SEQUENCE LISTING

<110> ONCOMED PHARMACEUTICALS, INC.
DUPONT, JAKOB
PARMAR, HEMA

<120> METHODS FOR TREATMENT OF CANCER COMPRISING TIGIT-BINDING AGENTS

<130> 2293.164PC02/PAC/E-H/M-S

<150> US 62/479,609
<151> 2017-03-31

<150> US 62/427,903
<151> 2016-11-30

<160> 29

<170> PatentIn version 3.5

<210> 1
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TIGIT amino acid sequence

<400> 1

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Met Arg Trp Cys Leu Leu Leu Ile Trp Ala Gln Gly Leu Arg Gln Ala
1               5                  10                  15


Pro Leu Ala Ser Gly Met Met Thr Gly Thr Ile Glu Thr Thr Gly Asn
            20                  25                  30


Ile Ser Ala Glu Lys Gly Gly Ser Ile Ile Leu Gln Cys His Leu Ser
        35                  40                  45


Ser Thr Thr Ala Gln Val Thr Gln Val Asn Trp Glu Gln Gln Asp Gln
    50                  55                  60


Leu Leu Ala Ile Cys Asn Ala Asp Leu Gly Trp His Ile Ser Pro Ser
65                  70                  75                  80
```

```
Phe Lys Asp Arg Val Ala Pro Gly Pro Gly Leu Gly Leu Thr Leu Gln
                85                  90                  95

Ser Leu Thr Val Asn Asp Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr
            100                 105                 110

Tyr Pro Asp Gly Thr Tyr Thr Gly Arg Ile Phe Leu Glu Val Leu Glu
        115                 120                 125

Ser Ser Val Ala Glu His Gly Ala Arg Phe Gln Ile Pro Leu Leu Gly
    130                 135                 140

Ala Met Ala Ala Thr Leu Val Val Ile Cys Thr Ala Val Ile Val Val
145                 150                 155                 160

Val Ala Leu Thr Arg Lys Lys Lys Ala Leu Arg Ile His Ser Val Glu
                165                 170                 175

Gly Asp Leu Arg Arg Lys Ser Ala Gly Gln Glu Glu Trp Ser Pro Ser
            180                 185                 190

Ala Pro Ser Pro Pro Gly Ser Cys Val Gln Ala Glu Ala Ala Pro Ala
        195                 200                 205

Gly Leu Cys Gly Glu Gln Arg Gly Glu Asp Cys Ala Glu Leu His Asp
    210                 215                 220

Tyr Phe Asn Val Leu Ser Tyr Arg Ser Leu Gly Asn Cys Ser Phe Phe
225                 230                 235                 240

Thr Glu Thr Gly
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<210> 2
<211> 223
<212> PRT
<213> Artificial Sequence

<220>

<223> Human TIGIT amino acid sequence without predicted signal sequence

<400> 2

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Met Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Glu Lys
1               5                  10                  15


Gly Gly Ser Ile Ile Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln
            20                  25                  30


Val Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Cys
        35                  40                  45


Asn Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val
    50                  55                  60


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


Asp Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr
                85                  90                  95


Tyr Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu
            100                 105                 110


His Gly Ala Arg Phe Gln Ile Pro Leu Leu Gly Ala Met Ala Ala Thr
        115                 120                 125


Leu Val Val Ile Cys Thr Ala Val Ile Val Val Val Ala Leu Thr Arg
    130                 135                 140


Lys Lys Lys Ala Leu Arg Ile His Ser Val Glu Gly Asp Leu Arg Arg
145                 150                 155                 160


Lys Ser Ala Gly Gln Glu Glu Trp Ser Pro Ser Ala Pro Ser Pro Pro
                165                 170                 175


Gly Ser Cys Val Gln Ala Glu Ala Ala Pro Ala Gly Leu Cys Gly Glu
            180                 185                 190
```

Gln Arg Gly Glu Asp Cys Ala Glu Leu His Asp Tyr Phe Asn Val Leu
        195   200   205

Ser Tyr Arg Ser Leu Gly Asn Cys Ser Phe Phe Thr Glu Thr Gly
    210   215   220

<210> 3
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TIGIT extracellular domain amino acid sequence

<400> 3

Met Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Glu Lys
1   5   10   15

Gly Gly Ser Ile Ile Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln
            20   25   30

Val Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Cys
        35   40   45

Asn Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val
    50   55   60

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

Asp Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr
                85   90   95

Tyr Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu
            100   105   110

His Gly Ala Arg Phe Gln Ile Pro
        115   120

<210> 4
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> OMP-313M32/313M33 Heavy chain CDR1

<400> 4

Thr Ser Asp Tyr Ala Trp Asn
1   5

<210> 5
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> OMP-313M32/313M33 Heavy chain CDR2

<400> 5

Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser Leu Arg Ser
1   5   10   15

<210> 6
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> OMP-313M32/313M33 Heavy chain CDR3

<400> 6

Ala Arg Arg Gln Val Gly Leu Gly Phe Ala Tyr
1   5   10

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

<220>

<223> OMP-313M32/313M33 Light chain CDR1

<400> 7

Lys Ala Ser Gln Asp Val Ser Thr Ala Val Ala
1 5 10

<210> 8
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> OMP-313M32/313M33 Light chain CDR2

<400> 8

Ser Ala Ser Tyr Arg Tyr Thr
1 5

<210> 9
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> OMP-313M32/313M33 Light chain CDR3

<400> 9

Gln Gln His Tyr Ser Thr Pro
1 5

<210> 10
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> OMP-313M32/313M33 Heavy chain variable region amino acid sequence

<400> 10

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

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


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


Ile Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser Leu
    50                  55                  60


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


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


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


Leu Val Thr Val Ser Ser
        115


<210>  11
<211>  99
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  OMP-313M32/313M33 Light chain variable region amino acid sequence

<400>  11

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 Ala Ser Gln Asp Val Ser Thr Ala
            20                  25                  30


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

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

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

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

Thr Phe Gly

<210> 12
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> OMP-313M32 Heavy chain (IgG1) amino acid sequence with predicted
       signal sequence

<220>
<221> MISC_FEATURE
<222> (1)..(19)
<223> predicted signal sequence

<400> 12

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1   5   10   15

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

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile
        35   40   45

Thr Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly
    50   55   60

Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn

```
65                  70                  75                  80

Pro Ser Leu Arg Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn
                85                  90                  95

Gln Phe Phe Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Arg Gln Val Gly Leu Gly Phe Ala Tyr Trp Gly
        115                 120                 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270
```

```
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys
```

465

<210> 13
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> OMP-313M32 Heavy chain (IgG1) amino acid sequence without signal sequence

<400> 13

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


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


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


Ile Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser Leu
    50                  55                  60


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


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


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


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


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

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

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

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

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

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

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

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

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

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

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

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

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

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

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


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


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


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


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


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


<210>  14
<211>  234
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  OMP-313M32/313M33 Light chain amino acid sequence with predicted
       signal sequence


<220>
<221>  MISC_FEATURE
<222>  (1)..(20)
<223>  predicted signal sequence

<400>  14

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15


Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
            20                  25                  30
```

```
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
        35                  40                  45

Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    50                  55                  60

Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Ser
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser
                85                  90                  95

Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Tyr
            100                 105                 110

Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
        115                 120                 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

Tyr Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
        195                 200                 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

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

225 230

<210> 15
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> OMP-313M32/313M33 Light chain amino acid sequence without signal sequence

<400> 15

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 Ala Ser Gln Asp Val Ser Thr Ala
20 25 30

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

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

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

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp
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


Asn 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>  16
<211>  464
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  313M33 Heavy chain (IgG4) amino acid sequence with predicted
       signal sequence


<220>
<221>  MISC_FEATURE
<222>  (1)..(19)
<223>  predicted signal sequence

<400>  16

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1               5                   10                  15


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


Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile
        35                  40                  45


Thr Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly
```

```
    50                  55                  60

Leu Glu Trp Ile Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn
65                  70                  75                  80

Pro Ser Leu Arg Ser Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn
                85                  90                  95

Gln Phe Phe Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Arg Gln Val Gly Leu Gly Phe Ala Tyr Trp Gly
        115                 120                 125

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

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
225                 230                 235                 240

Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
                245                 250                 255
```

```
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
            260                 265                 270

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
        275                 280                 285

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
    290                 295                 300

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
305                 310                 315                 320

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
                325                 330                 335

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
            340                 345                 350

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
        355                 360                 365

Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
    370                 375                 380

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
385                 390                 395                 400

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
                405                 410                 415

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
            420                 425                 430

Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
        435                 440                 445

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
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450 455 460

<210> 17
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> 313M33 Heavy chain (IgG4) amino acid sequence without signal sequence

<400> 17

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

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

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

Ile Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser Leu
50 55 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
        435                 440                 445
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<210> 18
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> OMP-313M32/313M33 Heavy chain variable region nucleotide sequence

<400> 18
caggtccagc tgcaggagtc tggcccagga ctggtgaagc cttctgagac cctgtccctc 60

acctgcgctg tctctggtta ctccatcacc tccgattatg cctggaactg gattcggcag 120

cccccaggga aggggctgga gtggattggg tacataagct actctggtag cactagctac 180

aacccatctc tccggtcacg ggtcacaata tcacgggaca catccaagaa ccagttcttc 240

ctgaagctgt cctctgtgac cgccgctgac accgccgtgt attactgtgc aaggagacag 300

gtcgggctgg ggtttgctta ctggggccaa ggaaccctgg tcaccgtcag ctca 354

<210> 19
<211> 297

<212> DNA
<213> Artificial Sequence

<220>
<223> OMP-313M32/313M33 Light chain variable region nucleotide sequence

<400> 19
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgttggaga cagagtcacc 60

atcacttgca aggcttctca ggatgtgtct actgctgttg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctactct gcatcctatc ggtacactgg ggtcccatca 180

aggttctccg gatctggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtcagcaa cattattcta ctccttggac attcggc 297

<210> 20
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> OMP-313M32 Heavy chain (IgG1) nucleotide sequence

<400> 20
atggactgga cctggaggat actctttctc gtggctgcag ccacaggagc ccactcccag 60

gtccagctgc aggagtctgg cccaggactg gtgaagcctt ctgagaccct gtccctcacc 120

tgcgctgtct ctggttactc catcacctcc gattatgcct ggaactggat tcggcagccc 180

ccagggaagg ggctggagtg gattgggtac ataagctact ctggtagcac tagctacaac 240

ccatctctcc ggtcacgggt cacaatatca cgggacacat ccaagaacca gttcttcctg 300

aagctgtcct ctgtgaccgc cgctgacacc gccgtgtatt actgtgcaag gagacaggtc 360

gggctggggt ttgcttactg gggccaagga accctggtca ccgtcagctc agccagcaca 420

aagggcccct ccgtgttccc tctggccct tcctccaagt ccacctccgg cggcaccgcc 480

gctctgggct gcctggtgaa ggactacttc cctgagcctg tgaccgtgtc ctggaactct 540

ggcgccctga cctctggcgt gcacaccttc ccagccgtgc tgcagtcctc cggcctgtac 600

tccctgtcct ccgtggtgac cgtgccttcc tcctccctgg gcacccagac ctacatctgc 660

aacgtgaacc acaagccttc caacaccaag gtggacaagc gggtggagcc taagtcctgc 720

gacaagaccc acacctgccc tccctgccct gcccctgagc tgctgggcgg accttccgtg 780

ttcctgttcc ctcctaagcc taaggacacc ctgatgatct cccggacccc tgaggtgacc 840

tgcgtggtgg tggacgtgtc ccacgaggat cctgaggtga agttcaattg gtacgtggac 900

ggcgtggagg tgcacaacgc taagaccaag ccaagggagg agcagtacaa ctccacctac 960

cgggtggtgt ctgtgctgac cgtgctgcac caggactggc tgaacggcaa agaatacaag 1020

tgcaaggtct ccaacaaggc cctgcccgct cccatcgaga aaaccatctc caaggccaag 1080

ggccagcctc gcgagcctca ggtgtacacc ctgccaccca gccgggagga gatgaccaag 1140

aaccaggtgt ccctgacctg tctggtgaag ggcttctacc cttccgatat cgccgtggag 1200

tgggagtcta acggccagcc cgagaacaac tacaagacca cccctcctgt gctggactcc 1260

gacggctcct tcttcctgta ctccaagctg accgtggaca agtcccggtg gcagcagggc 1320

aacgtgttct cctgctccgt gatgcacgag gccctgcaca accactacac ccagaagagc 1380

ctgtctctgt ctcctggcaa gtga 1404

<210> 21
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> OMP-313M32/313M33 Light chain nucleotide sequence

<400> 21
atggtgctcc agacccaggt cttcatttcc ctgctgctct ggatcagcgg agcctacggg 60

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgttggaga cagagtcacc 120

atcacttgca aggcttctca ggatgtgtct actgctgttg cctggtatca gcagaaacca 180

gggaaagccc ctaagctcct gatctactct gcatcctatc ggtacactgg ggtcccatca 240

aggttctccg gatctggatc tgggacagat tttactttca ccatcagcag cctgcagcct 300

gaagatattg caacatatta ctgtcagcaa cattattcta ctccttggac attcggccaa 360

gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttccctcca 420

tctgatgagc agctcaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 480

cccagagagg ccaaagtcca gtggaaggtg gataacgccc tccaatccgg caactcccag 540

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcaa caccctgaca 600

ctgagcaaag cagactacga gaaacacaaa gtctatgcct gcgaagtcac ccatcagggc 660

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<210> 22
<211> 1395
<212> DNA
<213> Artificial Sequence

<220>
<223> 313M33 Heavy chain (IgG4) nucleotide sequence

<400> 22
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gtccagctgc aggagtctgg cccaggactg gtgaagcctt ctgagaccct gtccctcacc 120

tgcgctgtct ctggttactc catcacctcc gattatgcct ggaactggat tcggcagccc 180

ccagggaagg ggctggagtg gattgggtac ataagctact ctggtagcac tagctacaac 240

ccatctctcc ggtcacgggt cacaatatca cgggacacat ccaagaacca gttcttcctg 300

aagctgtcct ctgtgaccgc cgctgacacc gccgtgtatt actgtgcaag gagacaggtc 360

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aagggcccat ccgtcttccc cctggcaccc tgctcccgga gcacctccga gagcacagcc 480

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tccctctcct ccgtggtgac agtgccctcc agcagcctgg gcactaagac ctacacctgc 660

aacgtcgatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatgga 720

cccccatgcc caccttgccc agcacctgag ttcctggggg gaccatcagt cttcctgttc 780

cccccaaaac ccaaggacac tctcatgatc tcccggaccc ctgaggtcac ttgcgtggtg 840

gtggacgtga gccaggaaga ccccgaggtc agttcaact ggtatgtgga tggcgtggag 900

gttcataatg ccaagacaaa gcctcgggag gagcagttca acagcaccta ccgggtggtc 960

agcgtcctca ccgtcctgca ccaagactgg ctgaacggca aggagtacaa gtgcaaggtc 1020

tccaacaaag ggctcccatc ctccatcgag aaaaccatct ccaaagccaa agggcagccc 1080

cgggagccac aggtgtacac cctgccccca tcccaagagg agatgaccaa gaaccaagtg 1140

tccctgacct gcctggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc 1200

aatgggcagc ctgagaacaa ctacaagacc actcctcccg tgctggactc cgacggctcc 1260

ttcttcctct actcccggct caccgtggac aagagcaggt ggcaggaggg caatgtcttc 1320

tcctgctccg tgatgcatga ggctctgcac aaccactaca cacagaagag cctctccctg 1380

tctctgggca aatga 1395

<210> 23
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 Heavy chain constant region

<400> 23

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 24
<211> 326
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG2 Heavy chain constant region

<400> 24

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

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

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

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

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

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

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110
```

```
Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115                 120                 125

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

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145                 150                 155                 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
            180                 185                 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
    210                 215                 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225                 230                 235                 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                245                 250                 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            260                 265                 270

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

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

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305                 310                 315                 320
```

Ser Leu Ser Pro Gly Lys
325

<210> 25
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG3 Heavy chain constant region

<400> 25

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

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

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

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

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

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

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
100 105 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
115 120 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
130 135 140

```
Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145                 150                 155                 160

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165                 170                 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180                 185                 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
        195                 200                 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210                 215                 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225                 230                 235                 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                245                 250                 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
            260                 265                 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        275                 280                 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    290                 295                 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305                 310                 315                 320

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
                325                 330                 335
```

```
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
            340                 345                 350


Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
        355                 360                 365


Lys Ser Leu Ser Leu Ser Pro Gly Lys
    370                 375


<210>  26
<211>  327
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Human IgG4 Heavy chain constant region

<400>  26

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


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


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


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


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


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


Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
            100                 105                 110
```

```
Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125

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

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

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

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240

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

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

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

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

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320
```

Leu Ser Leu Ser Leu Gly Lys
325

<210> 27
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TIGIT amino acids 55-70

<400> 27

Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Cys Asn
1 5 10 15

<210> 28
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Human TIGIT amino acids 105-122

<400> 28

Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr Tyr Thr Gly
1 5 10 15

Arg Ile

<210> 29
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> FLAG Tag

<400> 29

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5