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<120> TREATMENT OF LAG-3 POSITIVE TUMORS

<130> 3338.070PC04/ELE/PAC/E-H

<150> 62/512,648
<151> 2017-05-30

<150> 62/513,813
<151> 2017-06-01

<150> 62/555,176
<151> 2017-09-07

<150> 62/582,178
<151> 2017-11-06

<160> 32

<170> PatentIn version 3.5

<210> 1
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy Chain Amino Acid Sequence; Anti-LAG-3 mAb (BMS-986016)

<400> 1

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

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

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

```
Gly Glu Ile Asn His Arg Gly Ser Thr Asn Ser Asn Pro Ser Leu Lys
    50                  55                  60

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

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

Phe Gly Tyr Ser Asp Tyr Glu Tyr Asn Trp Phe Asp Pro Trp Gly Gln
            100                 105                 110

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

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

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

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

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

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

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

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

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

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
```

260 265 270

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

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

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

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

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

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

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

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

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

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

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

<210> 2
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain Amino Acid Sequence; Anti-LAG-3 mAb (BMS-986016)

<400> 2

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Asn Leu Glu Ile 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> 3
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy Chain Variable Region (VH) Amino Acid Sequence; Anti-LAG-3 mAb (BMS-986016)

<400> 3

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

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

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

Gly Glu Ile Asn His Arg Gly Ser Thr Asn Ser Asn Pro Ser Leu Lys
50 55 60

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

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

Phe Gly Tyr Ser Asp Tyr Glu Tyr Asn Trp Phe Asp Pro Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 4
<211> 360
<212> DNA
<213> Artificial Sequence

<220>

<223> Heavy Chain Variable Region (VH) Nucleotide Sequence; Anti-LAG-3 mAb (BMS-986016)

<400> 4

caggtgcagc tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60

acctgcgctg tctatggtgg gtccttcagt gattactact ggaactggat ccgccagccc 120

ccagggaagg ggctggagtg gattggggaa atcaatcatc gtggaagcac caactccaac 180

ccgtccctca agagtcgagt caccctatca ctagacacgt ccaagaacca gttctccctg 240

aagctgaggt ctgtgaccgc cgcggacacg gctgtgtatt actgtgcgtt tggatatagt 300

gactacgagt acaactggtt cgacccctgg ggccagggaa ccctggtcac cgtctcctca 360

<210> 5
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain Variable Region (VL) Amino Acid Sequence; Anti-LAG-3 mAb (BMS-986016)

<400> 5

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

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

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

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

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

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

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

<210> 6
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Light Chain Variable Region (VL) Nucleotide Sequence; Anti-LAG-3 mAb (BMS-986016)

<400> 6
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtattagc agctacttag cctggtacca acagaaacct 120

ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtcagcag cgtagcaact ggcctctcac ttttggccag 300

gggaccaacc tggagatcaa a 321

<210> 7
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy Chain CDR1 Amino Acid Sequence; Anti-LAG-3 mAb (BMS-986016)

<400> 7

Asp Tyr Tyr Trp Asn
1 5

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

<220>
<223> Heavy Chain CDR2 Amino Acid Sequence; Anti-LAG-3 mAb (BMS-986016)

<400> 8

Glu Ile Asn His Arg Gly Ser Thr Asn Ser Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 9
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy Chain CDR3 Amino Acid Sequence; Anti-LAG-3 mAb (BMS-986016)

<400> 9

Gly Tyr Ser Asp Tyr Glu Tyr Asn Trp Phe Asp Pro
1 5 10

<210> 10
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain CDR1 Amino Acid Sequence; Anti-LAG-3 mAb (BMS-986016)

<400> 10

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

<210> 11
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain CDR2 Amino Acid Sequence; Anti-LAG-3 mAb (BMS-986016)

<400> 11

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 12
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain CDR3 Amino Acid Sequence; Anti-LAG-3 mAb (BMS-986016)

<400> 12

Gln Gln Arg Ser Asn Trp Pro Leu Thr
1 5

<210> 13
<211> 525
<212> PRT
<213> Artificial Sequence

<220>
<223> Human LAG-3 Amino Acid Sequence

<400> 13

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Met Trp Glu Ala Gln Phe Leu Gly Leu Leu Phe Leu Gln Pro Leu Trp
1               5                  10                  15


Val Ala Pro Val Lys Pro Leu Gln Pro Gly Ala Glu Val Pro Val Val
            20                  25                  30


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


Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly Val Thr Trp Gln
    50                  55                  60


His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro Gly His Pro Leu
65                  70                  75                  80


Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp Gly Pro Arg Pro
                85                  90                  95


Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly Leu Arg Ser Gly
            100                 105                 110


Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu Arg Gly Arg Gln
        115                 120                 125


Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg Arg Ala Asp Ala
    130                 135                 140


Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg Ala Leu Ser Cys
145                 150                 155                 160


Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr Ala Ser Pro Pro
                165                 170                 175
```

```
Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn Cys Ser Phe Ser
            180                 185                 190

Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg Asn Arg Gly Gln
        195                 200                 205

Gly Arg Val Pro Val Arg Glu Ser Pro His His His Leu Ala Glu Ser
    210                 215                 220

Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser Gly Pro Trp Gly
225                 230                 235                 240

Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser Ile Met Tyr Asn
                245                 250                 255

Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Pro Leu Thr Val Tyr Ala
            260                 265                 270

Gly Ala Gly Ser Arg Val Gly Leu Pro Cys Arg Leu Pro Ala Gly Val
        275                 280                 285

Gly Thr Arg Ser Phe Leu Thr Ala Lys Trp Thr Pro Pro Gly Gly Gly
    290                 295                 300

Pro Asp Leu Leu Val Thr Gly Asp Asn Gly Asp Phe Thr Leu Arg Leu
305                 310                 315                 320

Glu Asp Val Ser Gln Ala Gln Ala Gly Thr Tyr Thr Cys His Ile His
                325                 330                 335

Leu Gln Glu Gln Gln Leu Asn Ala Thr Val Thr Leu Ala Ile Ile Thr
            340                 345                 350

Val Thr Pro Lys Ser Phe Gly Ser Pro Gly Ser Leu Gly Lys Leu Leu
        355                 360                 365

Cys Glu Val Thr Pro Val Ser Gly Gln Glu Arg Phe Val Trp Ser Ser
    370                 375                 380
```

```
Leu Asp Thr Pro Ser Gln Arg Ser Phe Ser Gly Pro Trp Leu Glu Ala
385                 390                 395                 400


Gln Glu Ala Gln Leu Leu Ser Gln Pro Trp Gln Cys Gln Leu Tyr Gln
                405                 410                 415


Gly Glu Arg Leu Leu Gly Ala Ala Val Tyr Phe Thr Glu Leu Ser Ser
            420                 425                 430


Pro Gly Ala Gln Arg Ser Gly Arg Ala Pro Gly Ala Leu Pro Ala Gly
        435                 440                 445


His Leu Leu Leu Phe Leu Thr Leu Gly Val Leu Ser Leu Leu Leu Leu
    450                 455                 460


Val Thr Gly Ala Phe Gly Phe His Leu Trp Arg Arg Gln Trp Arg Pro
465                 470                 475                 480


Arg Arg Phe Ser Ala Leu Glu Gln Gly Ile His Pro Pro Gln Ala Gln
                485                 490                 495


Ser Lys Ile Glu Glu Leu Glu Gln Glu Pro Glu Pro Glu Pro Glu Pro
            500                 505                 510


Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Gln Leu
        515                 520                 525


<210>  14
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  LAG-3 Epitope

<400>  14

Pro Gly His Pro Leu Ala Pro Gly
1               5


<210>  15
<211>  8
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223>  LAG-3 Epitope

<400>  15

His Pro Ala Ala Pro Ser Ser Trp
1               5


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

<220>
<223>  LAG-3 Epitope

<400>  16

Pro Ala Ala Pro Ser Ser Trp Gly
1               5


<210>  17
<211>  440
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Heavy Chain Amino Acid Sequence; Anti-PD-1 mAb (BMS936558)

<400>  17

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


Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe Ser Asn Ser
            20                  25                  30


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


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


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

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

Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
            100                 105                 110

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

Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
    130                 135                 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
145                 150                 155                 160

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

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

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

Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala
    210                 215                 220

Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
225                 230                 235                 240

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

Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
            260                 265                 270

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
        275                 280                 285

Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
    290                 295                 300
```

```
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
305                 310                 315                 320

Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
                325                 330                 335

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr
            340                 345                 350

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
        355                 360                 365

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

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

Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
                405                 410                 415

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
            420                 425                 430

Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440


<210>  18
<211>  213
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Light Chain Amino Acid Sequence; Anti-PD-1 mAb (BMS936558)

<400>  18

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile 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 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190

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

Asn Arg Gly Glu Cys
    210
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<210> 19
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy Chain Variable Region (VH) Amino Acid Sequence; Anti-PD-1 mAb (BMS936558)

<400> 19

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

Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe Ser Asn Ser
20 25 30

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

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

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

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

Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser

<210> 20
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Heavy Chain Variable Region (VH) Nucleotide Sequence; Anti-PD-1 mAb (BMS936558)

<400> 20
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

gactgtaaag cgtctggaat caccttcagt aactctggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atttggtatg atggaagtaa aagatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgttt 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gacaaacgac 300

gactactggg gccagggaac cctggtcacc gtctcctca 339

<210> 21
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain Variable Region (VL) Amino Acid Sequence; Anti-PD-1 mAb (BMS936558)

<400> 21

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

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

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

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

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

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

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

<210> 22
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Light Chain Variable Region (VL) Nucleotide Sequence; Anti-PD-1

mAb (BMS936558)

<400> 22
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagt agttacttag cctggtacca acagaaacct 120

ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240

gaagattttg cagtttatta ctgtcagcag agtagcaact ggcctcggac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 23
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy Chain CDR1 Amino Acid Sequence; Anti-PD-1 mAb (BMS936558)

<400> 23

Asn Ser Gly Met His
1 5

<210> 24
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy Chain CDR2 Amino Acid Sequence; Anti-PD-1 mAb (BMS936558)

<400> 24

Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 25
<211> 4
<212> PRT
<213> Artificial Sequence

<220>

<223> Heavy Chain CDR3 Amino Acid Sequence; Anti-PD-1 mAb (BMS936558)

<400> 25

Asn Asp Asp Tyr
1

<210> 26
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain CDR1 Amino Acid Sequence; Anti-PD-1 mAb (BMS936558)

<400> 26

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

<210> 27
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain CDR2 Amino Acid Sequence; Anti-PD-1 mAb (BMS936558)

<400> 27

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 28
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain CDR3 Amino Acid Sequence; Anti-PD-1 mAb (BMS936558)

<400> 28

Gln Gln Ser Ser Asn Trp Pro Arg Thr
1 5

<210> 29
<211> 2106
<212> DNA
<213> Artificial Sequence

<220>
<223>  Complete Homo sapiens PD-1 sequence

<400>  29
agtttccctt ccgctcacct ccgcctgagc agtggagaag gcggcactct ggtggggctg 60

ctccaggcat gcagatccca caggcgccct ggccagtcgt ctgggcggtg ctacaactgg 120

gctggcggcc aggatggttc ttagactccc cagacaggcc ctggaacccc cccaccttct 180

tcccagccct gctcgtggtg accgaagggg acaacgccac cttcacctgc agcttctcca 240

acacatcgga gagcttcgtg ctaaactggt accgcatgag ccccagcaac cagacggaca 300

agctggccgc cttccccgag gaccgcagcc agcccggcca ggactgccgc ttccgtgtca 360

cacaactgcc caacgggcgt gacttccaca tgagcgtggt cagggcccgg cgcaatgaca 420

gcggcaccta cctctgtggg gccatctccc tggcccccaa ggcgcagatc aaagagagcc 480

tgcgggcaga gctcagggtg acagagagaa gggcagaagt gcccacagcc caccccagcc 540

cctcacccag gccagccggc cagttccaaa ccctggtggt tggtgtcgtg ggcggcctgc 600

tgggcagcct ggtgctgcta gtctgggtcc tggccgtcat ctgctcccgg gccgcacgag 660

ggacaatagg agccaggcgc accggccagc ccctgaagga ggacccctca gccgtgcctg 720

tgttctctgt ggactatggg gagctggatt tccagtggcg agagaagacc ccggagcccc 780

ccgtgccctg tgtccctgag cagacggagt atgccaccat tgtctttcct agcggaatgg 840

gcacctcatc ccccgcccgc aggggctcag ccgacggccc tcggagtgcc cagccactga 900

ggcctgagga tggacactgc tcttggcccc tctgaccggc ttccttggcc accagtgttc 960

tgcagaccct ccaccatgag cccgggtcag cgcatttcct caggagaagc aggcagggtg 1020

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cacctgcacc aggcacagcc ccaccacagg actcatgtct caatgcccac agtgagccca 1140

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<220>
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<220>
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ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180

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Met Tyr Pro Pro Pro Tyr
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