SEQUENCE LISTING

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<120> Covalently Bonded Diabodies Having Immunoreactivity with PD-1 and LAG-3 and Methods of Use Thereof

<130> 1301.0115PCT

<150> 62/017,467
<151> 2014-06-26

<160> 32

<170> PatentIn version 3.5

<210> 1
<211> 288
<212> PRT
<213> Homo sapiens

<220>
<221> misc
<222> (1)..(288)
<223> human PD-1 including signal sequence

<400> 1

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Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1               5                   10                  15


Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
            20                  25                  30


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


Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
    50                  55                  60
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```
Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65                  70                  75                  80

Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
                85                  90                  95

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
            100                 105                 110

Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
        115                 120                 125

Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
    130                 135                 140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
145                 150                 155                 160

Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Val Gly Val Val Gly Gly
                165                 170                 175

Leu Leu Gly Ser Leu Val Leu Leu Val Trp Val Leu Ala Val Ile Cys
            180                 185                 190

Ser Arg Ala Ala Arg Gly Thr Ile Gly Ala Arg Arg Thr Gly Gln Pro
        195                 200                 205

Leu Lys Glu Asp Pro Ser Ala Val Pro Val Phe Ser Val Asp Tyr Gly
    210                 215                 220

Glu Leu Asp Phe Gln Trp Arg Glu Lys Thr Pro Glu Pro Pro Val Pro
225                 230                 235                 240

Cys Val Pro Glu Gln Thr Glu Tyr Ala Thr Ile Val Phe Pro Ser Gly
                245                 250                 255
```

```
Met Gly Thr Ser Ser Pro Ala Arg Arg Gly Ser Ala Asp Gly Pro Arg
            260                 265                 270


Ser Ala Gln Pro Leu Arg Pro Glu Asp Gly His Cys Ser Trp Pro Leu
        275                 280                 285


<210>  2
<211>  113
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<222>  (1)..(113)
<223>  Anti-PD-1 Antibody mAb 1 Heavy Chain Variable Region

<400>  2

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
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100 105 110

Ser

<210> 3
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(107)
<223> Anti-PD-1 Antibody mAb 1 Light Chain Variable Region

<400> 3

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> 4
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-PD-1 Antibody mAb 2 Heavy Chain Variable Region

<400> 4

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> 5
<211> 111
<212> PRT
<213> Artificial Sequence

<220>

<223> Humanized Anti-PD-1 Antibody mAb 2 Light Chain Variable Region

<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 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> 6
<211> 121
<212> PRT
<213> Mus musculus

<400> 6

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

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

Trp Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35 40 45

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

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

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

Ala Arg Trp Arg Asp Ser Ser Gly Tyr His Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 7
<211> 111
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(111)
<223> Anti-PD-1 Antibody mAb 3 Light Chain Variable Region

<400> 7

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

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

Lys Leu Leu Ile Lys Phe Gly Ser Asn Leu Glu Ser Gly Ile Pro Ala
50 55 60

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

Pro Val Glu Glu Glu Asp Thr Ala Thr Tyr Tyr Cys Gln His Ser Trp
85 90 95

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

<210> 8
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-PD-1 Antibody mAb 4 Heavy Chain Variable Region

<400> 8

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

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

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

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

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

Leu Gln Ile Thr Ser Leu Thr Ala Glu Asp Thr Gly Met Tyr Phe Cys
85 90 95

```
Val Arg Val Gly Tyr Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  9
<211>  106
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Humanized Anti-PD-1 Antibody mAb 4 Light Chain Variable Region

<400>  9

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


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


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


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


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


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


Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
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<210> 10
<211> 525
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(525)
<223> human LAG3 (CD223) protein including signal sequence

<400> 10

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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 Ile 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
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<210> 11
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(120)
<223> Anti-LAG-3 Antibody mAb 1 Heavy Chain Variable Region

<400> 11

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 Asn Gly Asn 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> 12
<211> 107

<212> PRT
<213> Homo sapiens

<220>
<221> MOD_RES
<222> (1)..(107)
<223> Anti-LAG-3 Antibody mAb 1 Light Chain Variable Region

<400> 12

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> 13
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 1

<400> 13

Gly Gly Gly Ser Gly Gly Gly Gly
1 5

<210> 14
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> E-Coil Heterodimer-Promoting Domain

<400> 14

Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val
1 5 10 15

Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys
20 25

<210> 15
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> K-Coil Heterodimer-Promoting Domain

<400> 15

Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
1 5 10 15

Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
20 25

<210> 16
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-Containing E-Coil Heterodimer-Promoting Domain

<400> 16

Glu Val Ala Ala Cys Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val
1 5 10 15

Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys
20 25

<210> 17
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-Containing K-Coil Heterodimer-Promoting Domain

<400> 17

Lys Val Ala Ala Cys Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
1 5 10 15

Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
20 25

<210> 18
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-Containing Spacer Peptide

<400> 18

Gly Gly Cys Gly Gly Gly
1 5

<210> 19
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-Containing Linker Peptide

<400> 19

Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10

<210> 20
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Alternative Cysteine-Containing Linker Peptide

<400> 20

Leu Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys
1 5 10 15

<210> 21
<211> 218
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(218)
<223> IgG1 Fc Region

<400> 21

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
1 5 10 15

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
20 25 30

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
35 40 45

```
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
    50                  55                  60

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
65                  70                  75                  80

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                85                  90                  95

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
            100                 105                 110

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
        115                 120                 125

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

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
145                 150                 155                 160

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
                165                 170                 175

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
            180                 185                 190

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
        195                 200                 205

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215
```

<210> 22
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> "Knob-Bearing" IgG1 CH2-CH3 Domain

<400> 22

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


Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
            20                  25                  30


Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
        35                  40                  45


Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
    50                  55                  60


Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
65                  70                  75                  80


His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                85                  90                  95


Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
            100                 105                 110


Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
        115                 120                 125


Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr
    130                 135                 140


Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
145                 150                 155                 160


Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
                165                 170                 175
```

```
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
            180                 185                 190


Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
        195                 200                 205


Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215


<210>  23
<211>  218
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  "Hole-Bearing" IgG1 CH2-CH3 Domain

<400>  23

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
1               5                   10                  15


Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
            20                  25                  30


Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
        35                  40                  45


Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
    50                  55                  60


Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
65                  70                  75                  80


His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                85                  90                  95
```

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
100 105 110

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
115 120 125

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

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
145 150 155 160

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
165 170 175

Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
180 185 190

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Tyr Thr
195 200 205

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215

<210> 24
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1 Fc Region L234A/L235A Variant

<400> 24

Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
1 5 10 15

Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys
20 25 30

```
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
        35                  40                  45

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
    50                  55                  60

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
65                  70                  75                  80

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                85                  90                  95

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
            100                 105                 110

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
        115                 120                 125

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

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
145                 150                 155                 160

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
                165                 170                 175

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
            180                 185                 190

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
        195                 200                 205

Gln Lys Ser Leu Ser Leu Ser Pro Gly
    210                 215
```

<210> 25
<211> 494
<212> PRT
<213> Artificial Sequence

<220>
<223> First and Third Polypeptide Chains of the Exemplary PD-1 x LAG-3 Fc-DART-1 diabody

<400> 25

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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 Gly Gly Gly Ser Gly
            100                 105                 110


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


Pro Gly Arg Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe
    130                 135                 140
```

```
Ser Asn Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
145                 150                 155                 160


Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala
                165                 170                 175


Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
            180                 185                 190


Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
        195                 200                 205


Tyr Tyr Cys Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val
    210                 215                 220


Thr Val Ser Ser Gly Gly Cys Gly Gly Gly Glu Val Ala Ala Cys Glu
225                 230                 235                 240


Lys Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu
                245                 250                 255


Val Ala Ala Leu Glu Lys Leu Glu Pro Lys Ser Ala Asp Lys Thr His
            260                 265                 270


Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
        275                 280                 285


Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu
    290                 295                 300


Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
305                 310                 315                 320


Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                325                 330                 335
```

```
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
            340                 345                 350

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        355                 360                 365

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
    370                 375                 380

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
385                 390                 395                 400

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
                405                 410                 415

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            420                 425                 430

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
        435                 440                 445

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
    450                 455                 460

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
465                 470                 475                 480

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                485                 490
```

<210> 26
<211> 1482
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding the First and Third Polypeptide Chains of

the Exemplary PD-1 x LAG-3 Fc-DART-1 diabody

<400> 26

gaaattgtcc tgacacagtc tcccgcaacc ctgagtttga gtcctgggga gcgagcaact 60

ctctcctgcc gagcctccca gagtatctcc tcctacctcg cctggtacca acagaagcca 120

gggcaggctc caaggctgct tatctatgac gcctctaacc gcgcaactgg gattcccgca 180

cgcttctccg gctctggttc cggcacagac tttacactta ctatctctag cctggagcca 240

gaagactttg ccgtgtacta ttgtcagcaa cgttccaatt ggccccttac ctttgggcag 300

ggcactaact tggaaatcaa aggtggcgga tccggcggcg gaggccaggt tcagctggtc 360

gagagtggtg gcggcgttgt gcaacctggg cgttccctcc gattggactg taaagcttcc 420

ggcattactt tctcaaattc cggcatgcat tgggtgaggc aagcccctgg aaaagggctc 480

gaatgggtgg ctgtgatttg gtacgatggc agcaaacggt actacgccga ttctgttaag 540

ggccgcttta ccatctcccg cgataactca aagaacacac tgtttctgca aatgaatagt 600

cttagagccg aggacaccgc cgtgtactac tgtgccacaa atgacgatta ttgggggcag 660

ggcacattgg tcacagtgtc ttccggagga tgtggcggtg gagaagtggc cgcatgtgag 720

aaagaggttg ctgctttgga gaaggaggtc gctgcacttg aaaaggaggt cgcagccctg 780

gagaaactgg agcccaaatc tgctgacaaa actcacacat gcccaccgtg cccagcacct 840

gaagccgcgg ggggaccgtc agtcttcctc ttcccccaa aacccaagga caccctctat 900

atcacccggg agcctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc 1140

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1200

ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260

tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1320

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gt 1482

<210> 27
<211> 269
<212> PRT
<213> Artificial Sequence

<220>
<223> Second and Fourth Polypeptide Chains of the Exemplary PD-1 x LAG-3 Fc-DART-1 diabody

<400> 27

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 Gly Gly Gly Ser Gly
100 105 110

Gly Gly Gly Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
115 120 125

```
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe
    130                 135                 140


Ser Asp Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
145                 150                 155                 160


Glu Trp Ile Gly Glu Ile Asn His Asn Gly Asn Thr Asn Ser Asn Pro
                165                 170                 175


Ser Leu Lys Ser Arg Val Thr Leu Ser Leu Asp Thr Ser Lys Asn Gln
            180                 185                 190


Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
        195                 200                 205


Tyr Cys Ala Phe Gly Tyr Ser Asp Tyr Glu Tyr Asn Trp Phe Asp Pro
    210                 215                 220


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Cys Gly Gly
225                 230                 235                 240


Gly Lys Val Ala Ala Cys Lys Glu Lys Val Ala Ala Leu Lys Glu Lys
                245                 250                 255


Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
            260                 265
```

<210> 28
<211> 807
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding the Second and Fourth Polypeptide Chains of the Exemplary PD-1 x LAG-3 Fc-DART-1 diabody

<400> 28
gagatcgtac ttacccagtc tcccgccacc ctttccctga gtcctggtga gcgggccact 60

ctttcctgtc gcgcaagcca atcagtttct agctacctcg catggtatca gcagaagcca 120

gggcaggcac ccaggcttct catctatgac gccagtaacc gcgcaaccgg gatacctgct 180

agattttccg gcagtggatc tgggaccgat ttcacactga caatttcatc cttggaacca 240

gaagatttcg cagtctacta ctgccagcaa tcttccaact ggccaagaac tttcggacag 300

gggaccaaag tggaaattaa aggtggcgga tccggcggcg gaggccaggt ccagctccag 360

caatggggag ccgggctgct gaaaccctct gaaacactga gtctcacatg tgccgtttat 420

ggaggttcct tctccgatta ttactggaac tggattcgtc agcctcccgg caagggcctg 480

gagtggatcg gtgagattaa ccacaatggc aataccaata gcaatcctag tttgaaatct 540

cgcgtcactc tttccctcga tacaagcaaa aaccagtttt ctttgaaatt gcgatctgta 600

actgctgctg atactgccgt gtattactgc gcattcggct actccgacta tgaatataat 660

tggttcgatc cttggggaca gggaacattg gtaaccgtgt catccggagg atgtggcggt 720

ggaaaagtgg ccgcatgtaa ggagaaagtt gctgctttga aagagaaggt cgccgcactt 780

aaggaaaagg tcgcagccct gaaagag 807

<210> 29
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> First and Third Polypeptide Chains of the Exemplary PD-1 x LAG-3 Fc-DART-2 diabody

<400> 29

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 Gly Gly Gly Ser Gly
            100                 105                 110

Gly Gly Gly Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
        115                 120                 125

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

Ser Asp Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
145                 150                 155                 160

Glu Trp Ile Gly Glu Ile Asn His Asn Gly Asn Thr Asn Ser Asn Pro
                165                 170                 175

Ser Leu Lys Ser Arg Val Thr Leu Ser Leu Asp Thr Ser Lys Asn Gln
            180                 185                 190

Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
        195                 200                 205

Tyr Cys Ala Phe Gly Tyr Ser Asp Tyr Glu Tyr Asn Trp Phe Asp Pro
    210                 215                 220

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Cys Gly Gly
```

225 230 235 240

Gly Glu Val Ala Ala Cys Glu Lys Glu Val Ala Ala Leu Glu Lys Glu
245 250 255

Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Leu Glu Pro
260 265 270

Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
275 280 285

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
290 295 300

Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp
305 310 315 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
325 330 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
340 345 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
355 360 365

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
370 375 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385 390 395 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
405 410 415

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile

420 425 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
435 440 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
450 455 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465 470 475 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
485 490 495

Ser Leu Ser Pro Gly
500

<210> 30
<211> 1503
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding the First and Third Polypeptide Chains of the Exemplary PD-1 x LAG-3 Fc-DART-2 diabody

<400> 30
gagatcgtac ttacccagtc tcccgccacc ctttccctga gtcctggtga gcgggccact 60

ctttcctgtc gcgcaagcca atcagtttct agctacctcg catggtatca gcagaagcca 120

gggcaggcac ccaggcttct catctatgac gccagtaacc gcgcaaccgg gatacctgct 180

agattttccg gcagtggatc tgggaccgat ttcacactga caatttcatc cttggaacca 240

gaagatttcg cagtctacta ctgccagcaa tcttccaact ggccaagaac tttcggacag 300

gggaccaaag tggaaattaa aggtggcgga tccggcggcg gaggccaggt ccagctccag 360

caatggggag ccgggctgct gaaaccctct gaaacactga gtctcacatg tgccgtttat 420

ggaggttcct tctccgatta ttactggaac tggattcgtc agcctcccgg caagggcctg 480

gagtggatcg gtgagattaa ccacaatggc aataccaata gcaatcctag tttgaaatct 540

cgcgtcactc tttccctcga tacaagcaaa aaccagtttt ctttgaaatt gcgatctgta 600

actgctgctg atactgccgt gtattactgc gcattcggct actccgacta tgaatataat 660

tggttcgatc cttggggaca gggaacattg gtaaccgtgt catccggagg atgtggcggt 720

ggagaagtgg ccgcatgtga gaaagaggtt gctgctttgg agaaggaggt cgctgcactt 780

gaaaaggagg tcgcagccct ggagaaactg gagcccaaat ctgctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg gggggaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcta tatcacccgg gagcctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gaggagatga ccaagaacca ggtcagcctg 1260

acctgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500

ggt 1503

<210> 31
<211> 262
<212> PRT
<213> Artificial Sequence

<220>
<223> Second and Fourth Polypeptide Chains of the Exemplary PD-1 x LAG-3 Fc-DART-2 diabody

<400> 31

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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 Gly Gly Gly Ser Gly
            100                 105                 110


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


Pro Gly Arg Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe
    130                 135                 140


Ser Asn Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
145                 150                 155                 160


Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala
                165                 170                 175


Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
            180                 185                 190
```

```
Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
        195                 200                 205


Tyr Tyr Cys Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val
    210                 215                 220


Thr Val Ser Ser Gly Gly Cys Gly Gly Gly Lys Val Ala Ala Cys Lys
225                 230                 235                 240


Glu Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys
                245                 250                 255


Val Ala Ala Leu Lys Glu
            260
```

<210> 32
<211> 786
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding the Second and Fourth Polypeptide Chains of the Exemplary PD-1 x LAG-3 Fc-DART-2 diabody

<400> 32

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gaaattgtcc tgacacagtc tcccgcaacc ctgagtttga gtcctgggga gcgagcaact       60

ctctcctgcc gagcctccca gagtatctcc tcctacctcg cctggtacca acagaagcca      120

gggcaggctc caaggctgct tatctatgac gcctctaacc gcgcaactgg gattcccgca      180

cgcttctccg gctctggttc cggcacagac tttacactta ctatctctag cctggagcca      240

gaagactttg ccgtgtacta ttgtcagcaa cgttccaatt ggccccttac ctttgggcag      300

ggcactaact tggaaatcaa aggtggcgga tccggcggcg gaggccaggt tcagctggtc      360

gagagtggtg gcggcgttgt gcaacctggg cgttccctcc gattggactg taaagcttcc      420

ggcattactt tctcaaattc cggcatgcat tgggtgaggc aagcccctgg aaaagggctc      480

gaatgggtgg ctgtgatttg gtacgatggc agcaaacggt actacgccga ttctgttaag      540
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ggccgcttta ccatctcccg cgataactca aagaacacac tgtttctgca aatgaatagt 600

cttagagccg aggacaccgc cgtgtactac tgtgccacaa atgacgatta ttgggggcag 660

ggcacattgg tcacagtgtc ttccggagga tgtggcggtg gaaaagtggc cgcatgtaag 720

gagaaagttg ctgctttgaa agagaaggtc gccgcactta aggaaaaggt cgcagccctg 780

aaagag 786