SEQUENCE LISTING

<110> Akeso Biopharma, Inc.
AKESO PHARMACEUTICALS, INC.

<120> ANTI-CD73 ANTIBODY AND USE THEREOF

<130> FP230110

<150> CN 202011152518.9
<151> 2020-10-23

<160> 36

<170> PatentIn version 3.5

<210> 1
<211> 363
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence of the heavy chain variable region of 19F3

<400> 1
gaggtgcagc tgcagcagtc cggaccagag ctggtgaagc ctggcgcctc catgcggatg 60

tcttgtaagg cctctggcta cagcttcacc ggctatacaa tgaactgggt gaagcagtct 120

cacggcaaga atctggagtg gatcggcctg atcaaccctt acaatgccgg caccagctat 180

aaccagaagt ttaagggcaa ggccaccctg acagtggaca agagctcctc taccgcctac 240

atggagctgc tgtccctgac atctgaggat agcgccgtgt actattgcgc ccggtccgag 300

tacagatatg gcggcgacta ctttgattat tggggccagg gcaccacact gacagtgagc 360

tcc 363

<210> 2
<211> 121
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of the heavy chain variable region of 19F3

<400> 2

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

Ser Met Arg Met Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
35 40 45

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

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

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

Gln Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 3
<211> 339
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence of the light chain variable region of 19F3

<400> 3
gacatcgtga tgacccagtc tccaagctcc ctggcaatga gcgtgggaca gaaggtgaca 60

atgtcttgta agtctagcca gagcctgctg aactcctcta atcagaagaa ctacctggcc 120

tggtatcagc agaagccagg ccagtctccc aagctgctgg tgtactttgc cagcaccagg 180

gagtccggag tgcctgacag attcatcggc tccggctctg gcacagactt caccctgaca 240

atcagctccg tgcaggcaga ggacctggca gattatttct gccagcagca ctacgacacc 300

ccttatacat ttggcggcgg caccaagctg gagatcaag 339

<210> 4
<211> 113

<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of the light chain variable region of 19F3

<400> 4

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

Gln Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

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

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

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

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

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

Lys

<210> 5
<211> 363
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence of the heavy chain variable region of 19F3H1L1(hG1DM)

<400> 5
caggtgcagc tgcagcagtc tggagcagag gtggtgaagc caggagcctc tatgaagatg 60

agctgtaagg ccagcggcta ctccttcacc ggctatacaa tgaactgggt gaagcaggcc 120

cacggccaga atctggagtg gatcggcctg atcaaccctt acaatgccgg cacctcttat 180

aaccagaagt ttcagggcaa ggccaccctg acagtggaca agtccacctc tacagcctac 240

atggagctga gctccctgcg gagcgaggat acagccgtgt actattgcgc ccggtccgag 300

tacagatatg gcggcgacta ctttgattat tggggccagg gcaccacact gaccgtgtct 360

agc 363

<210> 6
<211> 121
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of the heavy chain variable region of 19F3H1L1(hG1DM)

<400> 6

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

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

Thr Met Asn Trp Val Lys Gln Ala His Gly Gln Asn Leu Glu Trp Ile
35 40 45

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

Gln Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

Gln Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 7
<211> 339
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence of the light chain variable region of 19F3H1L1(hG1DM)

<400> 7
gacatcgtga tgacccagtc cccaagctcc ctggcaatgt ctgtgggaga gagggtgaca 60

atgtcctgta agtctagcca gtctctgctg aactcctcta atcagaagaa ctacctggcc 120

tggtatcagc agaagcccgg ccaggcccct aagctgctgg tgtactttgc ctctaccagg 180

gagagcggag tgccagacag attctctggc agcggctccg gcacagactt caccctgaca 240

atcagctccg tgcaggcaga ggacctggca gattatttct gccagcagca ctacgatacc 300

ccctatacat ttggcggcgg caccaagctg gagatcaag 339

<210> 8
<211> 113
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of the light chain variable region of 19F3H1L1(hG1DM)

<400> 8

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

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

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

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

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

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


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


Lys
```

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

<220>
<223> Nucleic acid sequence of the heavy chain variable region of 19F3H2L2(hG1DM) or 19F3H2L3(hG1DM)

<400> 9

```
caggtgcagc tggtgcagtc tggagcagag gtggtgaagc caggagcctc tgtgaaggtg       60

agctgtaagg ccagcggcta ctccttcacc ggctatacaa tgaactgggt gaggcaggca      120

ccaggacaga atctggagtg gatcggcctg atcaaccctt acaatgccgg cacctcttat      180

aaccagaagt ttcagggcaa ggtgaccctg acagtggaca agtccacctc tacagcctac      240

atggagctga gctccctgcg gagcgaggat acagccgtgt actattgcgc ccggtccgag      300

tacagatatg gcggcgacta ctttgattat tggggccagg gcaccacact gaccgtgtct      360

agc                                                                    363
```

<210> 10
<211> 121
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of the heavy chain variable region of 19F3H2L2(hG1DM) or 19F3H2L3(hG1DM)

<400> 10

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

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

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

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

Gln Gly Lys Val Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65   70   75   80

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

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

Gln Gly Thr Thr Leu Thr Val Ser Ser
        115   120

<210> 11
<211> 339
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence of the light chain variable region of 19F3H2L2(hG1DM)

<400> 11
gacatcgtga tgacccagtc cccaagctcc ctggccgtgt ctgtgggaga gcgggtgaca 60

atctcctgta agtctagcca gtctctgctg aactcctcta atcagaagaa ctacctggcc 120

tggtatcagc agaagcccgg ccaggcccct aagctgctga tctacttcgc ctctaccagg 180

gagagcggag tgccagacag attctctggc agcggctccg gcacagactt caccctgaca 240

atcagctccg tgcaggcaga ggacgtggca gattactatt gccagcagca ctacgatacc 300

ccctatacat ttggcggcgg caccaagctg gagatcaag 339

<210> 12
<211> 113

<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of the light chain variable region of 19F3H2L2(hG1DM)

<400> 12

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

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

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

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

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

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

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

Lys

<210> 13
<211> 339
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence of the light chain variable region of 19F3H2L3(hG1DM)

<400> 13
gacatcgtga tgacccagtc cccaagctcc ctggccgtgt ctgtgggaga gcgggtgaca 60

atctcctgta agtctagcca gtctctgctg aactcctcta atcagaagaa ctacctggcc 120

tggtatcagc agaagcccgg ccaggcccct aagctgctga tctacttcgc ctctaccagg 180

gagagcggag tgccagacag attctctggc agcggctccg gcacagactt caccctgaca 240

atcagctccc tgcaggcaga ggacgtggcc gtgtactatt gccagcagca ctacgatacc 300

ccctatacat ttggcggcgg caccaagctg gagatcaag 339

<210> 14
<211> 113
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of the light chain variable region of 19F3H2L3(hG1DM)

<400> 14

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

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

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

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

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

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

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

Lys

<210> 15

<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of HCDR1 of 19F3, 19F3H1L1(hG1DM),19F3H2L2 (hG1DM)or 19F3H2L3(hG1DM)

<400> 15

Gly Tyr Ser Phe Thr Gly Tyr Thr
1 5

<210> 16
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of HCDR2 of 19F3, 19F3H1L1(hG1DM), 19F3H2L2 (hG1DM) or19F3H2L3(hG1DM)

<400> 16

Ile Asn Pro Tyr Asn Ala Gly Thr
1 5

<210> 17
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of HCDR3 of 19F3, 19F3H1L1(hG1DM), 19F3H2L2 (hG1DM) or 19F3H2L3(hG1DM)

<400> 17

Ala Arg Ser Glu Tyr Arg Tyr Gly Gly Asp Tyr Phe Asp Tyr
1 5 10

<210> 18
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of LCDR1 of 19F3, 19F3H1L1(hG1DM), 19F3H2L2 (hG1DM) or 19F3H2L3(hG1DM)

<400> 18

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

<210> 19
<211> 3
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of LCDR2 of 19F3, 19F3H1L1(hG1DM), 19F3H2L2 (hG1DM) or 19F3H2L3(hG1DM)

<400> 19

Phe Ala Ser
1

<210> 20
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of LCDR3 of 19F3, 19F3H1L1(hG1DM), 19F3H2L2 (hG1DM) or 19F3H2L3(hG1DM)

<400> 20

Gln Gln His Tyr Asp Thr Pro Tyr Thr
1 5

<210> 21
<211> 330
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence of the heavy chain constant region of 19F3H1L1(hG1DM), 19F3H2L2(hG1DM) or 19F3H2L3(hG1DM)

<400> 21

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

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

```
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240
```

```
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
```

<210> 22
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence of the light chain constant region of 19F3H1L1(hG1DM), 19F3H2L2(hG1DM) or 19F3H2L3(hG1DM)

<400> 22

```
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1               5                   10                  15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
            20                  25                  30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        35                  40                  45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50                  55                  60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
```

65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 23
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of HCDR1 involved in the heavy chain variable region of BiAb004 (hG1TM)

<400> 23

Gly Phe Ala Phe Ser Ser Tyr Asp
1 5

<210> 24
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of HCDR2 involved in the heavy chainvariable region of BiAb004 (hG1TM)

<400> 24

Ile Ser Gly Gly Gly Arg Tyr Thr
1 5

<210> 25
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of HCDR3 involved in the heavy chain variable region of BiAb004 (hG1TM)

<400> 25

Ala Asn Arg Tyr Gly Glu Ala Trp Phe Ala Tyr

1 5 10

<210> 26
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of HCDR4 involved in the heavy chain variable region of BiAb004 (hG1TM)

<400> 26

Gly Tyr Ser Phe Thr Gly Tyr Thr
1 5

<210> 27
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of HCDR5 involved in the heavy chain variable region of BiAb004 (hG1TM)

<400> 27

Ile Asn Pro Tyr Asn Asn Ile Thr
1 5

<210> 28
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of HCDR6 involved in the heavy chain variable region of BiAb004 (hG1TM)

<400> 28

Ala Arg Leu Asp Tyr Arg Ser Tyr
1 5

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

<220>
<223> Amino acid sequence of HCDR7 involved in the heavy chain variable region of BiAb004 (hG1TM)

<400> 29

Thr Gly Ala Val Thr Thr Ser Asn Phe
1   5

<210> 30
<211> 3
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of HCDR8 involved in the heavy chain variable region of BiAb004 (hG1TM)

<400> 30

Gly Thr Asn
1

<210> 31
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of HCDR9 involved in the heavy chain variable region of BiAb004 (hG1TM)

<400> 31

Ala Leu Trp Tyr Ser Asn His Trp Val
1   5

<210> 32
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of LCDR1 involved in the heavy chain variable region of BiAb004 (hG1TM)

<400> 32

Gln Asp Ile Asn Thr Tyr
1   5

<210> 33
<211> 3
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of LCDR2 involved in the heavy chain variable region of BiAb004 (hG1TM)

<400> 33

Arg Ala Asn
1

<210> 34
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of LCDR3 involved in the heavy chain variable region of BiAb004 (hG1TM)

<400> 34

Leu Gln Tyr Asp Glu Phe Pro Leu Thr
1 5

<210> 35
<211> 713
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of the heavy chain of BiAb004(hG1TM)

<400> 35

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
            420                 425                 430

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    450                 455                 460

Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys
```

```
465                 470                 475                 480

Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser
                485                 490                 495

Phe Thr Gly Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Cys
            500                 505                 510

Leu Glu Trp Ile Gly Leu Ile Asn Pro Tyr Asn Asn Ile Thr Asn Tyr
        515                 520                 525

Ala Gln Lys Phe Gln Gly Arg Val Thr Phe Thr Val Asp Thr Ser Ile
    530                 535                 540

Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Gly
545                 550                 555                 560

Val Tyr Phe Cys Ala Arg Leu Asp Tyr Arg Ser Tyr Trp Gly Gln Gly
                565                 570                 575

Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly
            580                 585                 590

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ala Val Val Thr
        595                 600                 605

Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu Thr
    610                 615                 620

Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Phe Pro Asn Trp
625                 630                 635                 640

Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Ser Leu Ile Gly Gly Thr
                645                 650                 655

Asn Asn Lys Ala Ser Trp Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu
            660                 665                 670

Gly Gly Lys Ala Ala Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu
        675                 680                 685
```

Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn His Trp Val Phe Gly
690 695 700

Cys Gly Thr Lys Leu Thr Val Leu Arg
705 710

<210> 36
<211> 214
<212> PRT
<213> Artificial sequence

<220>
<223> Amino acid sequence of the light chain of BiAb004(hG1TM)

<400> 36

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
```