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<120> COMBINATION OF PD-1 ANTAGONIST AND CPG-C TYPE OLIGONUCLEOTIDE FOR TREATING CANCER

<130> 24127

<150> 62/169,309
<151> 2015-06-01

<150> 62/168,449
<151> 2015-05-29

<160> 63

<170> PatentIn version 3.5

<210> 1
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<400> 1

Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Phe Ser Tyr Leu His
1 5 10 15

<210> 2
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<220>
<223> hPD-1.08A light chain CDR2

<400> 2

Leu Ala Ser Asn Leu Glu Ser
1   5

<210> 3
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<213> Artificial Sequence

<220>
<223> hPD-1.08A light chain CDR3

<400> 3

Gln His Ser Trp Glu Leu Pro Leu Thr
1   5

<210> 4
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<220>
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<400> 4

Ser Tyr Tyr Leu Tyr
1   5

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<400> 5

Gly Val Asn Pro Ser Asn Gly Gly Thr Asn Phe Ser Glu Lys Phe Lys
1 5 10 15

Ser

<210> 6
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<400> 6

Arg Asp Ser Asn Tyr Asp Gly Gly Phe Asp Tyr
1 5 10

<210> 7
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<213> Artificial Sequence

<220>
<223> hPD-1.09A light chain CDR1

<400> 7

Arg Ala Ser Lys Gly Val Ser Thr Ser Gly Tyr Ser Tyr Leu His
1 5 10 15

<210> 8
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<212> PRT
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<220>
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<400> 8

Leu Ala Ser Tyr Leu Glu Ser
1 5

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

<220>
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<400> 9

Gln His Ser Arg Asp Leu Pro Leu Thr
1 5

<210> 10
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<213> Artificial Sequence

<220>
<223> hPD-1.09A heavy chain CDR1

<400> 10

Asn Tyr Tyr Met Tyr
1 5

<210> 11
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> hPD-1.09A heavy chain CDR2

<400> 11

Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe Lys
1 5 10 15

Asn

<210> 12
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> hPD-1.09A heavy chain CDR3

<400> 12

Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr
1 5 10

<210> 13
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<220>
<223> 109A-H heavy chain variable region

<400> 13

Gln Val Gln Leu Val Gln Ser Gly Val 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 Asn Tyr
20 25 30

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

Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe
50 55 60

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

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

Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

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

<220>
<223> 409A-H heavy chain full length

<400> 14

Gln Val Gln Leu Val Gln Ser Gly Val 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 Asn Tyr
20 25 30

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

Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe
50 55 60

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

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

Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr 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>  15
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  K09A-L-11 light chain variable region

<400>  15

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 Lys Gly Val Ser Thr Ser
            20   25   30

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

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

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

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

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

<210> 16
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> K09A-L-16 light chain variable region

<400> 16

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

Glu Pro Ala Ser Ile Ser Cys Arg Ala Ser Lys Gly Val Ser Thr Ser
            20   25   30

Gly Tyr Ser Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro
        35   40   45

Gln Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Asp
    50   55   60

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


Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95


Asp Leu Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 17
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> K09A-L-17 light chain variable region

<400> 17

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


Glu Pro Ala Ser Ile Ser Cys Arg Ala Ser Lys Gly Val Ser Thr Ser
            20                  25                  30


Gly Tyr Ser Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro
        35                  40                  45


Gln Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Asp
    50                  55                  60


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


Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95
```

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

<210> 18
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> K09A-L-11 light chain full length

<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 Lys Gly Val Ser Thr Ser
20 25 30

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

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

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

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

Asp Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

```
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145                 150                 155                 160


Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175


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


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


Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210>  19
<211>  218
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  K09A-L-16 light chain full length

<400>  19

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


Glu Pro Ala Ser Ile Ser Cys Arg Ala Ser Lys Gly Val Ser Thr Ser
            20                  25                  30


Gly Tyr Ser Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro
        35                  40                  45


Gln Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Asp
    50                  55                  60
```

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


Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95


Asp Leu Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105                 110


Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        115                 120                 125


Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
    130                 135                 140


Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145                 150                 155                 160


Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175


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


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


Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 20
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> K09A-L-17 light chain full length

<400> 20

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

Glu Pro Ala Ser Ile Ser Cys Arg Ala Ser Lys Gly Val Ser Thr Ser
            20                  25                  30

Gly Tyr Ser Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro
        35                  40                  45

Gln Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Asp
    50                  55                  60

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

Arg Val Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95

Asp Leu Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105                 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        115                 120                 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
    130                 135                 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145                 150                 155                 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
            180                 185                 190
```

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


Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210>  21
<211>  447
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Pembrolizumab Heavy chain

<400>  21

Gln Val Gln Leu Val Gln Ser Gly Val 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 Asn Tyr
            20                  25                  30


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


Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe
    50                  55                  60


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


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


Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr Trp Gly Gln
            100                 105                 110
```

```
Gly Thr Thr 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>  22
<211>  218
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Pembrolizumab Light Chain

<400>  22

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 Lys Gly Val Ser Thr Ser
            20                  25                  30

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

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

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

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

Asp Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
            100                 105                 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        115                 120                 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
    130                 135                 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145                 150                 155                 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 23
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> Nivolumab Heavy chain

<400> 23

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> 24
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Nivolumab Light Chain

<400> 24

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

<220>
<223> Synthetic construct

<400> 25

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Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp His Leu Leu
1               5                   10                  15


Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr
            20                  25                  30


Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu
        35                  40                  45


Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile
    50                  55                  60


Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser
65                  70                  75                  80


Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn
                85                  90                  95


Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr
            100                 105                 110


Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val
        115                 120                 125


Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val
    130                 135                 140
```

```
Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr
145                 150                 155                 160


Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser
                165                 170                 175


Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn
            180                 185                 190


Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr
        195                 200                 205


Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu
    210                 215                 220


Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His
225                 230                 235                 240


Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr
                245                 250                 255


Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys
            260                 265                 270


Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu
        275                 280                 285


Glu Thr
    290
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<210> 26
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<212> PRT
<213> Rattus norvegicus

<400> 26

Lys Thr Ser Gln Asn Ile Phe Glu Asn Leu Ala

1 5 10

<210> 27
<211> 8
<212> PRT
<213> Rattus norvegicus

<400> 27

Tyr Asn Ala Ser Pro Leu Gln Ala
1 5

<210> 28
<211> 8
<212> PRT
<213> Rattus norvegicus

<400> 28

His Gln Tyr Tyr Ser Gly Tyr Thr
1 5

<210> 29
<211> 10
<212> PRT
<213> Rattus norvegicus

<400> 29

Gly Phe Thr Phe Ser Asp Tyr His Met Ala
1 5 10

<210> 30
<211> 17
<212> PRT
<213> Rattus norvegicus

<400> 30

Ser Ile Thr Leu Asp Ala Thr Tyr Thr Tyr Tyr Arg Asp Ser Val Arg
1 5 10 15

Gly

<210> 31
<211> 10
<212> PRT
<213> Rattus norvegicus

<400> 31

His Arg Gly Phe Ser Val Trp Leu Asp Tyr
1 5 10

<210> 32
<211> 120
<212> PRT
<213> Homo sapiens

<400> 32

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

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

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

Ala Ser Ile Thr Leu Asp Ala Thr Tyr Thr Tyr Tyr Arg Asp Ser Val
50 55 60

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

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

Ala Arg His Arg Gly Phe Ser Val Trp Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala
        115   120

<210> 33
<211> 111
<212> PRT
<213> Homo sapiens

<400> 33

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Tyr Ser Gly Tyr Thr
                85   90   95

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

<210> 34
<211> 449
<212> PRT
<213> Homo sapiens

<400> 34

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

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1               5                   10                  15

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

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

Ala Ser Ile Thr Leu Asp Ala Thr Tyr Thr Tyr Tyr Arg Asp Ser Val
    50                  55                  60

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

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

Ala Arg His Arg Gly Phe Ser Val Trp Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110

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

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

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

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

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

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
```

195 200 205

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

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

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

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

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

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

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

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

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

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

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

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu

385 390 395 400

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

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

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

Lys

<210> 35
<211> 213
<212> PRT
<213> Homo sapiens

<400> 35

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Tyr Ser Gly Tyr Thr
85 90 95

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


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


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


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


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


Thr Leu Thr 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


<210>  36
<211>  118
<212>  PRT
<213>  Murine

<400>  36

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


Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30
```

```
Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ala Ala Phe Ile
    50                  55                  60


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


Lys Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95


Arg Asn Arg Gly Tyr Asp Val Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Thr Leu Thr Val Ser Ser
        115


<210>  37
<211>  111
<212>  PRT
<213>  Murine

<400>  37

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


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


Gly His Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Trp Arg Ala Ser Thr Leu Glu Ser Gly Ile Pro Ala
    50                  55                  60
```

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

Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Gly Asn
85 90 95

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

<210> 38
<211> 107
<212> DNA
<213> Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1) . . . (3)
<223> OTHER INFORMATION: n = absent or A, T, G or C
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4) . . . (8)
<223> OTHER INFORMATION: Sequence of bases 4-8 may be repeated up to 4 times
<220> FEATURE:
<221> NAME/KEY: misc_feature
<220> LOCATION: (7) . . . (8)
<223> OTHER INFORMATION: n = absent or A, T, G or C
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9) . . . (10)
<223> OTHER INFORMATION: n = absent or A, T, C or G
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 11
<223> OTHER INFORMATION: n = A, T, C or G and base is complementary to base 16
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11) . . . (18)
<223> OTHER INFORMATION: Sequence of bases 11-18 may be repeated up to 20 times
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 12
<223> OTHER INFORMATION: n = A, T, C or G and base is complementary to base 15

<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 15
<223> OTHER INFORMATION: n = A, T, C or G and base is complementary to base 12
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 16
<223> OTHER INFORMATION: n = A, T, C or G and base is complementary to base 11
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (17) . . . (18)
<223> OTHER INFORMATION: Bases 17-18 may be absent
<222> LOCATION: 19-107
<223> OTHER INFORMATION : n = absent or A, T, C or G

<400> 38
nntcgnnnn nncgnncgnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnn 107

<210> 39
<211> 35
<212> DNA
<213> Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 4-7
<223> OTHER INFORMATION: n is absent, A, T, C or G
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 8
<223> OTHER INFORMATION: n=A, T, C or G and base is complementary to base 13
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 9
<223> OTHER INFORMATION: n=A, T, C or G and base is complementary to base 12
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 12
<223> OTHER INFORMATION: n=A, T, C or G and base is complementary to base 9
<220> FEATURE:
<221> NAME/KEY: misc_feature

<222> LOCATION: 13
<223> OTHER INFORMATION: n=A, T, C or G and base is complementary to base 8
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 8-15
<223> OTHER INFORMATION: sequence of bases 8-15 may be repeated up to 4 times
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 16-35
<223> OTHER INFORMATION: n is absent, A, T, C or G

<400> 39
tcgnnnnnnc gnncgnnnnn nnnnnnnnnn nnnnn 35

<210> 40
<211> 46
<212> DNA
<213> Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 4-8
<223> OTHER INFORMATION: n is absent, A, T, C or G
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 27-46
<223> OTHER INFORMATION: n is absent, A, T, C or G

<400> 40
tcgnnnnntt cgaacgttcg aacgttnnnn nnnnnnnnnn nnnnnn 46

<210> 41
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 41
tcgtcgaacg ttcgagatga t 21

<210> 42
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 42
tcgttcgaac gttcgaacgt tcgaa 25

<210> 43
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 43
tcgaacgttc gaacgttcga acgtt 25

<210> 44
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 44
tcgaacgttc gaacgttcga atttt 25

<210> 45
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 45
tcgaacgttc gaacgttcga acgttcgaat 30

<210> 46
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 46
tcgtaacgtt cgaacgttcg aacgtta 27

<210> 47
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 47
tcgtaacgtt cgaacgttcg aacgtt 26

<210> 48
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
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<400> 48tcgtaacgtt cgaacgttcg aacgt 25

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 49
tcgtaacgtt cgaacgttcg aacg 24

<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 50
tcgtaacgtt cgaacgttcg aac 23

<210> 51
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 51
tcgtaacgtt cgaacgttcg aa 22

<210> 52
<211> 160
<212> PRT
<213> Homo sapiens

<400> 52

Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15

Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30

Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45

Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60

Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala

65 70 75 80

Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
85 90 95

Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110

Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
115 120 125

Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
130 135 140

Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
145 150 155 160

<210> 53
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 53
tccatgacgt tcctgacgtt 20

<210> 54
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 54
tgactgtgaa ccttagagat ga 22

<210> 55

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

<220>
<223> Antibody MEB037.22C3 CDRL1

<400> 55

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

Ala

<210> 56
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody MEB037.22C3 CDRL2

<400> 56

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 57
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody MEB037.22C3 CDRL3

<400> 57

Lys Gln Ser Tyr Asp Val Val Thr
1 5

<210> 58
<211> 112
<212> PRT

<213> Artificial Sequence

<220>
<223> Antibody MEB037.22C3 Mature Variable Region

<400> 58

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

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

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

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

Pro Asp Arg Phe Thr 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 Val Tyr Tyr Cys Lys Gln
85 90 95

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

<210> 59
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody MEB037.22C3 CDRH1

<400> 59

Ser Tyr Trp Ile His
1 5

<210> 60
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody MEB037.22C3 CDRH1

<400> 60

Gly Thr Thr Phe Thr Ser Tyr Trp Ile His
1 5 10

<210> 61
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody MEB037.22C3 CDRH2

<400> 61

Tyr Ile Asn Pro Ser Ser Gly Tyr His Glu Tyr Asn Gln Lys Phe Ile
1 5 10 15

Asp

<210> 62
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody MEB037.22C3 CDRH3

<400> 62

Ser Gly Trp Leu Ile His Gly Asp Tyr Tyr Phe Asp Phe
1 5 10

<210> 63

<211> 122
<212> PRT
<213> Artificial Sequence

<220> Antibody MEB037.22C3
<223> Mature Variable Region

<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Xaa can be Q or pE

<400> 63

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


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


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


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


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


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


Ala Arg Ser Gly Trp Leu Ile His Gly Asp Tyr Tyr Phe Asp Phe Trp
            100                 105                 110


Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
        115                 120
```