro Pro Thr Leu Pro Gly Thr Asn Ile
515 520 525

Val Leu Gly Ala Leu Pro Glu Asp Arg His Ile Asp Arg Leu Ala Lys
530 535 540

305072_1.txt

Arg Gln Arg Pro Gly Glu Arg Leu Asp Leu Ala Met Leu Ala Ala Ile
545 550 555 560

Arg Arg Val Tyr Gly Leu Leu Ala Asn Thr Val Arg Tyr Leu Gln Cys
565 570 575

Gly Gly Ser Trp Arg Glu Asp Trp Gly Gln Leu Ser Gly Thr Ala Val
580 585 590

Pro Pro Gln Gly Ala Glu Pro Gln Ser Asn Ala Gly Pro Arg Pro His
595 600 605

Ile Gly Asp Thr Leu Phe Thr Leu Phe Arg Ala Pro Glu Leu Leu Ala
610 615 620

Pro Asn Gly Asp Leu Tyr Asn Val Phe Ala Trp Ala Leu Asp Val Leu
625 630 635 640

Ala Lys Arg Leu Arg Ser Met His Val Phe Ile Leu Asp Tyr Asp Gln
645 650 655

Ser Pro Ala Gly Cys Arg Asp Ala Leu Leu Gln Leu Thr Ser Gly Met
660 665 670

Val Gln Thr His Val Thr Thr Pro Gly Ser Ile Pro Thr Ile Cys Asp
675 680 685

Leu Ala Arg Thr Phe Ala Arg Glu Met Gly Glu Ala Asn
690 695 700

<210> 37
<211> 1641
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-hCD20 CAR

<400> 37
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305072_1.txt

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tccggcagcg gcagcggcac aagctatagc ctgaccatct ccagagtgga ggccgaggat	300
gccgccacct actactgcca gcagtggacc agcaaccccc ccacattcgg aggcggcacc	360
aagctggaga tcaaaggcgg aggcggcagc ggcgaggcgg gcagcggagg cggaggaagc	420
caagtgcagc tgcagcagcc tggagctgag ctggtgaagc ctggcgcctc cgtcaagatg	480
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cccggaagag gcctggagt gatcggagcc atctacccc gcaacggcga taccagctat	600
aaccagaagt tcaagggcaa ggccaccctc accgccgaca agagcagcag caccgcctac	660
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tactatggcg gcgactggta cttcaacgtg tggggcgccg gaacaaccgt gaccgtgagc	780
gccgcggccg cattcgtgcc ggtcttcctg ccagcgaagc ccaccacgac gccagcgccg	840
cgaccaccaa caccggcgcc caccatcgcg tcgcagcccc tgtccctgcg cccagaggcg	900
tgccggccag cggcgggggg cgcagtcac acgagggggc tggacttcgc ctgtgatatc	960
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aacatgactc ccgcccgc cgggcccacc cgcaagcatt accagcccta tgccccacca	1140
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tgtagctgcc gatttccaga agaagaagaa ggaggatgtg aactgagagt gaagttcagc	1320
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gggggaaagc cgagaaggaa gaaccctcag gaaggcctgt acaatgaact gcagaaagat	1500
aagatggcgg aggcctacag tgagattggg atgaaaggcg agcgccggag gggcaagggg	1560
cacgatggcc tttaccaggg tctcagtaca gccaccaagg acacctacga cgcccttcac	1620

atgcaggccc tgccccctcg c

1641

<210> 38
 <211> 547
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-hCD20 CAR

<400> 38

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

Ala His Ser Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala
 20 25 30

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

Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro
 50 55 60

Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe
 65 70 75 80

Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val
 85 90 95

Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn
 100 105 110

Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
 130 135 140

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

305072_1.txt

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp
165 170 175

Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr
180 185 190

Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala
195 200 205

Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
210 215 220

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

Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly Thr Thr
245 250 255

Val Thr Val Ser Ala Ala Ala Ala Phe Val Pro Val Phe Leu Pro Ala
260 265 270

Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
275 280 285

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
290 295 300

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
305 310 315 320

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

Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Ser Lys Arg Ser
340 345 350

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
355 360 365

305072_1.txt

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
370 375 380

Ala Tyr Arg Ser Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu
385 390 395 400

Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln
405 410 415

Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly
420 425 430

Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
435 440 445

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
450 455 460

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
465 470 475 480

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
485 490 495

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
500 505 510

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
515 520 525

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
530 535 540

Pro Pro Arg
545

<210> 39
<211> 2625
<212> DNA

<213> Artificial Sequence

<220>

<223> anti-GM2 CAR (VL15VH)

<400> 39

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acctgttccg ccagctccag cgtgagctac atgcactggg tccagcagaa gcccggaag	180
gcccccaagc tgtggatcta cagcaccagc aacctggctt ccggcgtgcc tgccagattt	240
tccggctccg gcagcggcac aagctactcc ctgaccatca gcagactgca gcccggaagac	300
atcgccacct actactgtca gcagaggagc agctaccctt acaccttcgg cggcggcacc	360
aaggtggaga tcaagggcgg cggcggaagc ggaggcggcg gcagcggcgg aggcggaagc	420
gaagtgcagc tgggtgcagtc cggagccgag gtgaaaaagc ctggcgcctc cgtcaagggtg	480
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cccgccagg gactggagtg gatgggctac atctaccca ataacggcgg caccggctac	600
aaccagaagt tcaagtcaa ggtgaccatc accgtggaca ccagcaccag caccgcctac	660
atggaactgc acagcctcag aagcgaagac accgctgtgt actactgcgc cacctacggc	720
cactactacg gctacatgtt cgcctactgg ggacagggca ccctgggtgac cgtcagcagc	780
gcggccgcat tcgtgccggt cttcctgcca gcgaagccca ccacgacgcc agcgccgcga	840
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tatatattca aacaaccatt tatgagacca gtacaaacta ctcaagagga agatggctgt	1260
agctgccgat ttccagaaga agaagaagga ggatgtgaac tgagagtga gttcagcagg	1320
agcgagacg cccccgcgta ccagcagggc cagaaccagc tctataacga gctcaatcta	1380

305072_1.txt

ggacgaagag aggagtacga tgtttttgac aagagacgtg gccgggaccc tgagatgggg	1440
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gatggccttt accagggtct cagtacagcc accaaggaca cctacgacgc ctttcacatg	1620
caggccctgc cccctcgcga attcggaagc ggagtgaaac agactttgaa ttttgacctt	1680
ctcaagttgg cgggagacgt ggagtccaac cctggaccat gcatgttcca tgtttctttt	1740
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tgtgatattg aaggtaaaga tggcaaaca tatgagagtg ttctaattggt cagcatcgat	1860
caattattgg acagcatgaa agaaattggt agcaattgcc tgaataatga atttaacttt	1920
tttaaaagac atatctgtga tgctaataag gaaggatatgt ttttattccg tgctgctcgc	1980
aagttgaggc aatttcttaa aatgaatagc actggtgatt ttgatctcca cttattaaaa	2040
gtttcagaag gcacaacaat actgttgaac tgcactggcc aggttaaagg aagaaaacca	2100
gctgccctgg gtgaagccca accaacaag agtttggag aaaataaatc tttaaaggaa	2160
cagaaaaaac tgaatgactt gtgtttccta aagagactat tacaagagat aaaaacttgt	2220
tggaataaaa ttttgatggg cactaaagaa cacggaagcg gagtgaaca gactttgaat	2280
tttgacctt tcaagttggc gggagacgtg gagtccaacc ctggacctat ggccctgcta	2340
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gatgctgaag actgctgcct gtctgtgacc cagaaaccca tccctgggta catcgtgagg	2460
aacttccact accttctcat caaggatggc tgcagggtgc ctgctgtagt gttcaccaca	2520
ctgaggggcc gccagctctg tgcaccccca gaccagccct gggtagaacg catcatccag	2580
agactgcaga ggacctcagc caagatgaag cgccgcagca gttaa	2625

<210> 40
 <211> 874
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-GM2 CAR (VL15VH)

<400> 40

305072_1.txt

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

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

Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
50 55 60

Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe
65 70 75 80

Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Leu
85 90 95

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

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
130 135 140

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

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Met Asp Trp
165 170 175

Val Lys Gln Ser Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Tyr
180 185 190

Pro Asn Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe Lys Ser Lys Val
195 200 205

305072_1.txt

Thr Ile Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu Leu His
210 215 220

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

His Tyr Tyr Gly Tyr Met Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
245 250 255

Thr Val Ser Ser Ala Ala Ala Phe Val Pro Val Phe Leu Pro Ala Lys
260 265 270

Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
275 280 285

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
290 295 300

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
305 310 315 320

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
325 330 335

Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg
340 345 350

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
355 360 365

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
370 375 380

Tyr Arg Ser Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu
385 390 395 400

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
405 410 415

305072_1.txt

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
420 425 430

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
435 440 445

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
450 455 460

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
465 470 475 480

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
485 490 495

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
500 505 510

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
515 520 525

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
530 535 540

Pro Arg Glu Phe Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu
545 550 555 560

Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Cys Met Phe
565 570 575

His Val Ser Phe Arg Tyr Ile Phe Gly Leu Pro Pro Leu Ile Leu Val
580 585 590

Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Glu Gly Lys Asp Gly
595 600 605

Lys Gln Tyr Glu Ser Val Leu Met Val Ser Ile Asp Gln Leu Leu Asp
610 615 620

305072_1.txt

Ser Met Lys Glu Ile Gly Ser Asn Cys Leu Asn Asn Glu Phe Asn Phe
625 630 635 640

Phe Lys Arg His Ile Cys Asp Ala Asn Lys Glu Gly Met Phe Leu Phe
645 650 655

Arg Ala Ala Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ser Thr Gly
660 665 670

Asp Phe Asp Leu His Leu Leu Lys Val Ser Glu Gly Thr Thr Ile Leu
675 680 685

Leu Asn Cys Thr Gly Gln Val Lys Gly Arg Lys Pro Ala Ala Leu Gly
690 695 700

Glu Ala Gln Pro Thr Lys Ser Leu Glu Glu Asn Lys Ser Leu Lys Glu
705 710 715 720

Gln Lys Lys Leu Asn Asp Leu Cys Phe Leu Lys Arg Leu Leu Gln Glu
725 730 735

Ile Lys Thr Cys Trp Asn Lys Ile Leu Met Gly Thr Lys Glu His Gly
740 745 750

Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly
755 760 765

Asp Val Glu Ser Asn Pro Gly Pro Met Ala Leu Leu Leu Ala Leu Ser
770 775 780

Leu Leu Val Leu Trp Thr Ser Pro Ala Pro Thr Leu Ser Gly Thr Asn
785 790 795 800

Asp Ala Glu Asp Cys Cys Leu Ser Val Thr Gln Lys Pro Ile Pro Gly
805 810 815

Tyr Ile Val Arg Asn Phe His Tyr Leu Leu Ile Lys Asp Gly Cys Arg
820 825 830

305072_1.txt

Val Pro Ala Val Val Phe Thr Thr Leu Arg Gly Arg Gln Leu Cys Ala
835 840 845

Pro Pro Asp Gln Pro Trp Val Glu Arg Ile Ile Gln Arg Leu Gln Arg
850 855 860

Thr Ser Ala Lys Met Lys Arg Arg Ser Ser
865 870

<210> 41
<211> 2655
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-GM2 CAR (VL25VH)

<400> 41
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atccaactga cccagtcccc ttccagcctg agcgcttccc ccggagacag ggtgacaatt 120
acctgcagcg ccagctcctc cgtgagctac atgcactggg tccagcagaa gcccggaag 180
gcccccaagc tgtggatcta ctccacaagc aacctggcct ccggcgtgcc tgccagattt 240
agcgggaagcg gcagcggcac atcctacagc ctgaccatct ccaggctgca gcccgaggac 300
atcgccacat actactgcca gcagaggtcc agctaccctt acacattcgg aggcggcacc 360
aaggtggaga tcaagagctc cgctgacgac gctaagaagg acgctgcca gaaggacgac 420
gccaagaagg atgacgcca aaaagacggc gaagtccagc tggtgcagag cggcgctgag 480
gtgaagaagc ctggcgccag cgtcaaggtg agctgtaagg cctccggcta caccttcacc 540
gactacaaca tggattgggt gaagcagagc cccggacagg gcctggagtg gatgggctac 600
atctacccca acaacggcgg caccggctac aaccagaaat tcaagtcaa ggtgaccatc 660
accgtggaca ccagcacatc caccgcctac atggaactgc acagcctgag gtccgaggac 720
acagccgtgt actactgcgc tacctacggc cactactacg gctacatgtt cgcttactgg 780
ggacagggca ccctggtgac cgtgagctcc gcggccgcat tcgtgccggt cttcctgcc 840
gcgaagccca ccacgacgcc agcgccgca ccaccaacac cggcgcccac catcgcgctc 900

305072_1.txt

cagccccctgt ccctgcgccc agaggcgtgc cggccagcgg cggggggcgc agtgcacacg	960
agggggctgg acttcgcctg tgatatctac atctgggcgc ccttggccgg gacttgtggg	1020
gtccttctcc tgtcactggt tatcaccctt tactgcaacc acaggaacag gagtaagagg	1080
agcaggctcc tgcacagtga ctacatgaac atgactcccc gccgccccgg gccacccgc	1140
aagcattacc agccctatgc cccaccacgc gacttcgcag cctatcgctc ccgtttctct	1200
gttgttaaac ggggcagaaa gaagctcctg tatatatcca aacaaccatt tatgagacca	1260
gtacaaacta ctcaagagga agatggctgt agctgccgat ttccagaaga agaagaagga	1320
ggatgtgaac tgagagtga gttcagcagg agcgcagacg ccccgcgta ccagcagggc	1380
cagaaccagc tctataacga gctcaatcta ggacgaagag aggagtacga tgttttggac	1440
aagagacgtg gccgggaccc tgagatgggg ggaaagccga gaaggaagaa ccctcaggaa	1500
ggcctgtaca atgaactgca gaaagataag atggcggagg cctacagtga gattgggatg	1560
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accaaggaca cctacgacgc cttcacatg caggccctgc cccctcgca attcggaagc	1680
ggagtgaac agactttgaa ttttgacctt ctcaagttgg cgggagacgt ggagtccaac	1740
cctggaccat gcatgttcca tgtttctttt aggtatatct ttggacttcc tcccctgac	1800
cttgttctgt tgccagtagc atcatctgat tgtgatattg aaggtaaaga tggcaaacaa	1860
tatgagagtg ttctaattgt cagcatcgat caattattgg acagcatgaa agaaattggt	1920
agcaattgcc tgaataatga atttaacttt tttaaaagac atatctgtga tgctaataag	1980
gaaggatatg ttttattccg tgctgctcgc aagttgaggc aatttcttaa aatgaatagc	2040
actggtgatt ttgatctcca cttattaaaa gtttcagaag gcacaacaat actgttgaac	2100
tgactggcc aggttaaagg aagaaaacca gctgccctgg gtgaagccca accaacaag	2160
agtttggaag aaaataaatc tttaaaggaa cagaaaaaac tgaatgactt gtgtttccta	2220
aagagactat tacaagagat aaaaacttgt tggaataaaa ttttgatggg cactaaagaa	2280
cacggaagcg gagtgaacaa gactttgaat tttgaccttc tcaagttggc gggagacgtg	2340
gagtccaacc ctggacctat ggccctgcta ctggccctca gcctgctggt tctctggact	2400
tccccagccc caactctgag tggcaccaat gatgctgaag actgctgcct gtctgtgacc	2460

305072_1.txt

cagaaaccca tccctgggta catcgtgagg aacttccact accttctcat caaggatggc 2520
 tgcaggggtgc ctgctgtagt gttcaccaca ctgagggggcc gccagctctg tgcaccccca 2580
 gaccagccct gggtagaacg catcatccag agactgcaga ggacctcagc caagatgaag 2640
 cgccgcagca gttaa 2655

<210> 42
 <211> 884
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> anti-GM2 CAR (VL25VH)

<400> 42

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

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

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

Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
 50 55 60

Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe
 65 70 75 80

Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Leu
 85 90 95

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

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

Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala Lys Lys Asp

130

135

140

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

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

Tyr Thr Phe Thr Asp Tyr Asn Met Asp Trp Val Lys Gln Ser Pro Gly
 180 185 190

Gln Gly Leu Glu Trp Met Gly Tyr Ile Tyr Pro Asn Asn Gly Gly Thr
 195 200 205

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

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

Thr Ala Val Tyr Tyr Cys Ala Thr Tyr Gly His Tyr Tyr Gly Tyr Met
 245 250 255

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

Ala Phe Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala
 275 280 285

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
 290 295 300

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
 305 310 315 320

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
 325 330 335

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys

340

345

350

Asn His Arg Asn Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
 355 360 365

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
 370 375 380

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Phe Ser
 385 390 395 400

Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
 405 410 415

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
 420 425 430

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
 435 440 445

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
 450 455 460

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
 465 470 475 480

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
 485 490 495

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
 500 505 510

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
 515 520 525

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
 530 535 540

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Glu Phe Gly Ser

545 550 555 560
 Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp
 565 570 575
 Val Glu Ser Asn Pro Gly Pro Cys Met Phe His Val Ser Phe Arg Tyr
 580 585 590
 Ile Phe Gly Leu Pro Pro Leu Ile Leu Val Leu Leu Pro Val Ala Ser
 595 600 605
 Ser Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser Val
 610 615 620
 Leu Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile Gly
 625 630 635 640
 Ser Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile Cys
 645 650 655
 Asp Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys Leu
 660 665 670
 Arg Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His Leu
 675 680 685
 Leu Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly Gln
 690 695 700
 Val Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr Lys
 705 710 715 720
 Ser Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn Asp
 725 730 735
 Leu Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp Asn
 740 745 750
 Lys Ile Leu Met Gly Thr Lys Glu His Gly Ser Gly Val Lys Gln Thr

755

760

765

Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro
 770 775 780

Gly Pro Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val Leu Trp Thr
 785 790 795 800

Ser Pro Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys
 805 810 815

Leu Ser Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe
 820 825 830

His Tyr Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe
 835 840 845

Thr Thr Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp
 850 855 860

Val Glu Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys
 865 870 875 880

Arg Arg Ser Ser

<210> 43
 <211> 2625
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> anti-GM2 CAR (VH15VL)

<400> 43
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 gtgcagctgg tgcagtccgg agccgaggtg aagaagcctg ggcgcagcgt gaaggtgagc 120
 tgtaaggcct ccggctacac cttcaccgac tacaacatgg actgggtcaa gcagagccct 180
 ggccagggcc tggagtggat gggctatatc tacccaaca acggcggcac cggctacaac 240

305072_1.txt

cagaagttca agagcaaggt caccatcacc gtggacacct ccacctccac agcctacatg	300
gagctgcaca gcctgaggag cgaggatacc gccgtgtact actgcgctac ctacggccat	360
tactacggat acatgttcgc ctactggggc cagggaaccc tggtcaccgt gtcctccgga	420
ggaggaggaa gcggaggcgg cggctccggc ggaggcggat ccgacatcca gctgacacaa	480
tccccagca gcctgagcgc tagccccggc gatagggtga caattacctg cagcgcctcc	540
agctccgtgt cctacatgca ctggtttcag caaaagcccc gcaaggcccc taagctgtgg	600
atctacagca ccagcaacct ggccagcggg gtgcctgcca gatttagcgg cagcggcagc	660
ggcaccagct acagcctgac catcagcaga ctgcagcccc aggatatcgc cacctactac	720
tgccagcaga ggagctccta cccctacaca ttcggcggcg gaaccaaggt ggagatcaag	780
gcggccgcat tcgtgccggt cttcctgcca gcgaagccca ccacgacgcc agcgccgcga	840
ccaccaacac cggcgcccac catcgcgtcg cagccccctgt ccctgcgccc agaggcgtgc	900
cggccagcgg cggggggcgc agtgcacacg agggggctgg acttcgcctg tgatatctac	960
atctgggcgc ctttggccgg gacttgtggg gtccttctcc tgtcactggt tatcaccctt	1020
tactgcaacc acaggaacag gagtaagagg agcaggctcc tgcacagtga ctacatgaac	1080
atgactcccc gccgccccgg gccacccgc aagcattacc agccctatgc cccaccacgc	1140
gacttcgcag cctatcgctc ccgtttctct gttgttaaag ggggcagaaa gaagctcctg	1200
tatatattca aacaaccatt tatgagacca gtacaaacta ctcaagagga agatggctgt	1260
agctgccgat ttccagaaga agaagaagga ggatgtgaac tgagagtga gttcagcagg	1320
agcgagacg cccccgcgta ccagcagggc cagaaccagc tctataacga gctcaatcta	1380
ggacgaagag aggagtacga tgttttggac aagagacgtg gccgggaccc tgagatgggg	1440
ggaaagccga gaaggaagaa ccctcaggaa ggcctgtaca atgaactgca gaaagataag	1500
atggcggagg cctacagtga gattgggatg aaaggcgagc gccggagggg caaggggcac	1560
gatggccttt accagggtct cagtacagcc accaaggaca cctacgacgc cttcacatg	1620
caggccctgc cccctcgcga attcggaaag ggagtgaaac agactttgaa ttttgacctt	1680
ctcaagttgg cgggagacgt ggagtccaac cctggacat gcatgttcca tgtttctttt	1740
aggtatatct ttggacttcc tcccctgatc cttgttctgt tgccagtagc atcatctgat	1800

305072_1.txt

tgtgatattg aaggtaaaga tggcaaacaa tatgagagtg ttctaattggt cagcatcgat 1860
caattattgg acagcatgaa agaaattggt agcaattgcc tgaataatga atttaacttt 1920
tttaaaagac atatctgtga tgctaataag gaaggtatgt ttttattccg tgctgctcgc 1980
aagttgaggc aatttcttaa aatgaatagc actggtgatt ttgatctcca cttattaaaa 2040
gtttcagaag gcacaacaat actgttgaac tgcactggcc aggttaaagg aagaaaacca 2100
gctgccctgg gtgaagccca accaacaag agtttgaag aaaataaatc tttaaaggaa 2160
cagaaaaaac tgaatgactt gtgtttccta aagagactat tacaagagat aaaaacttgt 2220
tggaataaaa ttttgatggg cactaaagaa cacggaagcg gagtgaaca gactttgaat 2280
tttgacctt tcaagttggc gggagacgtg gagtccaacc ctggacctat ggccctgcta 2340
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gatgctgaag actgctgcct gtctgtgacc cagaaaccca tccctgggta catcgtgagg 2460
aacttccact accttctcat caaggatggc tgcagggtgc ctgctgtagt gttcaccaca 2520
ctgagggggc gccagctctg tgcaccccca gaccagccct gggtagaacg catcatccag 2580
agactgcaga ggacctcagc caagatgaag cgccgcagca gttaa 2625

<210> 44
<211> 874
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-GM2 CAR (VH15VL)

<400> 44

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

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

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

Thr Asp Tyr Asn Met Asp Trp Val Lys Gln Ser Pro Gly Gln Gly Leu

50

55

60

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

Gln Lys Phe Lys Ser Lys Val Thr Ile Thr Val Asp Thr Ser Thr Ser
 85 90 95

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

Tyr Tyr Cys Ala Thr Tyr Gly His Tyr Tyr Gly Tyr Met Phe Ala Tyr
 115 120 125

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln
 145 150 155 160

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

Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys
 180 185 190

Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala
 195 200 205

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr
 210 215 220

Ser Leu Thr Ile Ser Arg Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
 225 230 235 240

Cys Gln Gln Arg Ser Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
 245 250 255

Val Glu Ile Lys Ala Ala Ala Phe Val Pro Val Phe Leu Pro Ala Lys

260

265

270

Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
 275 280 285

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
 290 295 300

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
 305 310 315 320

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
 325 330 335

Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg
 340 345 350

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
 355 360 365

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
 370 375 380

Tyr Arg Ser Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu
 385 390 395 400

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
 405 410 415

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
 420 425 430

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
 435 440 445

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
 450 455 460

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly

465 470 475 480
 Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
 485 490 495
 Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
 500 505 510
 Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
 515 520 525
 Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
 530 535 540
 Pro Arg Glu Phe Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu
 545 550 555 560
 Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Cys Met Phe
 565 570 575
 His Val Ser Phe Arg Tyr Ile Phe Gly Leu Pro Pro Leu Ile Leu Val
 580 585 590
 Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Glu Gly Lys Asp Gly
 595 600 605
 Lys Gln Tyr Glu Ser Val Leu Met Val Ser Ile Asp Gln Leu Leu Asp
 610 615 620
 Ser Met Lys Glu Ile Gly Ser Asn Cys Leu Asn Asn Glu Phe Asn Phe
 625 630 635 640
 Phe Lys Arg His Ile Cys Asp Ala Asn Lys Glu Gly Met Phe Leu Phe
 645 650 655
 Arg Ala Ala Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ser Thr Gly
 660 665 670
 Asp Phe Asp Leu His Leu Leu Lys Val Ser Glu Gly Thr Thr Ile Leu

675

680

685

Leu Asn Cys Thr Gly Gln Val Lys Gly Arg Lys Pro Ala Ala Leu Gly
 690 695 700

Glu Ala Gln Pro Thr Lys Ser Leu Glu Glu Asn Lys Ser Leu Lys Glu
 705 710 715 720

Gln Lys Lys Leu Asn Asp Leu Cys Phe Leu Lys Arg Leu Leu Gln Glu
 725 730 735

Ile Lys Thr Cys Trp Asn Lys Ile Leu Met Gly Thr Lys Glu His Gly
 740 745 750

Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly
 755 760 765

Asp Val Glu Ser Asn Pro Gly Pro Met Ala Leu Leu Leu Ala Leu Ser
 770 775 780

Leu Leu Val Leu Trp Thr Ser Pro Ala Pro Thr Leu Ser Gly Thr Asn
 785 790 795 800

Asp Ala Glu Asp Cys Cys Leu Ser Val Thr Gln Lys Pro Ile Pro Gly
 805 810 815

Tyr Ile Val Arg Asn Phe His Tyr Leu Leu Ile Lys Asp Gly Cys Arg
 820 825 830

Val Pro Ala Val Val Phe Thr Thr Leu Arg Gly Arg Gln Leu Cys Ala
 835 840 845

Pro Pro Asp Gln Pro Trp Val Glu Arg Ile Ile Gln Arg Leu Gln Arg
 850 855 860

Thr Ser Ala Lys Met Lys Arg Arg Ser Ser
 865 870

<210> 45

305072_1.txt

<211> 2655

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-GM2 CAR (VH25VL)

<400> 45

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tgcaaagcca gcggctatac cttcaccgac tacaacatgg actgggtgaa gcagagcccc	180
ggccaaggcc tcgagtggat gggatacatc taccccaaca acggcggcac cggctacaac	240
cagaagttca agagcaaggt gaccatcacc gtggacacat ccacaagcac cgcctatatg	300
gagctccaca gcctgaggag cgaggacacc gccgtgtact actgcgccac ctacggccac	360
tactacggct atatgttcgc ctactggggc cagggcaccc tgggtgacagt gtcctcctcc	420
agcgccgatg atgccaagaa ggatgccgcc aaaaaggacg acgctaagaa ggatgacgcc	480
aagaaggacg gcgatatcca gctgacacag agccctagct ccctgagcgc tagccctggc	540
gacagagtga ccatcacctg cagcgccagc tccagcgtga gctacatgca ctggttccag	600
cagaaacccg gcaaggcccc caagctgtgg atctacagca ccagcaatct ggctagcggc	660
gtgcctgcca ggtttagcgg atccggcagc ggcacctcct actccctgac aatctccaga	720
ctgcagcccc aggacatcgc cacctactac tgccaacaga ggtcctccta cccctacacc	780
ttcggcggcg gcaccaaagt ggagatcaag gcggccgcat tcgtgccggt cttcctgcca	840
gcgaagccca ccacgacgcc agcgccgca ccaccaacac cggcgccac catcgcgtcg	900
cagccccctgt ccctgcgccc agaggcgtgc cggccagcgg cggggggcgc agtgcacacg	960
agggggctgg acttcgcctg tgatatctac atctgggcgc cttggccgg gacttgtggg	1020
gtccttctcc tgtcactggt taccacctt tactgcaacc acaggaacag gagtaagagg	1080
agcaggctcc tgcacagtga ctacatgaac atgactcccc gccgccccgg gccacccgc	1140
aagcattacc agccctatgc cccaccacgc gacttcgcag cctatcgctc ccgtttctct	1200
gttgtaaac ggggcagaaa gaagctcctg tatatatcca aacaaccatt tatgagacca	1260
gtacaaacta ctcaagagga agatggctgt agctgccgat ttccagaaga agaagaagga	1320

305072_1.txt

ggatgtgaac tgagagtga gttcagcagg agcgcagacg ccccgcgta ccagcagggc	1380
cagaaccagc tctataacga gctcaatcta ggacgaagag aggagtacga tgttttggac	1440
aagagacgtg gccgggaccc tgagatgggg ggaaagccga gaaggaagaa ccctcaggaa	1500
ggcctgtaca atgaactgca gaaagataag atggcggagg cctacagtga gattgggatg	1560
aaaggcgagc gccggagggg caaggggcac gatggccttt accaggggtct cagtacagcc	1620
accaaggaca cctacgacgc cttcacatg caggccctgc cccctcgcga attcggaagc	1680
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tatgagagtg ttctaattggt cagcatcgat caattattgg acagcatgaa agaaattggt	1920
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gaaggatatgt ttttattccg tgctgctcgc aagttgaggc aatttcttaa aatgaatagc	2040
actggtgatt ttgatctcca cttattaaaa gtttcagaag gcacaacaat actgttgaac	2100
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aagagactat tacaagagat aaaaacttgt tggaataaaa ttttgatggg cactaaagaa	2280
cacggaagcg gagtgaacaa gactttgaat tttgaccttc tcaagttggc gggagacgtg	2340
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tccccagccc caactctgag tggcaccaat gatgctgaag actgctgcct gtctgtgacc	2460
cagaaacca tccctgggta catcgtgagg aacttccact accttctcat caaggatggc	2520
tgcagggtgc ctgctgtagt gttcaccaca ctgaggggcc gccagctctg tgcaccccca	2580
gaccagccct gggtagaacg catcatccag agactgcaga ggacctcagc caagatgaag	2640
cgccgcagca gttaa	2655

<210> 46
 <211> 884
 <212> PRT
 <213> Artificial Sequence

305072_1.txt

<220>

<223> anti-GM2 CAR (VH25VL)

<400> 46

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

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

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

Thr Asp Tyr Asn Met Asp Trp Val Lys Gln Ser Pro Gly Gln Gly Leu
50 55 60

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

Gln Lys Phe Lys Ser Lys Val Thr Ile Thr Val Asp Thr Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Tyr Gly His Tyr Tyr Gly Tyr Met Phe Ala Tyr
115 120 125

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

Ala Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala Lys Lys Asp Asp Ala
145 150 155 160

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

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

305072_1.txt

Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys
195 200 205

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

Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg
225 230 235 240

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser
245 250 255

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

Ala Phe Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala
275 280 285

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
290 295 300

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
305 310 315 320

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
325 330 335

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
340 345 350

Asn His Arg Asn Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
355 360 365

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
370 375 380

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Phe Ser
385 390 395 400

305072_1.txt

Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro
405 410 415

Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys
420 425 430

Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe
435 440 445

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
450 455 460

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
465 470 475 480

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
485 490 495

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
500 505 510

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
515 520 525

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
530 535 540

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Glu Phe Gly Ser
545 550 555 560

Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp
565 570 575

Val Glu Ser Asn Pro Gly Pro Cys Met Phe His Val Ser Phe Arg Tyr
580 585 590

Ile Phe Gly Leu Pro Pro Leu Ile Leu Val Leu Leu Pro Val Ala Ser
595 600 605

305072_1.txt

Ser Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser Val
610 615 620

Leu Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile Gly
625 630 635 640

Ser Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile Cys
645 650 655

Asp Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys Leu
660 665 670

Arg Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His Leu
675 680 685

Leu Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly Gln
690 695 700

Val Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr Lys
705 710 715 720

Ser Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn Asp
725 730 735

Leu Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp Asn
740 745 750

Lys Ile Leu Met Gly Thr Lys Glu His Gly Ser Gly Val Lys Gln Thr
755 760 765

Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro
770 775 780

Gly Pro Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val Leu Trp Thr
785 790 795 800

Ser Pro Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys
805 810 815

305072_1.txt

Leu Ser Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe
820 825 830

His Tyr Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe
835 840 845

Thr Thr Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp
850 855 860

Val Glu Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys
865 870 875 880

Arg Arg Ser Ser

<210> 47
<211> 3825
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-GM2 CAR (VL15VH)_HSV tk

<400> 47
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atccagctga cccagtcccc tagcagcctg tccgctagcc ccggagacag agtgaccatc 120
acctgttccg ccagctccag cgtgagctac atgcactggt tccagcagaa gcccggcaag 180
gcccccaagc tgtggatcta cagcaccagc aacctggctt ccggcgtgcc tgccagattt 240
tccggctccg gcagcggcac aagctactcc ctgaccatca gcagactgca gcccgaagac 300
atcgccacct actactgtca gcagaggagc agctaccctt acaccttcgg cggcggcacc 360
aaggtggaga tcaagggcgg cggcgggaagc ggaggcggcg gcagcggcgg aggcggaagc 420
gaagtgcagc tggatgcagtc cggagccgag gtgaaaaagc ctggcgcctc cgtcaagggtg 480
agctgcaagg ccagcggcta tacattcacc gactataaca tggactgggt gaagcagagc 540
cccggccagg gactggagtg gatgggctac atctaccca ataacggcgg caccggctac 600
aaccagaagt tcaagtccaa ggtgaccatc accgtggaca ccagcaccag caccgcctac 660

305072_1.txt

atggaactgc acagcctcag aagcgaagac accgctgtgt actactgcgc cacctacggc	720
cactactacg gctacatgtt cgcctactgg ggacagggca ccctgggtgac cgtcagcagc	780
gcggccgcat tcgtgccggt cttcctgcca gcgaagccca ccacgacgcc agcgccgcga	840
ccaccaaacac cggcgcccac catcgcgtcg cagcccctgt ccctgcgccc agaggcgtgc	900
cggccagcgg cggggggcgc agtgcacacg agggggctgg acttcgcctg tgatatctac	960
atctggggcg ccttggccgg gacttgtggg gtccttctcc tgtcactggt tatcaccctt	1020
tactgcaacc acaggaacag gagtaagagg agcaggctcc tgcacagtga ctacatgaac	1080
atgactcccc gccgccccgg gccacccgc aagcattacc agccctatgc cccaccacgc	1140
gacttcgcag cctatcgctc ccgtttctct gttgttaaag ggggcagaaa gaagctcctg	1200
tatatattca aacaaccatt tatgagacca gtacaaacta ctcaagagga agatggctgt	1260
agctgccgat ttccagaaga agaagaagga ggatgtgaac tgagagtga gttcagcagg	1320
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ggaaagccga gaaggaagaa ccctcaggaa ggcctgtaca atgaactgca gaaagataag	1500
atggcgagg cctacagtga gattgggatg aaaggcgagc gccggagggg caaggggcac	1560
gatggccttt accagggctc cagtacagcc accaaggaca cctacgacgc cttcacatg	1620
caggccctgc cccctcgca attcggaagc ggagtgaac agactttgaa ttttgacctt	1680
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305072_1.txt

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cccgaaccta	tgacatatg	gagggctctc	ggcgcctccg	agaccatcgc	caacatttac	3000
accaccagc	acaggctgga	tcaggagag	atctccgccg	gcgatgctgc	cgtggtgatg	3060
accagcgccc	agatcactat	gggtatgcct	tatgccgtga	ccgacgctgt	gctggctcct	3120
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gacagacatc	ctatcgccgc	tctgctgtgc	taccccgccg	ctaggtacct	gatgggcagc	3240
atgaccctc	aggccgtgct	ggcttttgtg	gccctcattc	ccccacact	gcctggcaca	3300
aatatcgtgc	tcggcgccct	gcctgaggac	aggcacatcg	ataggctggc	taagagacag	3360
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cagctgacct	ccggcatggt	gcagaccac	gtgaccaccc	ctggaagcat	ccccacaatc	3780

tgcgacctgg ccaggacctt tgccagagaa atgggagaag ccaac

3825

<210> 48

<211> 1275

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-GM2 CAR (VL15VH)_HSV tk

<400> 48

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

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

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

Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
50 55 60

Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe
65 70 75 80

Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Leu
85 90 95

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

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
130 135 140

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

305072_1.txt

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Met Asp Trp
165 170 175

Val Lys Gln Ser Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Tyr
180 185 190

Pro Asn Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe Lys Ser Lys Val
195 200 205

Thr Ile Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu Leu His
210 215 220

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

His Tyr Tyr Gly Tyr Met Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
245 250 255

Thr Val Ser Ser Ala Ala Ala Phe Val Pro Val Phe Leu Pro Ala Lys
260 265 270

Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
275 280 285

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
290 295 300

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
305 310 315 320

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
325 330 335

Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg
340 345 350

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
355 360 365

305072_1.txt

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
370 375 380

Tyr Arg Ser Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu
385 390 395 400

Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu
405 410 415

Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys
420 425 430

Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
435 440 445

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
450 455 460

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
465 470 475 480

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
485 490 495

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
500 505 510

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
515 520 525

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
530 535 540

Pro Arg Glu Phe Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu
545 550 555 560

Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Cys Met Phe
565 570 575

305072_1.txt

His Val Ser Phe Arg Tyr Ile Phe Gly Leu Pro Pro Leu Ile Leu Val
580 585 590

Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Glu Gly Lys Asp Gly
595 600 605

Lys Gln Tyr Glu Ser Val Leu Met Val Ser Ile Asp Gln Leu Leu Asp
610 615 620

Ser Met Lys Glu Ile Gly Ser Asn Cys Leu Asn Asn Glu Phe Asn Phe
625 630 635 640

Phe Lys Arg His Ile Cys Asp Ala Asn Lys Glu Gly Met Phe Leu Phe
645 650 655

Arg Ala Ala Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ser Thr Gly
660 665 670

Asp Phe Asp Leu His Leu Leu Lys Val Ser Glu Gly Thr Thr Ile Leu
675 680 685

Leu Asn Cys Thr Gly Gln Val Lys Gly Arg Lys Pro Ala Ala Leu Gly
690 695 700

Glu Ala Gln Pro Thr Lys Ser Leu Glu Glu Asn Lys Ser Leu Lys Glu
705 710 715 720

Gln Lys Lys Leu Asn Asp Leu Cys Phe Leu Lys Arg Leu Leu Gln Glu
725 730 735

Ile Lys Thr Cys Trp Asn Lys Ile Leu Met Gly Thr Lys Glu His Gly
740 745 750

Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly
755 760 765

Asp Val Glu Ser Asn Pro Gly Pro Met Ala Leu Leu Leu Ala Leu Ser
770 775 780

305072_1.txt

Leu Leu Val Leu Trp Thr Ser Pro Ala Pro Thr Leu Ser Gly Thr Asn
785 790 795 800

Asp Ala Glu Asp Cys Cys Leu Ser Val Thr Gln Lys Pro Ile Pro Gly
805 810 815

Tyr Ile Val Arg Asn Phe His Tyr Leu Leu Ile Lys Asp Gly Cys Arg
820 825 830

Val Pro Ala Val Val Phe Thr Thr Leu Arg Gly Arg Gln Leu Cys Ala
835 840 845

Pro Pro Asp Gln Pro Trp Val Glu Arg Ile Ile Gln Arg Leu Gln Arg
850 855 860

Thr Ser Ala Lys Met Lys Arg Arg Ser Ser Gly Ser Gly Val Lys Gln
865 870 875 880

Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn
885 890 895

Pro Gly Pro Met Ala Ser Tyr Pro Gly His Gln His Ala Ser Ala Phe
900 905 910

Asp Gln Ala Ala Arg Ser Arg Gly His Ser Asn Arg Arg Thr Ala Leu
915 920 925

Arg Pro Arg Arg Gln Gln Glu Ala Thr Glu Val Arg Pro Glu Gln Lys
930 935 940

Met Pro Thr Leu Leu Arg Val Tyr Ile Asp Gly Pro His Gly Met Gly
945 950 955 960

Lys Thr Thr Thr Thr Gln Leu Leu Val Ala Leu Gly Ser Arg Asp Asp
965 970 975

Ile Val Tyr Val Pro Glu Pro Met Thr Tyr Trp Arg Val Leu Gly Ala
980 985 990

305072_1.txt

Ser Glu Thr Ile Ala Asn Ile Tyr Thr Thr Gln His Arg Leu Asp Gln
 995 1000 1005

Gly Glu Ile Ser Ala Gly Asp Ala Ala Val Val Met Thr Ser Ala
 1010 1015 1020

Gln Ile Thr Met Gly Met Pro Tyr Ala Val Thr Asp Ala Val Leu
 1025 1030 1035

Ala Pro His Ile Gly Gly Glu Ala Gly Ser Ser His Ala Pro Pro
 1040 1045 1050

Pro Ala Leu Thr Leu Ile Phe Asp Arg His Pro Ile Ala Ala Leu
 1055 1060 1065

Leu Cys Tyr Pro Ala Ala Arg Tyr Leu Met Gly Ser Met Thr Pro
 1070 1075 1080

Gln Ala Val Leu Ala Phe Val Ala Leu Ile Pro Pro Thr Leu Pro
 1085 1090 1095

Gly Thr Asn Ile Val Leu Gly Ala Leu Pro Glu Asp Arg His Ile
 1100 1105 1110

Asp Arg Leu Ala Lys Arg Gln Arg Pro Gly Glu Arg Leu Asp Leu
 1115 1120 1125

Ala Met Leu Ala Ala Ile Arg Arg Val Tyr Gly Leu Leu Ala Asn
 1130 1135 1140

Thr Val Arg Tyr Leu Gln Cys Gly Gly Ser Trp Arg Glu Asp Trp
 1145 1150 1155

Gly Gln Leu Ser Gly Thr Ala Val Pro Pro Gln Gly Ala Glu Pro
 1160 1165 1170

Gln Ser Asn Ala Gly Pro Arg Pro His Ile Gly Asp Thr Leu Phe
 1175 1180 1185

305072_1.txt

Thr Leu Phe Arg Ala Pro Glu Leu Leu Ala Pro Asn Gly Asp Leu
1190 1195 1200

Tyr Asn Val Phe Ala Trp Ala Leu Asp Val Leu Ala Lys Arg Leu
1205 1210 1215

Arg Ser Met His Val Phe Ile Leu Asp Tyr Asp Gln Ser Pro Ala
1220 1225 1230

Gly Cys Arg Asp Ala Leu Leu Gln Leu Thr Ser Gly Met Val Gln
1235 1240 1245

Thr His Val Thr Thr Pro Gly Ser Ile Pro Thr Ile Cys Asp Leu
1250 1255 1260

Ala Arg Thr Phe Ala Arg Glu Met Gly Glu Ala Asn
1265 1270 1275

<210> 49
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> VH region of anti-GM2 antibody for VL25VH

<400> 49
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agctgtaagg cctccggcta caccttcacc gactacaaca tggattgggt gaagcagagc 120
cccggacagg gcctggagtg gatgggctac atctacccca acaacggcgg caccggctac 180
aaccagaaat tcaagtccaa ggtgaccatc accgtggaca ccagcacatc caccgcctac 240
atggaactgc acagcctgag gtccgaggac acagccgtgt actactgcgc tacctacggc 300
cactactacg gctacatgtt cgcttactgg ggacagggca ccctggtgac cgtgagctcc 360

<210> 50
<211> 318
<212> DNA
<213> Artificial Sequence

305072_1.txt

<220>

<223> VL region of anti-GM2 antibody for VL25VH

<400> 50

gatatccaac tgaccagtc cccttcagc ctgagcgctt ccccggaga cagggtgaca	60
attacctgca gcgccagctc ctccgtgagc tacatgcact gggtccagca gaagcccggc	120
aagggcccca agctgtggat ctactccaca agcaacctgg cctccggcgt gcctgccaga	180
tttagcggaa gcggcagcgg cacatcctac agcctgacca tctccaggct gcagcccagag	240
gacatcgcca catactactg ccagcagagg tccagctacc cttacacatt cggaggcggc	300
accaaggtgg agatcaag	318

<210> 51

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> VH region of anti-GM2 antibody for VH15VL

<400> 51

gaggtgcagc tggtgcagtc cggagccgag gtgaagaagc ctggcgccag cgtgaaggtg	60
agctgtaagg cctccggcta caccttcacc gactacaaca tggactgggt caagcagagc	120
cctggccagg gcctggagtg gatgggctat atctaccca acaacggcgg caccggctac	180
aaccagaagt tcaagagcaa ggtcaccatc accgtggaca cctccacctc cacagcctac	240
atggagctgc acagcctgag gagcaggat accgccgtgt actactgcgc tacctacggc	300
cattactacg gatacatgtt cgcctactgg ggccaggga cctggtcac cgtgtcctcc	360

<210> 52

<211> 318

<212> DNA

<213> Artificial Sequence

<220>

<223> VL region of anti-GM2 antibody for VH15VL

<400> 52

gacatccagc tgacacaatc cccagcagc ctgagcgcta gcccggcga tagggtgaca	60
attacctgca gcgcctccag ctccgtgtcc tacatgcact gggttcagca aaagcccggc	120

305072_1.txt

aaggccccta agctgtggat ctacagcacc agcaacctgg ccagcggagt gcctgccaga 180
 tttagcggca gcggcagcgg caccagctac agcctgacca tcagcagact gcagcccag 240
 gatatcgcca cctactactg ccagcagagg agctcctacc cctacacatt cggcggcgga 300
 accaaggtgg agatcaag 318

<210> 53
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH region of anti-GM2 antibody for VH25VL

<400> 53
 gaagtgcagc tgggtgcagtc cggagctgag gtgaagaagc ccggcgccag cgtgaaggtc 60
 agctgcaaag ccagcggcta taccttcacc gactacaaca tggactgggt gaagcagagc 120
 cccggccaag gcctcgagt gatgggatac atctaccca acaacggcgg caccggctac 180
 aaccagaagt tcaagagcaa ggtgaccatc accgtggaca catccacaag caccgcctat 240
 atggagctcc acagcctgag gagcaggagc accgccgtgt actactgcgc cacctacggc 300
 cactactacg gctatatgtt cgcctactgg ggccagggca ccctggtgac agtgtctctc 360

<210> 54
 <211> 318
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL region of anti-GM2 antibody for VH25VL

<400> 54
 gatattccagc tgacacagag ccctagctcc ctgagcgcta gccctggcga cagagtgacc 60
 atcacctgca gcgccagctc cagcgtgagc tacatgcact gggtccagca gaaacccggc 120
 aaggcccca agctgtggat ctacagcacc agcaatctgg ctacggcgt gcctgccagg 180
 tttagcggat ccggcagcgg cacctcctac tcctgacaa tctccagact gcagcccag 240
 gacatcgcca cctactactg ccaacagagg tcctcctacc cctacacctt cggcggcgga 300
 accaaagtgg agatcaag 318

<210> 55
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> linker 15 for VH15VL

<400> 55
 ggaggaggag gaagcggagg cggcggctcc ggcggaggcg gatcc 45

<210> 56
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> linker 25 for VH25VL

<400> 56
 tccagcgccg atgatgcaa gaaggatgcc gccaaaaagg acgacgctaa gaaggatgac 60
 gccaaagaagg acggc 75

<210> 57
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> signal peptide

<400> 57

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

Ala His Ser

<210> 58
 <211> 531
 <212> DNA
 <213> Homo sapiens

<400> 58
 atgttccatg tttcttttag gtatatcttt ggacttcctc ccctgaccc tgttctgttg 60

305072_1.txt

ccagtagcat catctgattg tgatattgaa ggtaaagatg gcaaacaata tgagagtgtt 120
 ctaatgggtca gcatcgatca attattggac agcatgaaag aaattggttag caattgcctg 180
 aataatgaat ttaacttttt taaaagacat atctgtgatg ctaataagga aggtatgttt 240
 ttattccgtg ctgctcgcaa gttgaggcaa tttcttaaaa tgaatagcac tgggtgatttt 300
 gatctccact tattaanaagt ttcagaaggc acaacaatac tgttgaactg cactggccag 360
 gttaaaggaa gaaaaccagc tgccctgggt gaagcccaac caacaaagag tttggaagaa 420
 aataaatctt taaaggaaca gaaaaaactg aatgacttgt gtttcctaaa gagactatta 480
 caagagataa aaacttggtg gaataaaatt ttgatgggca ctaaagaaca c 531

<210> 59
 <211> 177
 <212> PRT
 <213> Homo sapiens

<400> 59

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Leu Pro Pro Leu Ile
 1 5 10 15

Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Glu Gly Lys
 20 25 30

Asp Gly Lys Gln Tyr Glu Ser Val Leu Met Val Ser Ile Asp Gln Leu
 35 40 45

Leu Asp Ser Met Lys Glu Ile Gly Ser Asn Cys Leu Asn Asn Glu Phe
 50 55 60

Asn Phe Phe Lys Arg His Ile Cys Asp Ala Asn Lys Glu Gly Met Phe
 65 70 75 80

Leu Phe Arg Ala Ala Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ser
 85 90 95

Thr Gly Asp Phe Asp Leu His Leu Leu Lys Val Ser Glu Gly Thr Thr
 100 105 110

305072_1.txt

Ile Leu Leu Asn Cys Thr Gly Gln Val Lys Gly Arg Lys Pro Ala Ala
 115 120 125

Leu Gly Glu Ala Gln Pro Thr Lys Ser Leu Glu Glu Asn Lys Ser Leu
 130 135 140

Lys Glu Gln Lys Lys Leu Asn Asp Leu Cys Phe Leu Lys Arg Leu Leu
 145 150 155 160

Gln Glu Ile Lys Thr Cys Trp Asn Lys Ile Leu Met Gly Thr Lys Glu
 165 170 175

His

<210> 60
 <211> 294
 <212> DNA
 <213> Homo sapiens

<400> 60
 atggccctgc tactggccct cagcctgctg gttctctgga cttccccagc cccaactctg 60
 agtggcacca atgatgctga agactgctgc ctgtctgtga ccagaaaacc catccctggg 120
 tacatcgtga ggaacttcca ctaccttctc atcaaggatg gctgcagggt gcctgctgta 180
 gtgttcacca cactgagggg cgcagctc tgtgcacccc cagaccagcc ctgggtagaa 240
 cgcatcatcc agagactgca gaggacctca gccaatga agcgccgcag cagt 294

<210> 61
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 61

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

Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser
 20 25 30

305072_1.txt

Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr
35 40 45

Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr
50 55 60

Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Glu
65 70 75 80

Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys Arg Arg
85 90 95

Ser Ser

<210> 62
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> F2A

<400> 62

Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala
1 5 10 15

Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25

<210> 63
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of VH region of anti-GM2 antibody

<400> 63

Asp Tyr Asn Met Asp
1 5

<210> 64
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR2 of VH region of anti-GM2 antibody

<400> 64

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

Ser

<210> 65
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR3 of VH region of anti-GM2 antibody

<400> 65

Tyr	Gly	His	Tyr	Tyr	Gly	Tyr	Met	Phe	Ala	Tyr
1				5					10	

<210> 66
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR1 of VL region of anti-GM2 antibody

<400> 66

Ser	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	His
1				5				10	

<210> 67
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>

<223> CDR2 of VL region of anti-GM2 antibody

<400> 67

Ser Thr Ser Asn Leu Ala Ser
1 5

<210> 68

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 of VL region of anti-GM2 antibody

<400> 68

Gln Gln Arg Ser Ser Tyr Pro Tyr Thr
1 5