SEQUENCE LISTING

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<120> NKG2D DARIC RECEPTORS

<130> BLBD-091/02WO 315698-2770

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<160> 48

<170> PatentIn version 3.5

<210> 1
<211> 302
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized FRB T2098L-CD8aTM-CD137-CD3z NKG2D DARIC signaling component

<400> 1

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Ser Ile Leu Trp His Glu Met Trp His Glu
20 25 30

Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys
35 40 45

Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly
50 55 60

Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp

```
65                  70                  75                  80

Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn
                85                  90                  95

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

Arg Ile Ser Lys Ala Ser Ala Gly Thr Gly Ser Asp Ile Tyr Ile Trp
        115                 120                 125

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
    130                 135                 140

Thr Met His Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
145                 150                 155                 160

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
                165                 170                 175

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
            180                 185                 190

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
        195                 200                 205

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
    210                 215                 220

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
225                 230                 235                 240

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
                245                 250                 255

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
```

260 265 270

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
275 280 285

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ser
290 295 300

<210> 2
<211> 323
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized FRB T2098L-CD8aTM-CD137-CD3z NKG2D DARIC signaling component

<400> 2

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Ser Ile Leu Trp His Glu Met Trp His Glu
20 25 30

Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys
35 40 45

Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly
50 55 60

Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp
65 70 75 80

Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn
85 90 95

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

```
Arg Ile Ser Lys Ala Ser Ala Gly Thr Gly Ser Asp Ile Tyr Ile Trp
        115                 120                 125

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
    130                 135                 140

Thr Met His Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
145                 150                 155                 160

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
                165                 170                 175

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
            180                 185                 190

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
        195                 200                 205

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
    210                 215                 220

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
225                 230                 235                 240

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
                245                 250                 255

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
            260                 265                 270

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
        275                 280                 285

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ser Gly Ser
    290                 295                 300
```

```
Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
305                 310                 315                 320


Asn Pro Gly
```

<210> 3
<211> 303
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized NKG2D-FKBP12-CD4TM NKG2D DARIC binding component

<400> 3

```
Pro Ser Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp
1               5                   10                  15


Val Pro Gly Ser Thr Gly Phe Asn Gln Glu Val Gln Ile Pro Leu Thr
            20                  25                  30


Glu Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn
        35                  40                  45


Asn Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln
    50                  55                  60


Ala Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys
65                  70                  75                  80


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


Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser
            100                 105                 110
```

```
Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp
        115                 120                 125

Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser
    130                 135                 140

Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Gly Gly Gly Gly
145                 150                 155                 160

Ser Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
                165                 170                 175

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
            180                 185                 190

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
        195                 200                 205

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
    210                 215                 220

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
225                 230                 235                 240

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
                245                 250                 255

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Arg Met
            260                 265                 270

Ala Leu Ile Val Leu Gly Gly Val Ala Gly Leu Leu Leu Phe Ile Gly
        275                 280                 285

Leu Gly Ile Phe Phe Cys Val Arg Cys Arg His Arg Arg Arg Gln
    290                 295                 300
```

<210> 4
<211> 301
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized NKG2D-FKBP12-CD4TM NKG2D DARIC binding component

<400> 4

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser
20 25 30

Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys
35 40 45

Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser
50 55 60

Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp
65 70 75 80

Gln Asp Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu Val
85 90 95

His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu
100 105 110

Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala
115 120 125

Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr Pro
130 135 140

Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Gly Gly Gly Gly Ser Gly
145 150 155 160

```
Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys
                165                 170                 175

Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp Gly
            180                 185                 190

Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe Met
        195                 200                 205

Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala Gln
    210                 215                 220

Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala
225                 230                 235                 240

Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr Leu
                245                 250                 255

Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Arg Met Ala Leu
            260                 265                 270

Ile Val Leu Gly Gly Val Ala Gly Leu Leu Leu Phe Ile Gly Leu Gly
        275                 280                 285

Ile Phe Phe Cys Val Arg Cys Arg His Arg Arg Arg Gln
    290                 295                 300
```

<210> 5
<211> 626
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized NKG2D DARIC polyprotein comprising an NKG2D DARIC binding component and an NKG2D DARIC signaling component separated by a viral P2A domain

<400> 5

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Gly Ser Ile Leu Trp His Glu Met Trp His Glu
            20                  25                  30

Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys
        35                  40                  45

Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly
    50                  55                  60

Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp
65                  70                  75                  80

Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn
                85                  90                  95

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

Arg Ile Ser Lys Ala Ser Ala Gly Thr Gly Ser Asp Ile Tyr Ile Trp
        115                 120                 125

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
    130                 135                 140

Thr Met His Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
145                 150                 155                 160

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
                165                 170                 175

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
            180                 185                 190
```

```
Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
        195                 200                 205

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
    210                 215                 220

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
225                 230                 235                 240

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
                245                 250                 255

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
            260                 265                 270

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
        275                 280                 285

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ser Gly Ser
    290                 295                 300

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
305                 310                 315                 320

Asn Pro Gly Pro Ser Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu
                325                 330                 335

Leu Leu Trp Val Pro Gly Ser Thr Gly Phe Asn Gln Glu Val Gln Ile
            340                 345                 350

Pro Leu Thr Glu Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys
        355                 360                 365

Tyr Lys Asn Asn Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr
    370                 375                 380
```

```
Glu Ser Gln Ala Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val
385                 390                 395                 400

Tyr Ser Lys Glu Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Tyr His
                405                 410                 415

Trp Met Gly Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu
            420                 425                 430

Asp Gly Ser Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln
        435                 440                 445

Lys Gly Asp Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu
    450                 455                 460

Asn Cys Ser Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Gly
465                 470                 475                 480

Gly Gly Gly Ser Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly
                485                 490                 495

Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly
            500                 505                 510

Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys
        515                 520                 525

Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu
    530                 535                 540

Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile
545                 550                 555                 560

Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro
                565                 570                 575
```

```
Pro His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly
            580                 585                 590


Gly Arg Met Ala Leu Ile Val Leu Gly Gly Val Ala Gly Leu Leu Leu
        595                 600                 605


Phe Ile Gly Leu Gly Ile Phe Phe Cys Val Arg Cys Arg His Arg Arg
    610                 615                 620


Arg Gln
625


<210>  6
<211>  333
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthesized NKG2D-FKBP12-CD4TM-OX40 NKG2D DARIC binding component

<400>  6

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1               5                   10                  15


Gly Ser Thr Gly Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser
            20                  25                  30


Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys
        35                  40                  45


Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser
    50                  55                  60


Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp
65                  70                  75                  80
```

```
Gln Asp Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu Val
                85                  90                  95

His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu
            100                 105                 110

Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala
        115                 120                 125

Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr Pro
    130                 135                 140

Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Gly Gly Gly Gly Ser Gly
145                 150                 155                 160

Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys
                165                 170                 175

Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp Gly
            180                 185                 190

Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe Met
        195                 200                 205

Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala Gln
    210                 215                 220

Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala
225                 230                 235                 240

Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr Leu
                245                 250                 255

Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Arg Met Ala Leu
            260                 265                 270
```

Ile Val Leu Gly Gly Val Ala Gly Leu Leu Leu Phe Ile Gly Leu Gly
275 280 285

Ile Phe Phe Ala Leu Tyr Leu Leu Arg Arg Asp Gln Arg Leu Pro Pro
290 295 300

Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln
305 310 315 320

Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile
325 330

<210> 7
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized NKG2D-FKBP12-CD4TM-TNFR2 NKG2D DARIC binding component

<400> 7

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser
20 25 30

Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys
35 40 45

Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser
50 55 60

Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp
65 70 75 80

Gln Asp Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu Val

```
                85                  90                  95

His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu
            100                 105                 110

Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala
        115                 120                 125

Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr Pro
    130                 135                 140

Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Gly Gly Gly Gly Ser Gly
145                 150                 155                 160

Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys
                165                 170                 175

Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp Gly
            180                 185                 190

Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe Met
        195                 200                 205

Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala Gln
    210                 215                 220

Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala
225                 230                 235                 240

Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr Leu
                245                 250                 255

Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Gly Arg Met Ala Leu
            260                 265                 270

Ile Val Leu Gly Gly Val Ala Gly Leu Leu Leu Phe Ile Gly Leu Gly
```

```
        275                 280                 285

Ile Phe Phe Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val
    290                 295                 300

Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln
305                 310                 315                 320

Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu
                325                 330                 335

Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro
            340                 345                 350

Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser
        355                 360                 365

Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn
    370                 375                 380

Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln
385                 390                 395                 400

Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro
                405                 410                 415

Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys
            420                 425                 430

Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr
        435                 440                 445

Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro
    450                 455                 460

Ser
```

465

<210> 8
<211> 658
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized NKG2D DARIC polyprotein comprising an NKG2D DARIC signaling component, a viral P2A domain, and an NKG2D DARIC.OX40 binding component

<400> 8

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gly Ser Ile Leu Trp His Glu Met Trp His Glu
20 25 30

Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys
35 40 45

Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly
50 55 60

Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp
65 70 75 80

Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn
85 90 95

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

Arg Ile Ser Lys Ala Ser Ala Gly Thr Gly Ser Asp Ile Tyr Ile Trp
115 120 125

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile

```
    130                 135                 140

Thr Met His Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
145                 150                 155                 160

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
                165                 170                 175

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
            180                 185                 190

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
        195                 200                 205

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
    210                 215                 220

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
225                 230                 235                 240

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
                245                 250                 255

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
            260                 265                 270

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
        275                 280                 285

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ser Gly Ser
    290                 295                 300

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
305                 310                 315                 320

Asn Pro Gly Pro Ser Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu
```

```
                325                 330                 335

Leu Leu Trp Val Pro Gly Ser Thr Gly Phe Asn Gln Glu Val Gln Ile
            340                 345                 350

Pro Leu Thr Glu Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys
        355                 360                 365

Tyr Lys Asn Asn Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr
    370                 375                 380

Glu Ser Gln Ala Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val
385                 390                 395                 400

Tyr Ser Lys Glu Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Tyr His
                405                 410                 415

Trp Met Gly Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu
            420                 425                 430

Asp Gly Ser Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln
        435                 440                 445

Lys Gly Asp Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu
    450                 455                 460

Asn Cys Ser Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Gly
465                 470                 475                 480

Gly Gly Gly Ser Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly
                485                 490                 495

Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly
            500                 505                 510

Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys
```

515 520 525

Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu
530 535 540

Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile
545 550 555 560

Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro
565 570 575

Pro His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly
580 585 590

Gly Arg Met Ala Leu Ile Val Leu Gly Gly Val Ala Gly Leu Leu Leu
595 600 605

Phe Ile Gly Leu Gly Ile Phe Phe Ala Leu Tyr Leu Leu Arg Arg Asp
610 615 620

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
625 630 635 640

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
645 650 655

Lys Ile

<210> 9
<211> 790
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized NKG2D DARIC polyprotein comprising an NKG2D DARIC signaling component, a viral P2A domain, and an NKG2D DARIC.TNFR2 binding component

<400> 9

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Gly Ser Ile Leu Trp His Glu Met Trp His Glu
            20                  25                  30

Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys
        35                  40                  45

Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly
    50                  55                  60

Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp
65                  70                  75                  80

Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn
                85                  90                  95

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

Arg Ile Ser Lys Ala Ser Ala Gly Thr Gly Ser Asp Ile Tyr Ile Trp
        115                 120                 125

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
    130                 135                 140

Thr Met His Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
145                 150                 155                 160

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
                165                 170                 175

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
```

```
            180                 185                 190

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
        195                 200                 205

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
    210                 215                 220

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
225                 230                 235                 240

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
                245                 250                 255

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
            260                 265                 270

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
        275                 280                 285

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ser Gly Ser
    290                 295                 300

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
305                 310                 315                 320

Asn Pro Gly Pro Ser Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu
                325                 330                 335

Leu Leu Trp Val Pro Gly Ser Thr Gly Phe Asn Gln Glu Val Gln Ile
            340                 345                 350

Pro Leu Thr Glu Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys
        355                 360                 365

Tyr Lys Asn Asn Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr
```

```
    370                 375                 380

Glu Ser Gln Ala Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val
385                 390                 395                 400

Tyr Ser Lys Glu Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Tyr His
                405                 410                 415

Trp Met Gly Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu
            420                 425                 430

Asp Gly Ser Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln
        435                 440                 445

Lys Gly Asp Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu
    450                 455                 460

Asn Cys Ser Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Gly
465                 470                 475                 480

Gly Gly Gly Ser Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly
                485                 490                 495

Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly
            500                 505                 510

Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys
        515                 520                 525

Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu
    530                 535                 540

Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile
545                 550                 555                 560

Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro
```

```
                565                 570                 575

Pro His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly
            580                 585                 590

Gly Arg Met Ala Leu Ile Val Leu Gly Gly Val Ala Gly Leu Leu Leu
        595                 600                 605

Phe Ile Gly Leu Gly Ile Phe Phe Lys Lys Lys Pro Leu Cys Leu Gln
    610                 615                 620

Arg Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr
625                 630                 635                 640

Gln Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser
                645                 650                 655

Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro
            660                 665                 670

Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly
        675                 680                 685

Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His
    690                 695                 700

Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser
705                 710                 715                 720

Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp
                725                 730                 735

Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe
            740                 745                 750

Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu Thr
```

```
        755                 760                 765


Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp
    770                 775                 780


Ala Gly Met Lys Pro Ser
785                 790


<210>  10
<211>  216
<212>  PRT
<213>  Homo sapiens

<400>  10

Met Gly Trp Ile Arg Gly Arg Arg Ser Arg His Ser Trp Glu Met Ser
1               5                   10                  15


Glu Phe His Asn Tyr Asn Leu Asp Leu Lys Lys Ser Asp Phe Ser Thr
            20                  25                  30


Arg Trp Gln Lys Gln Arg Cys Pro Val Val Lys Ser Lys Cys Arg Glu
        35                  40                  45


Asn Ala Ser Pro Phe Phe Phe Cys Cys Phe Ile Ala Val Ala Met Gly
    50                  55                  60


Ile Arg Phe Ile Ile Met Val Ala Ile Trp Ser Ala Val Phe Leu Asn
65                  70                  75                  80


Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys
                85                  90                  95


Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln
            100                 105                 110


Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met
        115                 120                 125
```

```
Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp
    130                 135                 140

Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu Val His Ile
145                 150                 155                 160

Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro
                165                 170                 175

Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr
            180                 185                 190

Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr Pro Asn Thr
        195                 200                 205

Tyr Ile Cys Met Gln Arg Thr Val
    210                 215
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<210> 11
<211> 134
<212> PRT
<213> Homo sapiens

<400> 11

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Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Cys Gly Pro
1               5                   10                  15

Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln Phe Phe
            20                  25                  30

Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met Ser Gln
        35                  40                  45

Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp Leu Leu
    50                  55                  60
```

```
Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu Val His Ile Pro Thr
65                  70                  75                  80


Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro Asn Leu
                85                  90                  95


Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr Ala Ser
            100                 105                 110


Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr Pro Asn Thr Tyr Ile
        115                 120                 125


Cys Met Gln Arg Thr Val
    130


<210>  12
<211>  3
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Exemplary linker sequence

<400>  12

Gly Gly Gly
1


<210>  13
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Exemplary linker sequence

<400>  13

Asp Gly Gly Gly Ser
1               5
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<210> 14
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary linker sequence

<400> 14

Thr Gly Glu Lys Pro
1 5

<210> 15
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary linker sequence

<400> 15

Gly Gly Arg Arg
1

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

<220>
<223> Exemplary linker sequence

<400> 16

Gly Gly Gly Gly Ser
1 5

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

<220>
<223> Exemplary linker sequence

<400> 17

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Val Asp
1   5   10

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

<220>
<223> Exemplary linker sequence

<400> 18

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

Leu Asp

<210> 19
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary linker sequence

<400> 19

Gly Gly Arg Arg Gly Gly Gly Ser
1   5

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

<220>
<223> Exemplary linker sequence

<400> 20

Leu Arg Gln Arg Asp Gly Glu Arg Pro
1 5

<210> 21
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary linker sequence

<400> 21

Leu Arg Gln Lys Asp Gly Gly Gly Ser Glu Arg Pro
1 5 10

<210> 22
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary linker sequence

<400> 22

Leu Arg Gln Lys Asp Gly Gly Gly Ser Gly Gly Gly Ser Glu Arg Pro
1 5 10 15

<210> 23
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavage sequence by TEV protease

<220>
<221> misc_feature
<222> (2)..(3)
<223> Xaa is any amino acid

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa is any amino acid

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa = Gly or Ser

<400> 23

Glu Xaa Xaa Tyr Xaa Gln Xaa
1   5

<210> 24
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavage sequence by TEV protease

<400> 24

Glu Asn Leu Tyr Phe Gln Gly
1   5

<210> 25
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavage sequence by TEV protease

<400> 25

Glu Asn Leu Tyr Phe Gln Ser
1   5

<210> 26
<211> 22
<212> PRT

<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 26

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
20

<210> 27
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 27

Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1 5 10 15

Pro Gly Pro

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

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 28

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
1 5 10

<210> 29

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

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 29

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
1 5 10 15

Glu Asn Pro Gly Pro
20

<210> 30
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 30

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1 5 10 15

Gly Pro

<210> 31
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 31

Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro
1 5 10

<210> 32
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 32

Gly Ser Gly Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp
1 5 10 15

Val Glu Ser Asn Pro Gly Pro
20

<210> 33
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 33

Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1 5 10 15

Asn Pro Gly Pro
20

<210> 34
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 34

Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro

1 5 10

<210> 35
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 35

Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala
1 5 10 15

Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25

<210> 36
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 36

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
1 5 10 15

Glu Ser Asn Pro Gly Pro
20

<210> 37
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 37

Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro
1 5 10

<210> 38
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 38

Leu Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn
1 5 10 15

Pro Gly Pro

<210> 39
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 39

Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn
1 5 10 15

Pro Gly Pro

<210> 40
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 40

Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro
1 5 10

<210> 41
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 41

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

Pro

<210> 42
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 42

Gln Leu Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1 5 10 15

Asn Pro Gly Pro
20

<210> 43
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 43

Ala Pro Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly
1   5   10   15

Asp Val Glu Ser Asn Pro Gly Pro
            20

<210> 44
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 44

Val Thr Glu Leu Leu Tyr Arg Met Lys Arg Ala Glu Thr Tyr Cys Pro
1   5   10   15

Arg Pro Leu Leu Ala Ile His Pro Thr Glu Ala Arg His Lys Gln Lys
            20   25   30

Ile Val Ala Pro Val Lys Gln Thr
        35   40

<210> 45
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 45

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

Gly Pro

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

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 46

Leu Leu Ala Ile His Pro Thr Glu Ala Arg His Lys Gln Lys Ile Val
1 5 10 15

Ala Pro Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly
20 25 30

Asp Val Glu Ser Asn Pro Gly Pro
35 40

<210> 47
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 47

Glu Ala Arg His Lys Gln Lys Ile Val Ala Pro Val Lys Gln Thr Leu
1 5 10 15

Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly
20 25 30

Pro

<210> 48
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Consensus Kozak sequence

<400> 48
gccrccatgg 10