

SEQUENCE LISTING

<110> CTTQ-Akeso (Shanghai) Biomed. Tech. Co., Ltd

<120> ANTI-PD-1 ANTIBODY AND MEDICAL USE THEREOF

<130>

<150> CN201910711138.5

<151> 2019-08-02

<150> CN201911133858.4

<151> 2019-11-19

<150> CN201911105715.2

<151> 2019-11-13

<150> CN201911105711.4

<151> 2019-11-13

<160> 24

<170> PatentIn version 3.5

<210> 1

<211> 354

<212> DNA

<213> Artificial

<220>

<223> Nucleic acid sequence of 14C12 heavy chain variable region

<400> 1

gagggtcaaac tggtggagag cggcggcggg ctggtgaagc ccggcgggtc actgaaactg	60
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cctgagaagc gcctggaatg ggtcgtact atcagcggag gcgggcgata cacctactat	180
cctgactctg tcaaaggag attcacaatt agtcgggata acgccagaaa tactctgtat	240
ctgcagatgt ctagtctgcg gtccgaggat acagctctgt actattgtgc aaaccggtac	300
ggcgaagcat ggtttgccta ttggggacag ggcaccctgg tgacagtctc tgcc	354

<210> 2

<211> 118

<212> PRT

<213> Artificial

<220>

<223> The amino acid sequence of 14C12 heavy chain variable region

<400> 2

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

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

Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

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

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

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

Ala Asn Arg Tyr Gly Glu Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ala
115

<210> 3

<211> 321

<212> DNA

<213> Artificial

<220>

<223> Nucleic acid sequence of 14C12 light chain variable region

<400> 3

gacattaaga tgacacagtc cccttcctca atgtacgcta gcctgggcga gcgagtgacc 60
ttcacatgca aagcatccca ggacatcaac acatacctgt cttggtttca gcagaagcca 120
ggcaaaagcc ccaagaccct gatctaccgg gccaatagac tgggtggacgg ggtccccagc 180
agattctccg gatctggcag tgggcaggat tactccctga ccatcagctc cctggagtat 240
gaagacatgg gcatctacta ttgcctgcag tatgatgagt tccctctgac ctttggagca 300
ggcacaaaac tggaactgaa g 321

<210> 4
 <211> 107
 <212> PRT
 <213> Artificial

<220>
 <223> The amino acid sequence of 14C12 light chain variable region

<400> 4

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

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

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

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

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

Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Pro Leu
 85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 100 105

<210> 5
 <211> 354
 <212> DNA
 <213> Artificial

<220>
 <223> Nucleic acid sequence of 14C12H1L1(hG1WT) heavy chain variable region

<400> 5

gaagtgcagc tggctcgagtc tgggggaggg ctggtgcagc ccggcgggctc actgcgactg 60

agctgcgcag cttccggatt cgccttttagc tcctacgaca tgtcctgggt gcgacaggca 120

ccaggaaagg gactggattg ggtcgtact atctcaggag gcgggagata cacctactat 180

cctgacagcg tcaagggccg gttcacaatc tctagagata acagtaagaa caatctgtat 240
 ctgcagatga acagcctgag ggctgaggac accgcactgt actattgtgc caaccgctac 300
 ggggaagcat ggtttgccta ttgggggcag ggaaccctgg tgacagtctc tagt 354

<210> 6
 <211> 118
 <212> PRT
 <213> Artificial

<220>
 <223> The amino acid sequence of 14C12H1L1(hG1WT) heavy chain variable region
 <400> 6

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 Ala Phe Ser Ser Tyr
 20 25 30

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

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

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

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

Ala Asn Arg Tyr Gly Glu Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 7
 <211> 321
 <212> DNA
 <213> Artificial

<220>

<223> Nucleic acid sequence of 14C12H1L1(hG1WT) light chain variable region

<400> 7

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ttcacatgcc gcgctagtca ggatatcaac acctacctga gctggtttca gcagaagcca      120
gggaaaagcc ccaagacact gatctaccgg gctaatagac tgggtgtctgg agtcccaagt      180
cggttcagtg gctcagggag cggacaggac tacactctga ccatcagctc cctgcagcct      240
gaggacatgg caacctacta ttgcctgcag tatgatgagt tcccactgac ctttggcgcc      300
gggacaaaac tggagctgaa g                                              321
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<210> 8

<211> 107

<212> PRT

<213> Artificial

<220>

<223> The amino acid sequence of 14C12H1L1(hG1WT) light chain variable region

<400> 8

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

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

```
Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
          35           40           45
```

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

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

```
Glu Asp Met Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Pro Leu
          85           90           95
```

```
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
          100          105
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<210> 9
 <211> 1344
 <212> DNA
 <213> Artificial

<220>
 <223> Nucleic acid sequence of 14C12H1L1 (hG1WT) heavy chain

<400> 9
 gaagtgcagc tggtcgagtc tgggggaggg ctggtgcagc ccggcgggtc actgcgactg 60
 agctgcgcag cttccggatt cgcctttagc tcctacgaca tgtcctgggt gcgacaggca 120
 ccaggaaagg gactggattg ggtcgctact atctcaggag gcgggagata cacctactat 180
 cctgacagcg tcaagggccg gttcacaatc tctagagata acagtaagaa caatctgtat 240
 ctgcagatga acagcctgag ggctgaggac accgcactgt actattgtgc caaccgctac 300
 ggggaagcat ggtttgccta ttgggggcag ggaaccctgg tgacagtctc tagtgccagc 360
 accaaaggac ctagcgtgtt tcctctcgcc ccctcctcca aaagcaccag cggaggaacc 420
 gctgctctcg gatgtctggt gaaggactac ttccctgaac ccgtcaccgt gagctggaat 480
 agcggcgctc tgacaagcgg agtccataca ttccctgctg tgctgcaaag cagcggactc 540
 tattccctgt ccagcgtcgt cacagtgtccc agcagcagcc tgggcaccca gacctacatc 600
 tgtaacgtca accacaagcc ctccaacacc aaggtggaca agaaagtgga gcccaaattc 660
 tgcgacaaga cacacacctg tccccctgt cctgctcccg aactcctcgg aggccctagc 720
 gtcttctctt ttctcccaa acccaaggac accctcatga tcagcagaac ccctgaagtc 780
 acctgtgtcg tcgtggatgt cagccatgag gaccccgagg tgaaattcaa ctggtatgtc 840
 gatggcgtcg aggtgcacaa cgccaaaacc aagcccaggg aggaacagta caactccacc 900
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 aagtgcaagg tgtccaacaa ggctctccct gccccattg agaagaccat cagcaaggcc 1020
 aaaggccaac ccaggagacc ccaggtctat acactgcctc cctccaggga cgaactcacc 1080
 aagaaccagg tgtccctgac ctgcctggtc aagggtttt atcccagcga catcgccgtc 1140
 gagtgggagt ccaacggaca gcccgagaat aactacaaga ccaccctcc tgtcctcgac 1200
 tccgacggct ctttcttct gtacagcaag ctgaccgtgg aaaaaagcag gtggcagcag 1260
 ggaaacgtgt tctcctgcag cgtgatgcac gaagccctcc acaaccacta caccagaaa 1320

agcctgtccc tgagccccgg caaa

1344

<210> 10

<211> 448

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of 14C12H1L1 (hG1WT) heavy chain

<400> 10

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 Ala Phe Ser Ser Tyr
20 25 30

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

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

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

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

Ala Asn Arg Tyr Gly Glu Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

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

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

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

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

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

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240

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

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

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

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

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

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

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

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

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400

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

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 11
 <211> 642
 <212> DNA
 <213> Artificial

<220>
 <223> Nucleic acid sequence of 14C12H1L1 (hG1WT) light chain

<400> 11
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 ttcacatgcc gcgctagtca ggatatcaac acctacctga gctggtttca gcagaagcca 120
 gggaaaagcc ccaagacact gatctaccgg gctaatagac tgggtgtctgg agtcccaagt 180
 cggttcagtg gctcagggag cggacaggac tacactctga ccatcagctc cctgcagcct 240
 gaggacatgg caacctacta ttgcctgcag tatgatgagt tcccactgac ctttggcgcc 300
 gggacaaaac tggagctgaa gcgaactgtg gccgctccct ccgtcttcat ttttcccct 360
 tctgacgaac agctgaaatc aggcacagcc agcgtggtct gtctgctgaa caatttctac 420
 cctagagagg caaaagtgca gtggaaggtc gataacgccc tgcagtccgg caacagccag 480
 gagagtgtga ctgaacagga ctcaaaagat agcacctatt ccctgtctag tacactgact 540
 ctgtccaagg ctgattacga gaagcacaaa gtgtatgcat gcgaagtgac acatcaggga 600
 ctgtcaagcc ccgtgactaa gtcttttaac cggggcgaat gt 642

<210> 12
 <211> 214
 <212> PRT
 <213> Artificial

<220>

<223> Amino acid sequence of the light chain of 14C12H1L1 (hG1WT)

<400> 12

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

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

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

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

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

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

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

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

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

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

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

Phe Asn Arg Gly Glu Cys
 210

<210> 13
 <211> 1335
 <212> DNA
 <213> Artificial

<220>
 <223> Nucleic acid sequence of 14C12H1L1(hG4) heavy chain

<400> 13
 gaagtgcagc tggtcgagtc tgggggaggg ctggtgcagc ccggcgggtc actgcgactg 60
 agctgcgcag cttccggatt cgccttttagc tcctacgaca tgtcctgggt gcgacaggca 120
 ccaggaaagg gactggattg ggtcgctact atctcaggag gcgggagata cacctactat 180
 cctgacagcg tcaagggccg gttcacaatc tctagagata acagtaagaa caatctgtat 240
 ctgcagatga acagcctgag ggctgaggac accgcactgt actattgtgc caaccgctac 300
 ggggaagcat ggtttgccta ttgggggcag ggaaccctgg tgacagtctc tagtgccagc 360
 accaaagggc cctcggctctt ccccctggcg ccctgctcca ggagcacctc cgagagcaca 420
 gccgccctgg gctgcctgggt caaggactac ttccccgaac cgggtgacgggt gtcgtggaac 480
 tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540
 tactccctca gcagcgtgggt gaccgtgccc tccagcagct tgggcacgaa gacctacacc 600
 tgcaacgtag atcacaagcc cagcaacacc aaggtggaca agagagttga gtccaaatat 660
 ggtcccccat gccaccatg cccagcacct gaggttcctgg ggggaccatc agtcttcctg 720
 ttccccccaa aaccaagga cactctcatg atctcccga cccctgaggt cacgtgcgtg 780
 gtggtggacg tgagccagga agaccccgag gtccagttca actggtacgt ggatggcgtg 840
 gaggtgcata atgccaagac aaagccgcgg gaggagcagt tcaacagcac gtaccgtgtg 900
 gtcagcgtcc tcaccgtcct gcaccaggac tggctgaacg gcaaggagta caagtgaag 960
 gtctccaaca aaggcctccc gtcctccatc gagaaaacca tctccaaagc caaagggcag 1020
 ccccgagagc cacaggtgta caccctgccc ccatcccagg aggagatgac caagaaccag 1080
 gtcagcctga cctgcctgggt caaaggcttc taccacagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200
tccttcttcc tctacagcag gctaaccgtg gacaagagca ggtggcagga ggggaatgtc 1260
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacacagaa ggcctctcc 1320
ctgtctctgg gtaaa 1335

<210> 14
<211> 445
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of 14C12H1L1(hG4) heavy chain

<400> 14

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 Ala Phe Ser Ser Tyr
20 25 30

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

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

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

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

Ala Asn Arg Tyr Gly Glu Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

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

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

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
 195 200 205

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

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 325 330 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
 405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440 445

<210> 15
 <211> 1344
 <212> DNA
 <213> Artificial

<220>
 <223> Nucleic acid sequence of 14C12H1L1(hG1TM) heavy chain

<400> 15
 gaagtgcagc tggctcgagtc tgggggaggg ctggtgcagc ccggcgggtc actgcgactg 60
 agctgcgcag cttccggatt cgccttttagc tcctacgaca tgtcctgggt gcgacaggca 120
 ccaggaaagg gactggattg ggtcgtact atctcaggag gcgggagata cacctactat 180
 cctgacagcg tcaagggccg gttcacaatc tctagagata acagtaagaa caatctgtat 240
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 ggggaagcat ggtttgctta ttgggggcag ggaaccctgg tgacagtctc tagtgccagc 360
 accaaagggc ccagcgtggt tcctctcgcc ccctcctcca aaagcaccag cggaggaacc 420
 gctgctctcg gatgtctggt gaaggactac ttccctgaac ccgtcaccgt gagctggaat 480
 agcggcgctc tgacaagcgg agtccataca ttccctgctg tgctgcaaag cagcggactc 540
 tattccctgt ccagcgtcgt cacagtgcc agcagcagcc tgggcacca gacctacatc 600
 tgtaacgtca accacaagcc ctccaacacc aaggtggaca agaaagtgga gccc aaatcc 660

tgcgacaaga cacacacctg tccccctgt cctgctcccg aagctgctgg agcccctagc	720
gtcttcctct ttcctcccaa acccaaggac accctcatga tcagcagaac ccctgaagtc	780
acctgtgtcg tcgtggatgt cagccatgag gaccccgagg tgaaattcaa ctggtatgtc	840
gatggcgtcg aggtgcacaa cgccaaaacc aagcccaggg aggaacagta caactccacc	900
tacaggggtgg tgtccgtgct gacagtcctc caccaggact ggctgaacgg caaggagtac	960
aagtgcaagg tgtccaacaa ggctctccct gccccattg agaagaccat cagcaaggcc	1020
aaaggccaac ccaggagacc ccaggtctat aactgcctc cctccaggga cgaactcacc	1080
aagaaccagg tgtccctgac ctgcctggtc aagggtttt atcccagcga catcgccgtc	1140
gagtgggagt ccaacggaca gcccgagaat aactacaaga ccaccctcc tgcctcgac	1200
tccgacggct ctttcttct gtacagcaag ctgaccgtgg aaaaagcag gtggcagcag	1260
ggaaacgtgt tctcctgcag cgtgatgcac gaagccctcc acaaccacta caccagaaa	1320
agcctgtccc tgagccccgg caaa	1344

<210> 16
 <211> 448
 <212> PRT
 <213> Artificial

<220>
 <223> Amino acid sequence of 14C12H1L1(hG1TM) heavy chain

<400> 16

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	Ala	Phe	Ser	Ser	Tyr
			20					25					30		

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

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

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

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

Ala Asn Arg Tyr Gly Glu Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

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

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

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

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

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

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser
225 230 235 240

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

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

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

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 305 310 315 320

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

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

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

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

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400

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

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
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Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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 <212> DNA
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<220>
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 ccaggaaagg gactggattg ggtcgtact atctcaggag gcgggagata cacctactat 180

cctgacagcg tcaagggccg gttcacaatc tctagagata acagtaagaa caatctgtat	240
ctgcagatga acagcctgag ggctgaggac accgcactgt actattgtgc caaccgctac	300
ggggaagcat ggtttgccta ttggggggcag ggaaccctgg tgacagtctc tagtgctagc	360
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gctgctctcg gatgtctggt gaaggactac ttccctgaac ccgtcaccgt gagctggaat	480
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tattccctgt ccagcgtcgt cacagtgcgc agcagcagcc tgggcaccca gacctacatc	600
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gagtgggagt ccaacggaca gcccgagaat aactacaaga ccaccctcc tgtcctcgac	1200
tccgacggct ctttcttct gtacagcaag ctgaccgtgg aaaaagcag gtggcagcag	1260
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 <212> PRT
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 <223> Amino acid sequence of 14C12H1L1(hG1DM) heavy chain

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
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Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Asp Trp Val
35 40 45

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

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

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

Ala Asn Arg Tyr Gly Glu Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

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

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

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

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

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

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
 225 230 235 240

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

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

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

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 305 310 315 320

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

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

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

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

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
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Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
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Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<212> PRT
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<400> 19

Gly Phe Ala Phe Ser Ser Tyr Asp
1 5

<210> 20
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<212> PRT
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<400> 20

Ile Ser Gly Gly Gly Arg Tyr Thr
1 5

<210> 21
<211> 11
<212> PRT
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<400> 21

Ala Asn Arg Tyr Gly Glu Ala Trp Phe Ala Tyr
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<210> 22
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<212> PRT
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<220>
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<400> 22

Gln Asp Ile Asn Thr Tyr
1 5

<210> 23
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<400> 23

Arg Ala Asn
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<210> 24
<211> 9
<212> PRT
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<223> LCDR3

<400> 24

Leu Gln Tyr Asp Glu Phe Pro Leu Thr
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