SEQUENCE LISTING

<110> NVIP Pty Ltd

<120> Tumour Necrosis Factor Receptor Fusion Proteins and Methods of using the same

<130> P122189.WO.01

<150> US 61/601,712
<151> 2012-02-22

<160> 31

<170> PatentIn version 3.5

<210> 1
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Ala Met Gly Leu Pro Thr Val Pro Gly Leu Leu Leu Pro Leu Val Leu
1               5                  10                  15

Leu Ala Leu Leu Leu Glu Ile Tyr Pro Ile Ser Val Thr Ala Leu Val
            20                  25                  30

Pro His Pro Arg Asn Arg Val Lys Arg Ala Ile Leu Cys Pro Gln Gly
        35                  40                  45

Lys Tyr Ile His Pro Gln Asp Asp Ser Ile Cys Cys Thr Lys Cys His
    50                  55                  60

Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Leu Asp Thr
65                  70                  75                  80

Asp Cys Arg Glu Cys Glu Asn Gly Thr Phe Thr Ala Ser Glu Asn His
                85                  90                  95

Leu Arg Gln Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Asn Gln
            100                 105                 110

Val Glu Ile Ser Pro Cys Thr Val Tyr Arg Asp Thr Val Cys Gly Cys
        115                 120                 125

Arg Lys Asn Gln Tyr Arg Phe Tyr Trp Ser Glu Thr Leu Phe Gln Cys
    130                 135                 140

Asn Asn Cys Ser Leu Cys Leu Asn Gly Thr Val Gln Ile Ser Cys Gln
145                 150                 155                 160

Glu Lys Gln Asn Thr Ile Cys Thr Cys His Ala Gly Phe Phe Leu Arg
                165                 170                 175

Glu His Glu Cys Val Ser Cys Val Asn Cys Lys Lys Asn Thr Glu Cys
            180                 185                 190
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Gly Lys Leu Cys Leu Pro Pro Val Glu Thr Val Lys Val Pro Gln Asp
195 200 205

Pro Gly Ser Thr
210

<210> 2
<211> 233
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<400> 2

Phe Asn Glu Cys Arg Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu
1 5 10 15

Pro Leu Gly Gly Pro Ser Val Leu Ile Phe Pro Pro Lys Pro Lys Asp
20 25 30

Ile Leu Arg Ile Thr Arg Thr Pro Glu Val Thr Cys Val Val Leu Asp
35 40 45

Leu Gly Arg Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly
50 55 60

Lys Glu Val His Thr Ala Lys Thr Gln Ser Arg Glu Gln Gln Phe Asn
65 70 75 80

Gly Thr Tyr Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp
85 90 95

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

Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Arg Ala His Lys
115 120 125

Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser
130 135 140

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

Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Arg Lys
165 170 175

His Arg Met Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu
180 185 190

Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Pro
195 200 205

```
Phe Thr Cys Ala Val Met His Glu Thr Leu Gln Asn His Tyr Thr Asp
    210                 215                 220


Leu Ser Leu Ser His Ser Pro Gly Lys
225                 230


<210>  3
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<212>  PRT
<213>  Canis familiaris

<400>  3

Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys
1               5                   10                  15


Cys Pro Ala Pro Glu Met Leu Gly Gly Pro Ser Val Phe Ile Phe Pro
            20                  25                  30


Pro Lys Pro Lys Asp Thr Leu Leu Ile Ala Arg Thr Pro Glu Val Thr
        35                  40                  45


Cys Val Val Val Asp Leu Asp Pro Glu Asp Pro Glu Val Gln Ile Ser
    50                  55                  60


Trp Phe Val Asp Gly Lys Gln Met Gln Thr Ala Lys Thr Gln Pro Arg
65                  70                  75                  80


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


Gly His Gln Asp Trp Leu Lys Gly Lys Gln Phe Thr Cys Lys Val Asn
            100                 105                 110


Asn Lys Ala Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg
        115                 120                 125


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


Glu Leu Ser Lys Asn Thr Val Ser Leu Thr Cys Leu Ile Lys Asp Phe
145                 150                 155                 160


Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu
                165                 170                 175


Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly
            180                 185                 190


Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln
        195                 200                 205


Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn
    210                 215                 220
```

```
His Tyr Thr Gln Glu Ser Leu Ser His Ser Pro Gly Lys
225                 230                 235
```

<210> 4
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<213> Canis familiaris

<400> 4

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Ala Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn Cys Pro Cys Pro
1               5                   10                  15

Gly Cys Gly Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
            20                  25                  30

Pro Lys Asp Ile Leu Val Thr Ala Arg Thr Pro Thr Val Thr Cys Val
        35                  40                  45

Val Val Asp Leu Asp Pro Glu Asn Pro Glu Val Gln Ile Ser Trp Phe
    50                  55                  60

Val Asp Ser Lys Gln Val Gln Thr Ala Asn Thr Gln Pro Arg Glu Glu
65                  70                  75                  80

Gln Ser Asn Gly Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His
                85                  90                  95

Gln Asp Trp Leu Ser Gly Lys Gln Phe Lys Cys Lys Val Asn Asn Lys
            100                 105                 110

Ala Leu Pro Ser Pro Ile Glu Glu Ile Ile Ser Lys Thr Pro Gly Gln
        115                 120                 125

Ala His Gln Pro Asn Val Tyr Val Leu Pro Pro Ser Arg Asp Glu Met
    130                 135                 140

Ser Lys Asn Thr Val Thr Leu Thr Cys Leu Val Lys Asp Phe Phe Pro
145                 150                 155                 160

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

Ser Lys Tyr Arg Met Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr
            180                 185                 190

Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly
        195                 200                 205

Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn His Tyr
    210                 215                 220
```

```
Thr Gln Ile Ser Leu Ser His Ser Pro Gly Lys
225                 230                 235


<210>  5
<211>  233
<212>  PRT
<213>  Canis familiaris

<400>  5

Pro Lys Glu Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu
1               5                   10                  15


Ser Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp
            20                  25                  30


Ile Leu Arg Ile Thr Arg Thr Pro Glu Ile Thr Cys Val Val Leu Asp
        35                  40                  45


Leu Gly Arg Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly
    50                  55                  60


Lys Glu Val His Thr Ala Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn
65                  70                  75                  80


Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp
                85                  90                  95


Leu Thr Gly Lys Glu Phe Lys Cys Arg Val Asn His Ile Gly Leu Pro
            100                 105                 110


Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln
        115                 120                 125


Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser
    130                 135                 140


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


Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Pro Glu Pro Glu Ser Lys
                165                 170                 175


Tyr His Thr Thr Ala Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu
            180                 185                 190


Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Thr
        195                 200                 205


Phe Thr Cys Ala Val Met His Glu Ala Leu Gln Asn His Tyr Thr Asp
    210                 215                 220


Leu Ser Leu Ser His Ser Pro Gly Lys
225                 230
```

<210> 6
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> caTNFRp60:HCA Fc Fusion Polypeptide

<400> 6

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


Ala Leu Leu Leu Glu Ile Tyr Pro Ile Ser Val Thr Ala Leu Val Pro
            20                  25                  30


His Pro Arg Asn Arg Val Lys Arg Ala Ile Leu Cys Pro Gln Gly Lys
        35                  40                  45


Tyr Ile His Pro Gln Asp Asp Ser Ile Cys Cys Thr Lys Cys His Lys
    50                  55                  60


Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Leu Asp Thr Asp
65                  70                  75                  80


Cys Arg Glu Cys Glu Asn Gly Thr Phe Thr Ala Ser Glu Asn His Leu
                85                  90                  95


Arg Gln Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Asn Gln Val
            100                 105                 110


Glu Ile Ser Pro Cys Thr Val Tyr Arg Asp Thr Val Cys Gly Cys Arg
        115                 120                 125


Lys Asn Gln Tyr Arg Phe Tyr Trp Ser Glu Thr Leu Phe Gln Cys Asn
    130                 135                 140


Asn Cys Ser Leu Cys Leu Asn Gly Thr Val Gln Ile Ser Cys Gln Glu
145                 150                 155                 160


Lys Gln Asn Thr Ile Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
                165                 170                 175


His Glu Cys Val Ser Cys Val Asn Cys Lys Lys Asn Thr Glu Cys Gly
            180                 185                 190


Lys Leu Cys Leu Pro Pro Val Glu Thr Val Lys Val Pro Gln Asp Pro
        195                 200                 205


Gly Ser Thr Phe Asn Glu Cys Arg Cys Thr Asp Thr Pro Pro Cys Pro
    210                 215                 220


Val Pro Glu Pro Leu Gly Gly Pro Ser Val Leu Ile Phe Pro Pro Lys
```

225 230 235 240

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

Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln Ile Ser Trp Phe
260 265 270

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

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

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

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

Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu
340 345 350

Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe Tyr
355 360 365

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

Glu Arg Lys His Arg Met Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser
385 390 395 400

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

Gly Asp Pro Phe Thr Cys Ala Val Met His Glu Thr Leu Gln Asn His
420 425 430

Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys
435 440

<210> 7
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> caTNFRp60:HCB Fc Fusion Polypeptide

<400> 7

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

```
Ala Leu Leu Leu Glu Ile Tyr Pro Ile Ser Val Thr Ala Leu Val Pro
            20                  25                  30

His Pro Arg Asn Arg Val Lys Arg Ala Ile Leu Cys Pro Gln Gly Lys
        35                  40                  45

Tyr Ile His Pro Gln Asp Asp Ser Ile Cys Cys Thr Lys Cys His Lys
    50                  55                  60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Leu Asp Thr Asp
65                  70                  75                  80

Cys Arg Glu Cys Glu Asn Gly Thr Phe Thr Ala Ser Glu Asn His Leu
                85                  90                  95

Arg Gln Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Asn Gln Val
            100                 105                 110

Glu Ile Ser Pro Cys Thr Val Tyr Arg Asp Thr Val Cys Gly Cys Arg
        115                 120                 125

Lys Asn Gln Tyr Arg Phe Tyr Trp Ser Glu Thr Leu Phe Gln Cys Asn
    130                 135                 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val Gln Ile Ser Cys Gln Glu
145                 150                 155                 160

Lys Gln Asn Thr Ile Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
                165                 170                 175

His Glu Cys Val Ser Cys Val Asn Cys Lys Lys Asn Thr Glu Cys Gly
            180                 185                 190

Lys Leu Cys Leu Pro Pro Val Glu Thr Val Lys Val Pro Gln Asp Pro
        195                 200                 205

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

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

Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu Ile Ala Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asp Pro Glu Val
            260                 265                 270

Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met Gln Thr Ala Lys Thr
        275                 280                 285

Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr Arg Val Val Ser Val
```

```
    290                 295                 300

Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly Lys Gln Phe Thr Cys
305                 310                 315                 320

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

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

Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser Leu Thr Cys Leu Ile
        355                 360                 365

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

Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu Asp
385                 390                 395                 400

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

Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala
            420                 425                 430

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


<210>  8
<211>  446
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  caTNFRp60:HCC Fc Fusion Polypeptide

<400>  8

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

Ala Leu Leu Leu Glu Ile Tyr Pro Ile Ser Val Thr Ala Leu Val Pro
            20                  25                  30

His Pro Arg Asn Arg Val Lys Arg Ala Ile Leu Cys Pro Gln Gly Lys
        35                  40                  45

Tyr Ile His Pro Gln Asp Asp Ser Ile Cys Cys Thr Lys Cys His Lys
    50                  55                  60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Leu Asp Thr Asp
65                  70                  75                  80
```

```
Cys Arg Glu Cys Glu Asn Gly Thr Phe Thr Ala Ser Glu Asn His Leu
                85                  90                  95

Arg Gln Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Asn Gln Val
            100                 105                 110

Glu Ile Ser Pro Cys Thr Val Tyr Arg Asp Thr Val Cys Gly Cys Arg
        115                 120                 125

Lys Asn Gln Tyr Arg Phe Tyr Trp Ser Glu Thr Leu Phe Gln Cys Asn
    130                 135                 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val Gln Ile Ser Cys Gln Glu
145                 150                 155                 160

Lys Gln Asn Thr Ile Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
                165                 170                 175

His Glu Cys Val Ser Cys Val Asn Cys Lys Lys Asn Thr Glu Cys Gly
            180                 185                 190

Lys Leu Cys Leu Pro Pro Val Glu Thr Val Lys Val Pro Gln Asp Pro
        195                 200                 205

Gly Ser Thr Ala Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn Cys
    210                 215                 220

Pro Cys Pro Gly Cys Gly Leu Leu Gly Gly Pro Ser Val Phe Ile Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Ile Leu Val Thr Ala Arg Thr Pro Thr Val
                245                 250                 255

Thr Cys Val Val Val Asp Leu Asp Pro Glu Asn Pro Glu Val Gln Ile
            260                 265                 270

Ser Trp Phe Val Asp Ser Lys Gln Val Gln Thr Ala Asn Thr Gln Pro
        275                 280                 285

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

Ile Gly His Gln Asp Trp Leu Ser Gly Lys Gln Phe Lys Cys Lys Val
305                 310                 315                 320

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

Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val Leu Pro Pro Ser Arg
            340                 345                 350

Asp Glu Met Ser Lys Asn Thr Val Thr Leu Thr Cys Leu Val Lys Asp
```

```
        355                 360                 365

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

Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro Gln Leu Asp Glu Asp
385                 390                 395                 400

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

Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His
            420                 425                 430

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

<210> 9
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> caTNFRp60:HCD Fc Fusion Polypeptide

<400> 9

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

Ala Leu Leu Leu Glu Ile Tyr Pro Ile Ser Val Thr Ala Leu Val Pro
            20                  25                  30

His Pro Arg Asn Arg Val Lys Arg Ala Ile Leu Cys Pro Gln Gly Lys
        35                  40                  45

Tyr Ile His Pro Gln Asp Asp Ser Ile Cys Cys Thr Lys Cys His Lys
    50                  55                  60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Leu Asp Thr Asp
65                  70                  75                  80

Cys Arg Glu Cys Glu Asn Gly Thr Phe Thr Ala Ser Glu Asn His Leu
                85                  90                  95

Arg Gln Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Asn Gln Val
            100                 105                 110

Glu Ile Ser Pro Cys Thr Val Tyr Arg Asp Thr Val Cys Gly Cys Arg
        115                 120                 125

Lys Asn Gln Tyr Arg Phe Tyr Trp Ser Glu Thr Leu Phe Gln Cys Asn
    130                 135                 140
```

```
Asn Cys Ser Leu Cys Leu Asn Gly Thr Val Gln Ile Ser Cys Gln Glu
145                 150                 155                 160

Lys Gln Asn Thr Ile Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
                165                 170                 175

His Glu Cys Val Ser Cys Val Asn Cys Lys Lys Asn Thr Glu Cys Gly
            180                 185                 190

Lys Leu Cys Leu Pro Pro Val Glu Thr Val Lys Val Pro Gln Asp Pro
        195                 200                 205

Gly Ser Thr Pro Lys Glu Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro
    210                 215                 220

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

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

Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln Ile Ser Trp Phe
            260                 265                 270

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

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

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

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

Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu
            340                 345                 350

Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu Ile Lys Asp Phe Tyr
        355                 360                 365

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

Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu Asp Glu Asp Gly Ser
385                 390                 395                 400

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

Gly Asp Thr Phe Thr Cys Ala Val Met His Glu Ala Leu Gln Asn His
```

420 425 430

Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys
435 440

<210> 10
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> caTNFRp60:HCA Aglycosyl Fc Fusion Polypeptide

<400> 10

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

Ala Leu Leu Leu Glu Ile Tyr Pro Ile Ser Val Thr Ala Leu Val Pro
20 25 30

His Pro Arg Asn Arg Val Lys Arg Ala Ile Leu Cys Pro Gln Gly Lys
35 40 45

Tyr Ile His Pro Gln Asp Asp Ser Ile Cys Cys Thr Lys Cys His Lys
50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Leu Asp Thr Asp
65 70 75 80

Cys Arg Glu Cys Glu Asn Gly Thr Phe Thr Ala Ser Glu Asn His Leu
85 90 95

Arg Gln Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Asn Gln Val
100 105 110

Glu Ile Ser Pro Cys Thr Val Tyr Arg Asp Thr Val Cys Gly Cys Arg
115 120 125

Lys Asn Gln Tyr Arg Phe Tyr Trp Ser Glu Thr Leu Phe Gln Cys Asn
130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val Gln Ile Ser Cys Gln Glu
145 150 155 160

Lys Gln Asn Thr Ile Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
165 170 175

His Glu Cys Val Ser Cys Val Asn Cys Lys Lys Asn Thr Glu Cys Gly
180 185 190

Lys Leu Cys Leu Pro Pro Val Glu Thr Val Lys Val Pro Gln Asp Pro
195 200 205

```
Gly Ser Thr Phe Asn Glu Cys Arg Cys Thr Asp Thr Pro Pro Cys Pro
    210                 215                 220

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

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

Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln Ile Ser Trp Phe
            260                 265                 270

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

Gln Phe Ala Gly Thr Tyr Arg Val Val Ser Val Leu Pro Ile Glu His
    290                 295                 300

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

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

Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu
            340                 345                 350

Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe Tyr
        355                 360                 365

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

Glu Arg Lys His Arg Met Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser
385                 390                 395                 400

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

Gly Asp Pro Phe Thr Cys Ala Val Met His Glu Thr Leu Gln Asn His
            420                 425                 430

Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys
        435                 440
```

<210> 11
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> caTNFRp60:HCB Aglycosyl Fc Fusion Polypeptide

<400> 11

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

Ala Leu Leu Leu Glu Ile Tyr Pro Ile Ser Val Thr Ala Leu Val Pro
            20                  25                  30

His Pro Arg Asn Arg Val Lys Arg Ala Ile Leu Cys Pro Gln Gly Lys
        35                  40                  45

Tyr Ile His Pro Gln Asp Asp Ser Ile Cys Cys Thr Lys Cys His Lys
    50                  55                  60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Leu Asp Thr Asp
65                  70                  75                  80

Cys Arg Glu Cys Glu Asn Gly Thr Phe Thr Ala Ser Glu Asn His Leu
                85                  90                  95

Arg Gln Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Asn Gln Val
            100                 105                 110

Glu Ile Ser Pro Cys Thr Val Tyr Arg Asp Thr Val Cys Gly Cys Arg
        115                 120                 125

Lys Asn Gln Tyr Arg Phe Tyr Trp Ser Glu Thr Leu Phe Gln Cys Asn
    130                 135                 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val Gln Ile Ser Cys Gln Glu
145                 150                 155                 160

Lys Gln Asn Thr Ile Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
                165                 170                 175

His Glu Cys Val Ser Cys Val Asn Cys Lys Lys Asn Thr Glu Cys Gly
            180                 185                 190

Lys Leu Cys Leu Pro Pro Val Glu Thr Val Lys Val Pro Gln Asp Pro
        195                 200                 205

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

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

Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu Ile Ala Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asp Pro Glu Val
            260                 265                 270
```

```
Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met Gln Thr Ala Lys Thr
        275                 280                 285

Gln Pro Arg Glu Glu Gln Phe Ala Gly Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly Lys Gln Phe Thr Cys
305                 310                 315                 320

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

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

Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser Leu Thr Cys Leu Ile
        355                 360                 365

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

Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu Asp
385                 390                 395                 400

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

Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala
            420                 425                 430

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


<210>  12
<211>  446
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  caTNFRp60:HCC Aglycosyl Fc Fusion Polypeptide

<400>  12

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

Ala Leu Leu Leu Glu Ile Tyr Pro Ile Ser Val Thr Ala Leu Val Pro
            20                  25                  30

His Pro Arg Asn Arg Val Lys Arg Ala Ile Leu Cys Pro Gln Gly Lys
        35                  40                  45

Tyr Ile His Pro Gln Asp Asp Ser Ile Cys Cys Thr Lys Cys His Lys
    50                  55                  60
```

```
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Leu Asp Thr Asp
65                  70                  75                  80

Cys Arg Glu Cys Glu Asn Gly Thr Phe Thr Ala Ser Glu Asn His Leu
                85                  90                  95

Arg Gln Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Asn Gln Val
            100                 105                 110

Glu Ile Ser Pro Cys Thr Val Tyr Arg Asp Thr Val Cys Gly Cys Arg
        115                 120                 125

Lys Asn Gln Tyr Arg Phe Tyr Trp Ser Glu Thr Leu Phe Gln Cys Asn
    130                 135                 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val Gln Ile Ser Cys Gln Glu
145                 150                 155                 160

Lys Gln Asn Thr Ile Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
                165                 170                 175

His Glu Cys Val Ser Cys Val Asn Cys Lys Lys Asn Thr Glu Cys Gly
            180                 185                 190

Lys Leu Cys Leu Pro Pro Val Glu Thr Val Lys Val Pro Gln Asp Pro
        195                 200                 205

Gly Ser Thr Ala Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn Cys
    210                 215                 220

Pro Cys Pro Gly Cys Gly Leu Leu Gly Gly Pro Ser Val Phe Ile Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Ile Leu Val Thr Ala Arg Thr Pro Thr Val
                245                 250                 255

Thr Cys Val Val Val Asp Leu Asp Pro Glu Asn Pro Glu Val Gln Ile
            260                 265                 270

Ser Trp Phe Val Asp Ser Lys Gln Val Gln Thr Ala Asn Thr Gln Pro
        275                 280                 285

Arg Glu Glu Gln Ser Ala Gly Thr Tyr Arg Val Val Ser Val Leu Pro
    290                 295                 300

Ile Gly His Gln Asp Trp Leu Ser Gly Lys Gln Phe Lys Cys Lys Val
305                 310                 315                 320

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

```
Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val Leu Pro Pro Ser Arg
            340                 345                 350

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

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

Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro Gln Leu Asp Glu Asp
385                 390                 395                 400

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

Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His
            420                 425                 430

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


<210>  13
<211>  444
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  caTNFRp60:HCD Aglycosyl Fc Fusion Polypeptide

<400>  13

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

Ala Leu Leu Leu Glu Ile Tyr Pro Ile Ser Val Thr Ala Leu Val Pro
            20                  25                  30

His Pro Arg Asn Arg Val Lys Arg Ala Ile Leu Cys Pro Gln Gly Lys
        35                  40                  45

Tyr Ile His Pro Gln Asp Asp Ser Ile Cys Cys Thr Lys Cys His Lys
    50                  55                  60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Leu Asp Thr Asp
65                  70                  75                  80

Cys Arg Glu Cys Glu Asn Gly Thr Phe Thr Ala Ser Glu Asn His Leu
                85                  90                  95

Arg Gln Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Asn Gln Val
            100                 105                 110

Glu Ile Ser Pro Cys Thr Val Tyr Arg Asp Thr Val Cys Gly Cys Arg
        115                 120                 125
```

```
Lys Asn Gln Tyr Arg Phe Tyr Trp Ser Glu Thr Leu Phe Gln Cys Asn
    130                 135                 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val Gln Ile Ser Cys Gln Glu
145                 150                 155                 160

Lys Gln Asn Thr Ile Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
                165                 170                 175

His Glu Cys Val Ser Cys Val Asn Cys Lys Lys Asn Thr Glu Cys Gly
            180                 185                 190

Lys Leu Cys Leu Pro Pro Val Glu Thr Val Lys Val Pro Gln Asp Pro
        195                 200                 205

Gly Ser Thr Pro Lys Glu Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro
    210                 215                 220

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

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

Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln Ile Ser Trp Phe
            260                 265                 270

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

Gln Phe Ala Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Glu His
    290                 295                 300

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

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

Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu
            340                 345                 350

Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu Ile Lys Asp Phe Tyr
        355                 360                 365

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

Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu Asp Glu Asp Gly Ser
385                 390                 395                 400
```

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


Gly Asp Thr Phe Thr Cys Ala Val Met His Glu Ala Leu Gln Asn His
            420                 425                 430


Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys
        435                 440


<210>  14
<211>  260
<212>  PRT
<213>  Canis familiaris

<400>  14

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


Trp Gly Ala Gly Arg Ala Val Pro Gly Gln Ala Thr Gln Leu Pro Tyr
            20                  25                  30


Val Pro Asp Pro Glu Leu Gly Ser Ser Cys Gln Gln Ser Glu Tyr Phe
        35                  40                  45


Asp Gln Arg Thr Gln Met Cys Cys Ser Met Cys Pro Pro Gly Ser His
    50                  55                  60


Ala Arg Leu Phe Cys Thr Lys Thr Ser Asn Thr Val Cys Ala Arg Cys
65                  70                  75                  80


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


Ser Cys Gly Ser Arg Cys Gly Ala Asp Gln Val Glu Thr Gln Ala Cys
            100                 105                 110


Thr Arg Glu Gln Asn Arg Ile Cys Ser Cys Lys Ser Gly Trp Tyr Cys
        115                 120                 125


Thr Leu Arg Arg Gln Gly Gly Cys Arg Leu Cys Ala Pro Leu Arg Arg
    130                 135                 140


Cys Arg Pro Gly Phe Gly Val Ala Lys Pro Gly Thr Ala Thr Ser Asp
145                 150                 155                 160


Val Val Cys Ala Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser
                165                 170                 175


Ser Thr Asp Thr Cys Arg Pro His Arg Ile Cys Ser Ser Val Ala Val
            180                 185                 190


Pro Gly Asn Ala Ser Val Asp Ala Val Cys Ser Pro Ala Pro Pro Thr
        195                 200                 205
```

```
Val Arg Thr Ala Pro Arg Pro Ala Ser Thr Arg Gln Pro Gly Ser Thr
    210                 215                 220

Gln Pro Arg Pro Ala Glu Pro Thr Pro Gly Pro Ser Thr Pro Pro Arg
225                 230                 235                 240

Thr Ser Val Leu Phe Pro Ala Val Pro Ser Pro Pro Ala Glu Gly Leu
                245                 250                 255

Ser Thr Gly Asp
            260
```

<210> 15
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> caTNFrecp80-HCA Fusion Polypeptide

<400> 15

```
Met Ala Pro Ala Ala Leu Trp Ala Leu Leu Ala Ala Gly Leu Gln Leu
1               5                   10                  15

Trp Gly Ala Gly Arg Ala Val Pro Gly Gln Ala Thr Gln Leu Pro Tyr
            20                  25                  30

Val Pro Asp Pro Glu Leu Gly Ser Ser Cys Gln Gln Ser Glu Tyr Phe
        35                  40                  45

Asp Gln Arg Thr Gln Met Cys Cys Ser Met Cys Pro Pro Gly Ser His
    50                  55                  60

Ala Arg Leu Phe Cys Thr Lys Thr Ser Asn Thr Val Cys Ala Arg Cys
65                  70                  75                  80

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

Ser Cys Gly Ser Arg Cys Gly Ala Asp Gln Val Glu Thr Gln Ala Cys
            100                 105                 110

Thr Arg Glu Gln Asn Arg Ile Cys Ser Cys Lys Ser Gly Trp Tyr Cys
        115                 120                 125

Thr Leu Arg Arg Gln Gly Gly Cys Arg Leu Cys Ala Pro Leu Arg Arg
    130                 135                 140

Cys Arg Pro Gly Phe Gly Val Ala Lys Pro Gly Thr Ala Thr Ser Asp
145                 150                 155                 160

Val Val Cys Ala Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser
```

```
                165                 170                 175

Ser Thr Asp Thr Cys Arg Pro His Arg Ile Cys Ser Ser Val Ala Val
            180                 185                 190

Pro Gly Asn Ala Ser Val Asp Ala Val Cys Ser Pro Ala Pro Pro Thr
        195                 200                 205

Val Arg Thr Ala Pro Arg Pro Ala Ser Thr Arg Gln Pro Gly Ser Thr
    210                 215                 220

Gln Pro Arg Pro Ala Glu Pro Thr Pro Gly Pro Ser Thr Pro Pro Arg
225                 230                 235                 240

Thr Ser Val Leu Phe Pro Ala Val Pro Ser Pro Pro Ala Glu Gly Leu
                245                 250                 255

Ser Thr Gly Asp Phe Asn Glu Cys Arg Cys Thr Asp Thr Pro Pro Cys
            260                 265                 270

Pro Val Pro Glu Pro Leu Gly Gly Pro Ser Val Leu Ile Phe Pro Pro
        275                 280                 285

Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu Val Thr Cys
    290                 295                 300

Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln Ile Ser Trp
305                 310                 315                 320

Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln Ser Arg Glu
                325                 330                 335

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

His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg Val Asn His
        355                 360                 365

Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly
    370                 375                 380

Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu
385                 390                 395                 400

Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe
                405                 410                 415

Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu
            420                 425                 430

Pro Glu Arg Lys His Arg Met Thr Pro Pro Gln Leu Asp Glu Asp Gly
        435                 440                 445
```

```
Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln
    450                 455                 460

Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu Thr Leu Gln Asn
465                 470                 475                 480

His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys
                485                 490
```

<210> 16
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> caTNFrecp80-HCB Fusion Polypeptide

<400> 16

```
Met Ala Pro Ala Ala Leu Trp Ala Leu Leu Ala Ala Gly Leu Gln Leu
1               5                   10                  15

Trp Gly Ala Gly Arg Ala Val Pro Gly Gln Ala Thr Gln Leu Pro Tyr
            20                  25                  30

Val Pro Asp Pro Glu Leu Gly Ser Ser Cys Gln Gln Ser Glu Tyr Phe
        35                  40                  45

Asp Gln Arg Thr Gln Met Cys Cys Ser Met Cys Pro Pro Gly Ser His
    50                  55                  60

Ala Arg Leu Phe Cys Thr Lys Thr Ser Asn Thr Val Cys Ala Arg Cys
65                  70                  75                  80

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

Ser Cys Gly Ser Arg Cys Gly Ala Asp Gln Val Glu Thr Gln Ala Cys
            100                 105                 110

Thr Arg Glu Gln Asn Arg Ile Cys Ser Cys Lys Ser Gly Trp Tyr Cys
        115                 120                 125

Thr Leu Arg Arg Gln Gly Gly Cys Arg Leu Cys Ala Pro Leu Arg Arg
    130                 135                 140

Cys Arg Pro Gly Phe Gly Val Ala Lys Pro Gly Thr Ala Thr Ser Asp
145                 150                 155                 160

Val Val Cys Ala Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser
                165                 170                 175

Ser Thr Asp Thr Cys Arg Pro His Arg Ile Cys Ser Ser Val Ala Val
```

```
            180                 185                 190

Pro Gly Asn Ala Ser Val Asp Ala Val Cys Ser Pro Ala Pro Pro Thr
        195                 200                 205

Val Arg Thr Ala Pro Arg Pro Ala Ser Thr Arg Gln Pro Gly Ser Thr
    210                 215                 220

Gln Pro Arg Pro Ala Glu Pro Thr Pro Gly Pro Ser Thr Pro Pro Arg
225                 230                 235                 240

Thr Ser Val Leu Phe Pro Ala Val Pro Ser Pro Pro Ala Glu Gly Leu
                245                 250                 255

Ser Thr Gly Asp Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro
            260                 265                 270

Asp Cys Pro Lys Cys Pro Ala Pro Glu Met Leu Gly Gly Pro Ser Val
        275                 280                 285

Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu Ile Ala Arg Thr
    290                 295                 300

Pro Glu Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asp Pro Glu
305                 310                 315                 320

Val Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met Gln Thr Ala Lys
                325                 330                 335

Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr Arg Val Val Ser
            340                 345                 350

Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly Lys Gln Phe Thr
        355                 360                 365

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

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

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

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

Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu
        435                 440                 445

Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys
    450                 455                 460
```

```
Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu
465                 470                 475                 480

Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser His Ser Pro Gly
                485                 490                 495

Lys
```

<210> 17
<211> 495
<212> PRT
<213> Artificial Sequence

<220>
<223> caTNFrecp80-HCC Fusion Polypeptide

<400> 17

```
Met Ala Pro Ala Ala Leu Trp Ala Leu Leu Ala Ala Gly Leu Gln Leu
1               5                   10                  15

Trp Gly Ala Gly Arg Ala Val Pro Gly Gln Ala Thr Gln Leu Pro Tyr
            20                  25                  30

Val Pro Asp Pro Glu Leu Gly Ser Ser Cys Gln Gln Ser Glu Tyr Phe
        35                  40                  45

Asp Gln Arg Thr Gln Met Cys Cys Ser Met Cys Pro Pro Gly Ser His
    50                  55                  60

Ala Arg Leu Phe Cys Thr Lys Thr Ser Asn Thr Val Cys Ala Arg Cys
65                  70                  75                  80

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

Ser Cys Gly Ser Arg Cys Gly Ala Asp Gln Val Glu Thr Gln Ala Cys
            100                 105                 110

Thr Arg Glu Gln Asn Arg Ile Cys Ser Cys Lys Ser Gly Trp Tyr Cys
        115                 120                 125

Thr Leu Arg Arg Gln Gly Gly Cys Arg Leu Cys Ala Pro Leu Arg Arg
    130                 135                 140

Cys Arg Pro Gly Phe Gly Val Ala Lys Pro Gly Thr Ala Thr Ser Asp
145                 150                 155                 160

Val Val Cys Ala Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser
                165                 170                 175

Ser Thr Asp Thr Cys Arg Pro His Arg Ile Cys Ser Ser Val Ala Val
```

```
            180                 185                 190

Pro Gly Asn Ala Ser Val Asp Ala Val Cys Ser Pro Ala Pro Pro Thr
        195                 200                 205

Val Arg Thr Ala Pro Arg Pro Ala Ser Thr Arg Gln Pro Gly Ser Thr
    210                 215                 220

Gln Pro Arg Pro Ala Glu Pro Thr Pro Gly Pro Ser Thr Pro Pro Arg
225                 230                 235                 240

Thr Ser Val Leu Phe Pro Ala Val Pro Ser Pro Pro Ala Glu Gly Leu
                245                 250                 255

Ser Thr Gly Asp Ala Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn
            260                 265                 270

Cys Pro Cys Pro Gly Cys Gly Leu Leu Gly Gly Pro Ser Val Phe Ile
        275                 280                 285

Phe Pro Pro Lys Pro Lys Asp Ile Leu Val Thr Ala Arg Thr Pro Thr
    290                 295                 300

Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asn Pro Glu Val Gln
305                 310                 315                 320

Ile Ser Trp Phe Val Asp Ser Lys Gln Val Gln Thr Ala Asn Thr Gln
                325                 330                 335

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

Pro Ile Gly His Gln Asp Trp Leu Ser Gly Lys Gln Phe Lys Cys Lys
        355                 360                 365

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

Thr Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val Leu Pro Pro Ser
385                 390                 395                 400

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

Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly Gln
            420                 425                 430

Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro Gln Leu Asp Glu
        435                 440                 445

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

```
Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu
465                 470                 475                 480


His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser Pro Gly Lys
                485                 490                 495


<210>  18
<211>  493
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  caTNFrecp80-HCD Fusion Polypeptide

<400>  18

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


Trp Gly Ala Gly Arg Ala Val Pro Gly Gln Ala Thr Gln Leu Pro Tyr
            20                  25                  30


Val Pro Asp Pro Glu Leu Gly Ser Ser Cys Gln Gln Ser Glu Tyr Phe
        35                  40                  45


Asp Gln Arg Thr Gln Met Cys Cys Ser Met Cys Pro Pro Gly Ser His
    50                  55                  60


Ala Arg Leu Phe Cys Thr Lys Thr Ser Asn Thr Val Cys Ala Arg Cys
65                  70                  75                  80


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


Ser Cys Gly Ser Arg Cys Gly Ala Asp Gln Val Glu Thr Gln Ala Cys
            100                 105                 110


Thr Arg Glu Gln Asn Arg Ile Cys Ser Cys Lys Ser Gly Trp Tyr Cys
        115                 120                 125


Thr Leu Arg Arg Gln Gly Gly Cys Arg Leu Cys Ala Pro Leu Arg Arg
    130                 135                 140


Cys Arg Pro Gly Phe Gly Val Ala Lys Pro Gly Thr Ala Thr Ser Asp
145                 150                 155                 160


Val Val Cys Ala Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser
                165                 170                 175


Ser Thr Asp Thr Cys Arg Pro His Arg Ile Cys Ser Ser Val Ala Val
            180                 185                 190


Pro Gly Asn Ala Ser Val Asp Ala Val Cys Ser Pro Ala Pro Pro Thr
```

```
        195                 200                 205

Val Arg Thr Ala Pro Arg Pro Ala Ser Thr Arg Gln Pro Gly Ser Thr
    210                 215                 220

Gln Pro Arg Pro Ala Glu Pro Thr Pro Gly Pro Ser Thr Pro Pro Arg
225                 230                 235                 240

Thr Ser Val Leu Phe Pro Ala Val Pro Ser Pro Pro Ala Glu Gly Leu
                245                 250                 255

Ser Thr Gly Asp Pro Lys Glu Ser Thr Cys Lys Cys Ile Ser Pro Cys
            260                 265                 270

Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro
        275                 280                 285

Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu Ile Thr Cys
    290                 295                 300

Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln Ile Ser Trp
305                 310                 315                 320

Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln Pro Arg Glu
                325                 330                 335

Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Glu
            340                 345                 350

His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg Val Asn His
        355                 360                 365

Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly
    370                 375                 380

Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu
385                 390                 395                 400

Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu Ile Lys Asp Phe
                405                 410                 415

Tyr Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Pro Glu
            420                 425                 430

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

Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln
    450                 455                 460

Gln Gly Asp Thr Phe Thr Cys Ala Val Met His Glu Ala Leu Gln Asn
465                 470                 475                 480
```

```
His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys
                485                 490


<210>  19
<211>  493
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  caTNFrecp80-aglycosyl HCA Fc Fusion Polypeptide

<400>  19

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


Trp Gly Ala Gly Arg Ala Val Pro Gly Gln Ala Thr Gln Leu Pro Tyr
            20                  25                  30


Val Pro Asp Pro Glu Leu Gly Ser Ser Cys Gln Gln Ser Glu Tyr Phe
        35                  40                  45


Asp Gln Arg Thr Gln Met Cys Cys Ser Met Cys Pro Pro Gly Ser His
    50                  55                  60


Ala Arg Leu Phe Cys Thr Lys Thr Ser Asn Thr Val Cys Ala Arg Cys
65                  70                  75                  80


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


Ser Cys Gly Ser Arg Cys Gly Ala Asp Gln Val Glu Thr Gln Ala Cys
            100                 105                 110


Thr Arg Glu Gln Asn Arg Ile Cys Ser Cys Lys Ser Gly Trp Tyr Cys
        115                 120                 125


Thr Leu Arg Arg Gln Gly Gly Cys Arg Leu Cys Ala Pro Leu Arg Arg
    130                 135                 140


Cys Arg Pro Gly Phe Gly Val Ala Lys Pro Gly Thr Ala Thr Ser Asp
145                 150                 155                 160


Val Val Cys Ala Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser
                165                 170                 175


Ser Thr Asp Thr Cys Arg Pro His Arg Ile Cys Ser Ser Val Ala Val
            180                 185                 190


Pro Gly Asn Ala Ser Val Asp Ala Val Cys Ser Pro Ala Pro Pro Thr
        195                 200                 205


Val Arg Thr Ala Pro Arg Pro Ala Ser Thr Arg Gln Pro Gly Ser Thr
```

```
    210                 215                 220

Gln Pro Arg Pro Ala Glu Pro Thr Pro Gly Pro Ser Thr Pro Pro Arg
225                 230                 235                 240

Thr Ser Val Leu Phe Pro Ala Val Pro Ser Pro Pro Ala Glu Gly Leu
                245                 250                 255

Ser Thr Gly Asp Phe Asn Glu Cys Arg Cys Thr Asp Thr Pro Pro Cys
            260                 265                 270

Pro Val Pro Glu Pro Leu Gly Gly Pro Ser Val Leu Ile Phe Pro Pro
        275                 280                 285

Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu Val Thr Cys
    290                 295                 300

Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln Ile Ser Trp
305                 310                 315                 320

Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln Ser Arg Glu
                325                 330                 335

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

His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg Val Asn His
        355                 360                 365

Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly
    370                 375                 380

Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu
385                 390                 395                 400

Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe
                405                 410                 415

Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu
            420                 425                 430

Pro Glu Arg Lys His Arg Met Thr Pro Pro Gln Leu Asp Glu Asp Gly
        435                 440                 445

Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln
    450                 455                 460

Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu Thr Leu Gln Asn
465                 470                 475                 480

His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys
                485                 490
```

<210> 20
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> caTNFrecp80-aglycosyl HCB Fc Fusion Polypeptide

<400> 20

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

Trp Gly Ala Gly Arg Ala Val Pro Gly Gln Ala Thr Gln Leu Pro Tyr
20 25 30

Val Pro Asp Pro Glu Leu Gly Ser Ser Cys Gln Gln Ser Glu Tyr Phe
35 40 45

Asp Gln Arg Thr Gln Met Cys Cys Ser Met Cys Pro Pro Gly Ser His
50 55 60

Ala Arg Leu Phe Cys Thr Lys Thr Ser Asn Thr Val Cys Ala Arg Cys
65 70 75 80

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

Ser Cys Gly Ser Arg Cys Gly Ala Asp Gln Val Glu Thr Gln Ala Cys
100 105 110

Thr Arg Glu Gln Asn Arg Ile Cys Ser Cys Lys Ser Gly Trp Tyr Cys
115 120 125

Thr Leu Arg Arg Gln Gly Gly Cys Arg Leu Cys Ala Pro Leu Arg Arg
130 135 140

Cys Arg Pro Gly Phe Gly Val Ala Lys Pro Gly Thr Ala Thr Ser Asp
145 150 155 160

Val Val Cys Ala Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser
165 170 175

Ser Thr Asp Thr Cys Arg Pro His Arg Ile Cys Ser Ser Val Ala Val
180 185 190

Pro Gly Asn Ala Ser Val Asp Ala Val Cys Ser Pro Ala Pro Pro Thr
195 200 205

Val Arg Thr Ala Pro Arg Pro Ala Ser Thr Arg Gln Pro Gly Ser Thr
210 215 220

Gln Pro Arg Pro Ala Glu Pro Thr Pro Gly Pro Ser Thr Pro Pro Arg

225 230 235 240

Thr Ser Val Leu Phe Pro Ala Val Pro Ser Pro Pro Ala Glu Gly Leu
245 250 255

Ser Thr Gly Asp Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro
260 265 270

Asp Cys Pro Lys Cys Pro Ala Pro Glu Met Leu Gly Gly Pro Ser Val
275 280 285

Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu Ile Ala Arg Thr
290 295 300

Pro Glu Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asp Pro Glu
305 310 315 320

Val Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met Gln Thr Ala Lys
325 330 335

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

Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly Lys Gln Phe Thr
355 360 365

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

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

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

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

Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu
435 440 445

Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys
450 455 460

Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu
465 470 475 480

Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser His Ser Pro Gly
485 490 495

Lys

<210> 21
<211> 495
<212> PRT
<213> Artificial Sequence

<220>
<223> caTNFrecp80-aglycosyl HCC Fc Fusion Polypeptide

<400> 21

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

Trp Gly Ala Gly Arg Ala Val Pro Gly Gln Ala Thr Gln Leu Pro Tyr
20 25 30

Val Pro Asp Pro Glu Leu Gly Ser Ser Cys Gln Gln Ser Glu Tyr Phe
35 40 45

Asp Gln Arg Thr Gln Met Cys Cys Ser Met Cys Pro Pro Gly Ser His
50 55 60

Ala Arg Leu Phe Cys Thr Lys Thr Ser Asn Thr Val Cys Ala Arg Cys
65 70 75 80

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

Ser Cys Gly Ser Arg Cys Gly Ala Asp Gln Val Glu Thr Gln Ala Cys
100 105 110

Thr Arg Glu Gln Asn Arg Ile Cys Ser Cys Lys Ser Gly Trp Tyr Cys
115 120 125

Thr Leu Arg Arg Gln Gly Gly Cys Arg Leu Cys Ala Pro Leu Arg Arg
130 135 140

Cys Arg Pro Gly Phe Gly Val Ala Lys Pro Gly Thr Ala Thr Ser Asp
145 150 155 160

Val Val Cys Ala Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser
165 170 175

Ser Thr Asp Thr Cys Arg Pro His Arg Ile Cys Ser Ser Val Ala Val
180 185 190

Pro Gly Asn Ala Ser Val Asp Ala Val Cys Ser Pro Ala Pro Pro Thr
195 200 205

Val Arg Thr Ala Pro Arg Pro Ala Ser Thr Arg Gln Pro Gly Ser Thr
210 215 220

Gln Pro Arg Pro Ala Glu Pro Thr Pro Gly Pro Ser Thr Pro Pro Arg

225 230 235 240

Thr Ser Val Leu Phe Pro Ala Val Pro Ser Pro Pro Ala Glu Gly Leu
245 250 255

Ser Thr Gly Asp Ala Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn
260 265 270

Cys Pro Cys Pro Gly Cys Gly Leu Leu Gly Gly Pro Ser Val Phe Ile
275 280 285

Phe Pro Pro Lys Pro Lys Asp Ile Leu Val Thr Ala Arg Thr Pro Thr
290 295 300

Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asn Pro Glu Val Gln
305 310 315 320

Ile Ser Trp Phe Val Asp Ser Lys Gln Val Gln Thr Ala Asn Thr Gln
325 330 335

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

Pro Ile Gly His Gln Asp Trp Leu Ser Gly Lys Gln Phe Lys Cys Lys
355 360 365

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

Thr Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val Leu Pro Pro Ser
385 390 395 400

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

Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly Gln
420 425 430

Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro Gln Leu Asp Glu
435 440 445

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

Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu
465 470 475 480

His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser Pro Gly Lys
485 490 495

<210> 22
<211> 493

<212> PRT
<213> Artificial Sequence

<220>
<223> caTNFrecp80-aglycosyl HCD Fc Fusion Polypeptide

<400> 22

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

Trp Gly Ala Gly Arg Ala Val Pro Gly Gln Ala Thr Gln Leu Pro Tyr
20 25 30

Val Pro Asp Pro Glu Leu Gly Ser Ser Cys Gln Gln Ser Glu Tyr Phe
35 40 45

Asp Gln Arg Thr Gln Met Cys Cys Ser Met Cys Pro Pro Gly Ser His
50 55 60

Ala Arg Leu Phe Cys Thr Lys Thr Ser Asn Thr Val Cys Ala Arg Cys
65 70 75 80

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

Ser Cys Gly Ser Arg Cys Gly Ala Asp Gln Val Glu Thr Gln Ala Cys
100 105 110

Thr Arg Glu Gln Asn Arg Ile Cys Ser Cys Lys Ser Gly Trp Tyr Cys
115 120 125

Thr Leu Arg Arg Gln Gly Gly Cys Arg Leu Cys Ala Pro Leu Arg Arg
130 135 140

Cys Arg Pro Gly Phe Gly Val Ala Lys Pro Gly Thr Ala Thr Ser Asp
145 150 155 160

Val Val Cys Ala Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser
165 170 175

Ser Thr Asp Thr Cys Arg Pro His Arg Ile Cys Ser Ser Val Ala Val
180 185 190

Pro Gly Asn Ala Ser Val Asp Ala Val Cys Ser Pro Ala Pro Pro Thr
195 200 205

Val Arg Thr Ala Pro Arg Pro Ala Ser Thr Arg Gln Pro Gly Ser Thr
210 215 220

Gln Pro Arg Pro Ala Glu Pro Thr Pro Gly Pro Ser Thr Pro Pro Arg
225 230 235 240

Thr Ser Val Leu Phe Pro Ala Val Pro Ser Pro Pro Ala Glu Gly Leu

245 250 255

Ser Thr Gly Asp Pro Lys Glu Ser Thr Cys Lys Cys Ile Ser Pro Cys
260 265 270

Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro
275 280 285

Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu Ile Thr Cys
290 295 300

Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln Ile Ser Trp
305 310 315 320

Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln Pro Arg Glu
325 330 335

Gln Gln Phe Ala Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Glu
340 345 350

His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg Val Asn His
355 360 365

Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly
370 375 380

Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu
385 390 395 400

Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu Ile Lys Asp Phe
405 410 415

Tyr Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Pro Glu
420 425 430

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

Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln
450 455 460

Gln Gly Asp Thr Phe Thr Cys Ala Val Met His Glu Ala Leu Gln Asn
465 470 475 480

His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys
485 490

<210> 23
<211> 633
<212> DNA
<213> Canis familiaris

<400> 23

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gaaatctacc ccatcagcgt gaccgccctg gtgccccacc cccggaacag agtgaagcgg 120

gccatcctgt gtccacaggg caagtacatc caccctcagg acgacagcat ctgctgcacc 180

aagtgccaca agggcaccta cctgtacaac gactgccccg gacccggcct ggacaccgat 240

tgcagagagt gcgagaacgg caccttcacc gccagcgaga accacctgag acagtgcctg 300

tcctgcagca agtgcagaaa agagatgaac caggtcgaga tcagcccctg caccgtgtac 360

cgggacaccg tgtgcggctg ccggaagaac cagtacagat tctattggag cgagacactg 420

ttccagtgca acaactgcag cctgtgcctg aatggcaccg tgcagatcag ctgccaggaa 480

aagcagaaca ccatctgcac ctgtcacgcc ggattctttc tgcgcgagca cgagtgcgtg 540

tcctgtgtga actgcaagaa aaacaccgag tgtggcaagc tgtgcctgcc ccctgtggaa 600

accgtgaaag tgcctcagga ccctggcagc aca 633

<210> 24
<211> 702
<212> DNA
<213> Canis familiaris

<400> 24
ttcaacgagt gccggtgtac cgacaccccc ccttgtcctg tgcctgagcc tctgggcgga 60

ccctccgtgc tgatcttccc acccaagccc aaggacatcc tgcggatcac ccggaccccc 120

gaagtgacct gcgtggtgct ggatctgggc cgcgaggacc ctgaggtgca gatcagttgg 180

ttcgtggacg gcaaagaggt gcacaccgct aagacccaga gcagagagca gcagttcaac 240

ggcacctaca gagtggtgtc cgtgctgccc atcgagcacc aggactggct gaccggcaaa 300

gagttcaagt gcagagtcaa ccacatcgac ctgcctagcc ctatcgagcg gaccatcagc 360

aaggccagag gcagagccca caagcccagc gtgtacgtgc tcccacccag ccccaaagag 420

ctgagcagca gcgacaccgt gtccatcacc tgtctgatca aggacttcta ccccccccgac 480

atcgacgtgg aatggcagag caacggacag caggaacccg agcggaagca cagaatgacc 540

cccccacagc tggacgagga cggcagctac ttcctgtaca gcaagctgag cgtggacaag 600

agccggtggc agcagggcga ccccttcaca tgtgccgtga tgcacgagac actgcagaac 660

cactacaccg acctgtctct gagccacagc cccggcaagt ga 702

<210> 25
<211> 714
<212> DNA
<213> Canis familiaris

<400> 25
cccaagcgcg agaacggcag agtgcccaga ccccccgact gccctaagtg tcccgccccct 60

gagatgctgg gcggaccctc cgtgttcatc ttcccaccca agcccaagga caccctgctg 120

atcgcccgga cccccgaagt gacctgcgtg gtggtggacc tggaccccga ggaccctgag 180

gtgcagatca gttggttcgt ggacggcaag cagatgcaga ccgccaagac ccagcccaga 240

gaggaacagt tcaacggcac ctaccgggtg gtgtccgtcc tgcctatcgg ccaccaggac 300

tggctgaagg gcaagcagtt tacctgcaaa gtgaacaaca aggccctgcc tagccccatc 360

gagcggacca tcagcaaggc cagaggccag gcccaccagc ccagcgtgta cgtgctgccc 420

cccagccggg aagaactgag caagaatacc gtgtccctga cctgcctgat caaggacttc 480

taccccccg acatcgacgt ggaatggcag agcaacggcc agcaggaacc cgagagcaag 540

taccggacca ccccccaca gctggacgag gacggcagct acttcctgta cagcaagctg 600

agcgtggaca agagccggtg gcagcggggc gacaccttca tctgcgccgt gatgcacgag 660

gccctgcaca accactacac ccaggaaagc ctgtctcaca gccccggcaa gtga 714

<210> 26
<211> 708
<212> DNA
<213> Canis familiaris

<400> 26
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ctgggaggac ctagcgtgtt catcttccca cccaagccca aggacatcct ggtcaccgcc 120

cggaccccca ccgtgacatg cgtggtggtg gacctggacc ccgagaaccc cgaggtgcag 180

atcagttggt tcgtggacag caaacaggtg cagaccgcca acacccagcc cagagaggaa 240

cagagcaacg gcacctacag agtggtgtct gtgctgccta tcggccacca ggactggctg 300

agcggcaagc agttcaagtg caaagtgaac aacaaggccc tgcctagccc catcgaggaa 360

atcatcagca agacccctgg acaggcccac cagcctaacg tgtacgtcct gcctcccagc 420

cgggacgaga tgtccaagaa caccgtgacc ctgacttgcc tggtcaagga cttcttcccc 480

cccgaaatcg acgtggaatg gcagtccaac ggccagcagg aacccgagag caagtaccgg 540

atgacccccc cacagctgga cgaggacggc agctacttcc tgtacagcaa gctgagcgtg 600

gacaagagcc ggtggcagcg gggcgacacc ttcatctgcg ccgtgatgca cgaggccctg 660

cacaaccact acacccagat cagcctgagc cacagccccg gcaagtga 708

<210> 27
<211> 702
<212> DNA
<213> Canis familiaris

<400> 27
cccaaagaaa gcacatgcaa gtgcatcagc ccctgtcccg tgcctgagtc tctgggaggc 60

ccttccgtgt tcatcttccc acccaagccc aaggacatcc tgcggatcac ccggaccccc 120

gagatcacct gtgtggtgct ggacctgggc cgcgaggacc ctgaggtgca gatcagttgg 180

ttcgtggacg gcaaagaggt gcacaccgct aagacccagc ccagagagca gcagttcaac 240

agcacctacc gggtggtgtc cgtcctgccc atcgagcacc aggactggct gaccggcaaa 300

gagttcaagt gcagagtcaa ccacatcggc ctgcccagcc ctatcgagcg gaccatcagc 360

aaggccagag gccaggccca ccagcccagc gtgtacgtgc tgccacctag ccccaaagag 420

ctgagcagca gcgacaccgt gaccctgacc tgcctgatca aggacttcta ccccccgaa 480

atcgacgtgg aatggcagag caacggacag cctgagcccg agagcaagta ccacaccaca 540

gccccccagc tggacgagga cggcagctac ttcctgtaca gcaagctgag cgtggacaag 600

agccggtggc agcagggcga caccttcaca tgtgccgtga tgcacgaggc cctgcagaac 660

cactacaccg acctgagcct gagccacagc cccggcaagt ga 702

<210> 28
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> caTNFRp60-HCA - nucleotide sequence encoding SEQ ID NO:6

<400> 28
atgggcctgc ccaccgtgcc tggactgctg ctgcctctgg tgctgctggc cctgctgctg 60

gaaatctacc ccatcagcgt gaccgccctg gtgccccacc cccggaacag agtgaagcgg 120

gccatcctgt gtccacaggg caagtacatc caccctcagg acgacagcat ctgctgcacc 180

aagtgccaca agggcaccta cctgtacaac gactgccccg gacccggcct ggacaccgat 240

tgcagagagt gcgagaacgg caccttcacc gccagcgaga accacctgag acagtgcctg 300

tcctgcagca agtgcagaaa agagatgaac caggtcgaga tcagcccctg caccgtgtac 360

cgggacaccg tgtgcggctg ccggaagaac cagtacagat tctattggag cgagacactg 420

ttccagtgca acaactgcag cctgtgcctg aatggcaccg tgcagatcag ctgccaggaa 480

aagcagaaca ccatctgcac ctgtcacgcc ggattctttc tgcgcgagca cgagtgcgtg 540

tcctgtgtga actgcaagaa aaacaccgag tgtggcaagc tgtgcctgcc ccctgtggaa 600

accgtgaaag tgcctcagga ccctggcagc acattcaacg agtgccggtg taccgacacc 660

ccccttgtc ctgtgcctga gcctctgggc ggaccctccg tgctgatctt cccacccaag 720

cccaaggaca tcctgcggat cacccggacc cccgaagtga cctgcgtggt gctggatctg 780

ggccgcgagg accctgaggt gcagatcagt tggttcgtgg acggcaaaga ggtgcacacc 840

gctaagaccc agagcagaga gcagcagttc aacggcacct acagagtggt gtccgtgctg 900

cccatcgagc accaggactg gctgaccggc aaagagttca agtgcagagt caaccacatc 960

gacctgccta gccctatcga gcggaccatc agcaaggcca gaggcagagc ccacaagccc 1020

agcgtgtacg tgctcccacc cagccccaaa gagctgagca gcagcgacac cgtgtccatc 1080

acctgtctga tcaaggactt ctacccccc gacatcgacg tggaatggca gagcaacgga 1140

cagcaggaac ccgagcggaa gcacagaatg acccccccac agctggacga ggacggcagc 1200

tacttcctgt acagcaagct gagcgtggac aagagccggt ggcagcaggg cgacccttc 1260

acatgtgccg tgatgcacga gacactgcag aaccactaca ccgacctgtc tctgagccac 1320

agccccggca agtga 1335

<210> 29
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> caTNFRp60-HCB - nucleotide sequence encoding SEQ ID NO:7

<400> 29
atgggcctgc ccaccgtgcc tggactgctg ctgcctctgg tgctgctggc cctgctgctg 60

gaaatctacc ccatcagcgt gaccgccctg gtgccccacc cccggaacag agtgaagcgg 120

gccatcctgt gtccacaggg caagtacatc caccctcagg acgacagcat ctgctgcacc 180

aagtgccaca agggcaccta cctgtacaac gactgccccg gacccggcct ggacaccgat 240

tgcagagagt gcgagaacgg caccttcacc gccagcgaga accacctgag acagtgcctg 300

tcctgcagca agtgcagaaa agagatgaac caggtcgaga tctctccctg caccgtgtac 360

cgggacaccg tgtgcggctg ccggaagaac cagtacagat tctattggag cgagacactg 420

ttccagtgca acaactgcag cctgtgcctg aatggcaccg tgcagatcag ctgccaggaa 480

aagcagaaca ccatctgcac ctgtcacgcc ggattctttc tgcgcgagca cgagtgcgtg 540

tcctgtgtga actgcaagaa aaacaccgag tgtggcaagc tgtgcctgcc ccctgtggaa 600

accgtgaaag tgcctcagga ccccggcagc acacccaagc gcgagaacgg cagagtgccc 660

agacccccg actgccctaa gtgtcccgcc cctgagatgc tgggcggacc ctccgtgttc 720

atcttcccac ccaagcccaa ggacaccctg ctgatcgccc ggaccccga agtgacctgc 780

gtggtggtgg acctggaccc cgaggaccct gaggtgcaga tcagttggtt cgtggacggc 840

aagcagatgc agaccgccaa gacccagccc agagaggaac agttcaacgg cacctaccgg 900

gtggtgtccg tcctgcctat cggccaccag gactggctga agggcaagca gtttacctgc 960

aaagtgaaca acaaggccct gcctagcccc atcgagcgga ccatcagcaa ggccagaggc 1020

caggcccacc agcccagcgt gtacgtgctg ccccccagcc gggaagaact gagcaagaat 1080

accgtgtccc tgacctgcct gatcaaggac ttctaccccc ccgacatcga cgtggaatgg 1140

cagagcaacg gccagcagga acccgagagc aagtaccgga ccacccccc acagctggac 1200

gaggacggca gctacttcct gtacagcaag ctgagcgtgg acaagagccg gtggcagcgg 1260

ggcgacacct tcatctgcgc cgtgatgcac gaggccctgc acaaccacta cacccaggaa 1320

agcctgtctc acagccccgg caagtga 1347

<210> 30
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> caTNFRp60-HCC - nucleotide sequence encoding SEQ ID NO:8

<400> 30
atgggcctgc ccaccgtgcc tggactgctg ctgcctctgg tgctgctggc cctgctgctg 60

gaaatctacc ccatcagcgt gaccgccctg gtgccccacc cccggaacag agtgaagcgg 120

gccatcctgt gtccacaggg caagtacatc caccctcagg acgacagcat ctgctgcacc 180

aagtgccaca agggcaccta cctgtacaac gactgccccg gacccggcct ggacaccgat 240

tgcagagagt gcgagaacgg caccttcacc gccagcgaga accacctgag acagtgcctg 300

tcctgcagca agtgcagaaa agagatgaac caggtcgaga tcagcccctg caccgtgtac 360

cgggacaccg tgtgcggctg ccggaagaac cagtacagat tctattggag cgagacactg 420

ttccagtgca acaactgcag cctgtgcctg aatggcaccg tgcagatcag ctgccaggaa 480

aagcagaaca ccatctgcac ctgtcacgcc ggattctttc tgcgcgagca cgagtgcgtg 540

tcctgtgtga actgcaagaa aaacaccgag tgtggcaagc tgtgcctgcc ccctgtggaa 600

accgtgaaag tgcctcagga ccccggcagc acagctaaag aatgcgagtg caagtgcaac 660

tgcaacaact gcccctgtcc tggctgcgga ctgctgggag gacctagcgt gttcatcttc 720

ccacccaagc ccaaggacat cctggtcacc gcccggaccc ccaccgtgac atgcgtggtg 780

gtggacctgg accccgagaa ccccgaggtg cagatcagtt ggttcgtgga cagcaaacag 840

gtgcagaccg ccaacaccca gcccagagag gaacagagca acggcaccta cagagtggtg 900

tctgtgctgc ctatcggcca ccaggactgg ctgagcggca agcagttcaa gtgcaaagtg 960

aacaacaagg ccctgcctag ccccatcgag gaaatcatca gcaagacccc tggacaggcc 1020

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ggcagctact tcctgtacag caagctgagc gtggacaaga gccggtggca gcggggcgac 1260

accttcatct gcgccgtgat gcacgaggcc ctgcacaacc actacaccca gatcagcctg 1320

agccacagcc ccggcaagtg a 1341

<210> 31
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> caTNFRp60-HCD - nucleotide sequence encoding SEQ ID NO:9

<400> 31
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gaaatctacc ccatcagcgt gaccgccctg gtgccccacc cccggaacag agtgaagcgg 120

gccatcctgt gtccacaggg caagtacatc caccctcagg acgacagcat ctgctgcacc 180

aagtgccaca agggcaccta cctgtacaac gactgccccg gacccggcct ggacaccgat 240

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tcctgcagca agtgcagaaa agagatgaac caggtcgaga tcagcccttg caccgtgtac 360

cgggacaccg tgtgcggctg ccggaagaac cagtacagat tctattggag cgagacactg 420

ttccagtgca acaactgcag cctgtgcctg aatggcaccg tgcagatcag ctgccaggaa 480

aagcagaaca ccatctgcac ctgtcacgcc ggattctttc tgcgcgagca cgagtgcgtg 540

tcctgtgtga actgcaagaa aaacaccgag tgtggcaagc tgtgcctgcc ccctgtggaa 600

accgtgaaag tgccccagga ccccggcagc acacccaaag aaagcacatg caagtgcatc 660

agcccctgtc ccgtgcctga gtctctggga ggcccttccg tgttcatctt cccacccaag 720

cccaaggaca tcctgcggat cacccggacc cccgagatca cctgtgtggt gctggacctg 780

ggccgcgagg accctgaggt gcagatcagt tggttcgtgg acggcaaaga ggtgcacacc 840

gctaagaccc agcccagaga gcagcagttc aacagcacct accgggtggt gtccgtcctg 900

cccatcgagc accaggactg gctgaccggc aaagagttca agtgcagagt caaccacatc 960

ggcctgccca gccctatcga gcggaccatc agcaaggcca gaggccaggc ccaccagccc 1020

agcgtgtacg tgctgccacc tagccccaaa gagctgagca gcagcgacac cgtgaccctg 1080

acctgcctga tcaaggactt ctacccccc gaaatcgacg tggaatggca gagcaacgga 1140

cagcctgagc ccgagagcaa gtaccacacc acagcccccc agctggacga ggacggcagc 1200

tacttcctgt acagcaagct gagcgtggac aagagccggt ggcagcaggg cgacaccttc 1260

acatgtgccg tgatgcacga ggccctgcag aaccactaca ccgacctgag cctgagccac 1320

agccccggca agtga 1335