SEQUENCE LISTING

<110> Emergent Product Development Seattle, LLC
Blankenship, John W.
Tan, Philip

<120> HETERODIMER BINDING PROTEINS AND USES THEREOF

<130> 2479.1040002/EJH/BNC

<140> 13/519,727
<141> 2010-12-29

<150> PCT/US2010/062436
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<150> US 61/365,266
<151> 2010-07-16

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<151> 2010-07-22

<160> 882

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 2088
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence of 2E12CH1CH2CH3Ck (X0130)

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ccaggaaagg gtctggagtg gctgggaatg atatggggtg atggaagcac agactataat 180
tcagctctca aatccagact atcgatcacc aaggacaact ccaagagcca agttttctta 240
aaaatgaaca gtctgcaaac tgatgacaca gccagatact actgtgctcg ggatggttat 300
agtaactttc attactatgt tatggactac tggggtcaag gaacctcagt caccgtctcc 360
tctgggggtg gaggctctgg tggcggtgga tccggcggag gtgggtcggg tggcggcgga 420
tctgacattg tgctcaccca atctccagct tctttggctg tgtctctagg tcagagagcc 480
accatctcct gcagagccag tgaaagtgtt gaatattatg tcacaagttt aatgcagtgg 540
taccaacaga aaccaggaca gccacccaaa ctcctcatct ctgctgctag caacgtagaa 600
tctggggtcc ctgccaggtt tagtggcagt gggtctggga cagactttag cctcaacatc 660
catcctgtgg aggaggatga tattgcaatg tatttctgtc agcaaagtag gaaggttcca 720
tggacgttcg gtggaggcac caagctggaa atcaagtcct cgagcgcctc caccaagggc 780
ccatcggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 840
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ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 960
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 1020
aatcacaagc ccagcaacac caaggtggac aagaaagttc gtacggagcc caaatcttct 1080
gacaaaactc acacatgccc accgtgccca tccggagcac ctgaactcct gggtggaccg 1140
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 1200
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 1260
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 1320
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1380
tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1440
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1500
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatccaag cgacatcgcc 1560
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1620
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1680

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caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1740
aagagcctct ccctgtctcc gggtaaatct agaactgtgg ctgcaccatc tgtcttcatc 1800
ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 1860
aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 1920
aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 1980
accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 2040
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<210> 2
<211> 696
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of 2E12CH1CH2CH3Ck (X0130)

<400> 2

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 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr
            20                  25                  30
Gly Val Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Met Ile Trp Gly Asp Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys
    50                  55                  60
Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala
                85                  90                  95
Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr Val Met Asp Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
    130                 135                 140
Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala
145                 150                 155                 160
Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser
                165                 170                 175
Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
            180                 185                 190
Ile Ser Ala Ala Ser Asn Val Glu Ser Gly Val Pro Ala Arg Phe Ser
        195                 200                 205
Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His Pro Val Glu
    210                 215                 220
Glu Asp Asp Ile Ala Met Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro
225                 230                 235                 240
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Ser Ser Ala
                245                 250                 255
Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
            260                 265                 270
Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
        275                 280                 285
Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
    290                 295                 300
Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
305                 310                 315                 320
Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
                325                 330                 335
Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
            340                 345                 350
Val Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
        355                 360                 365
Cys Pro Ser Gly Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
    370                 375                 380
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
385                 390                 395                 400
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
```

```
                405                 410                 415
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
            420                 425                 430
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
        435                 440                 445
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
    450                 455                 460
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
465                 470                 475                 480
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
                485                 490                 495
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
            500                 505                 510
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
        515                 520                 525
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
    530                 535                 540
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
545                 550                 555                 560
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
                565                 570                 575
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Thr
            580                 585                 590
Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
        595                 600                 605
Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
    610                 615                 620
Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
625                 630                 635                 640
Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
                645                 650                 655
Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
            660                 665                 670
Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
        675                 680                 685
Thr Lys Ser Phe Asn Arg Gly Glu
    690                 695
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<210> 3
<211> 2142
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of CKCH2CH3CH1-H68-2E12 (X0168)

<400> 3

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aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 180
aaggacagca cctacagcct cagcagcacc ctgacgctga gcaaagcaga ctacgagaaa 240
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 300
ttcaacaggg gagagcgtac ggagcccaaa tcttctgaca aaactcacac atgcccaccg 360
tgcccatccg gagcacctga actcctgggt ggaccgtcag tcttcctctt ccccccaaaa 420
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 480
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 540
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 600
accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 660
gccctcccag ccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 720
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 780
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 840
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 900
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 960
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1020
aaatctagag cctccaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 1080
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```
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cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 1260
acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 1320
gttaactcat tattcaacca agaagttcaa attcccttga ccgaaagtta cagcccgaat 1380
tctcaggtgc agctgaagga gtcaggacct ggcagcgtgg cgccctcaca gagcctgtcc 1440
atcacatgca ccgtctcagg gttctcatta accggctatg gtgtaaactg ggttcgccag 1500
cctccaggaa agggtctgga gtggctggga atgatatggg gtgatggaag cacagactat 1560
aattcagctc tcaaatccag actatcgatc accaaggaca actccaagag ccaagttttc 1620
ttaaaaatga acagtctgca aactgatgac acagccagat actactgtgc tcgggatggt 1680
tatagtaact ttcattacta tgttatggac tactggggtc aaggaacctc agtcaccgtc 1740
tcctctgggg gtggaggctc tggtggcggt ggatccggcg gaggtgggtc gggtggcggc 1800
ggatctgaca ttgtgctcac ccaatctcca gcttctttgg ctgtgtctct aggtcagaga 1860
gccaccatct cctgcagagc cagtgaaagt gttgaatatt atgtcacaag tttaatgcag 1920
tggtaccaac agaaaccagg acagccaccc aaactcctca tctctgctgc tagcaacgta 1980
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atccatcctg tggaggagga tgatattgca atgtatttct gtcagcaaag taggaaggtt 2100
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```

<210> 4
<211> 713
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of CKCH2CH3CH1-H68-2E12 (X0168)

<400> 4

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Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1               5                  10                  15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20                  25                  30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35                  40                  45
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50                  55                  60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65                  70                  75                  80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85                  90                  95
Val Thr Lys Ser Phe Asn Arg Gly Glu Arg Thr Glu Pro Lys Ser Ser
            100                 105                 110
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ser Gly Ala Pro Glu Leu
        115                 120                 125
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
    130                 135                 140
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
145                 150                 155                 160
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
                165                 170                 175
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
            180                 185                 190
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
        195                 200                 205
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
    210                 215                 220
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
225                 230                 235                 240
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
                245                 250                 255
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
            260                 265                 270
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
        275                 280                 285
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
    290                 295                 300
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
305                 310                 315                 320
```

```
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
                325                 330                 335
Leu Ser Pro Gly Lys Ser Arg Ala Ser Thr Lys Gly Pro Ser Val Phe
            340                 345                 350
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
        355                 360                 365
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
    370                 375                 380
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
385                 390                 395                 400
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
                405                 410                 415
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
            420                 425                 430
Ser Asn Thr Lys Val Asp Lys Lys Val Asn Ser Leu Phe Asn Gln Glu
        435                 440                 445
Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser Gln Val Gln
    450                 455                 460
Leu Lys Glu Ser Gly Pro Gly Ser Val Ala Pro Ser Gln Ser Leu Ser
465                 470                 475                 480
Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn
                485                 490                 495
Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile
            500                 505                 510
Trp Gly Asp Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu
        515                 520                 525
Ser Ile Thr Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
    530                 535                 540
Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Asp Gly
545                 550                 555                 560
Tyr Ser Asn Phe His Tyr Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr
                565                 570                 575
Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            580                 585                 590
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln
        595                 600                 605
Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser
    610                 615                 620
Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln
625                 630                 635                 640
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala
                645                 650                 655
Ala Ser Asn Val Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
            660                 665                 670
Ser Gly Thr Asp Phe Ser Leu Asn Ile His Pro Val Glu Glu Asp Asp
        675                 680                 685
Ile Ala Met Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro Trp Thr Phe
    690                 695                 700
Gly Gly Gly Thr Lys Leu Glu Ile Lys
705                 710
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<210> 5
<211> 1770
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of 2E12CH1CH2CH3 (X0112)

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ccaggaaagg gtctggagtg gctgggaatg atatggggtg atggaagcac agactataat 180
tcagctctca aatccagact atcgatcacc aaggacaact ccaagagcca agttttctta 240
aaaatgaaca gtctgcaaac tgatgacaca gccagatact actgtgctcg ggatggttat 300
agtaactttc attactatgt tatggactac tggggtcaag gaacctcagt caccgtctcc 360
tctgggggtg gaggctctgg tggcggtgga tccggcggag gtgggtcggg tggcggcgga 420

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tctgacattg tgctcaccca atctccagct tctttggctg tgtctctagg tcagagagcc 480
accatctcct gcagagccag tgaaagtgtt gaatattatg tcacaagttt aatgcagtgg 540
taccaacaga aaccaggaca gccacccaaa ctcctcatct ctgctgctag caacgtagaa 600
tctggggtcc ctgccaggtt tagtggcagt gggtctggga cagactttag cctcaacatc 660
catcctgtgg aggaggatga tattgcaatg tatttctgtc agcaaagtag gaaggttcca 720
tggacgttcg gtggaggcac caagctggaa atcaagtcct cgagcgcctc caccaagggc 780
ccatcggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 840
ggctgcctgg tcaaggacta cttccccgag ccggtgacgg tgtcgtggaa ctcaggcgcc 900
ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 960
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 1020
aatcacaagc ccagcaacac caaggtggac aagaaagttc gtacggagcc caaatcttct 1080
gacaaaactc acacatgccc accgtgccca tccggagcac ctgaactcct gggtggaccg 1140
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 1200
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 1260
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 1320
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1380
tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1440
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1500
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatccaag cgacatcgcc 1560
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1620
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1680
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1740
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<210> 6
<211> 589
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of 2E12CH1CH2CH3 (X0112)

<400> 6

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Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr
            20                  25                  30
Gly Val Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Met Ile Trp Gly Asp Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys
    50                  55                  60
Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala
                85                  90                  95
Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr Val Met Asp Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
    130                 135                 140
Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala
145                 150                 155                 160
Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser
                165                 170                 175
Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
            180                 185                 190
Ile Ser Ala Ala Ser Asn Val Glu Ser Gly Val Pro Ala Arg Phe Ser
        195                 200                 205
Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His Pro Val Glu
    210                 215                 220
Glu Asp Asp Ile Ala Met Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro
225                 230                 235                 240
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Ser Ser Ala
                245                 250                 255
Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
            260                 265                 270
Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
```

```
        275                 280                 285
Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
    290                 295                 300
Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
305                 310                 315                 320
Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
                325                 330                 335
Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
            340                 345                 350
Val Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
        355                 360                 365
Cys Pro Ser Gly Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
    370                 375                 380
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
385                 390                 395                 400
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
                405                 410                 415
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
            420                 425                 430
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
        435                 440                 445
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
    450                 455                 460
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
465                 470                 475                 480
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
                485                 490                 495
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
            500                 505                 510
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
        515                 520                 525
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
    530                 535                 540
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
545                 550                 555                 560
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
                565                 570                 575
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            580                 585
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<210> 7
<211> 1026
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of CkCH2CH3 (X0113)

<400> 7

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aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 180
aaggacagca cctacagcct cagcagcacc ctgacgctga gcaaagcaga ctacgagaaa 240
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 300
ttcaacaggg gagagcgtac ggagcccaaa tcttctgaca aaactcacac atgcccaccg 360
tgcccatccg gagcacctga actcctgggt ggaccgtcag tcttcctctt ccccccaaaa 420
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 480
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 540
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 600
accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 660
gccctcccag ccccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 720
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 780
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 840
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 900
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 960
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1020
aaatga                                                          1026
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<210> 8
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of CkCH2CH3 (X0113)

<400> 8
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu Arg Thr Glu Pro Lys Ser Ser
            100   105   110
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ser Gly Ala Pro Glu Leu
        115   120   125
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
    130   135   140
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
145   150   155   160
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
                165   170   175
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
            180   185   190
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
        195   200   205
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
    210   215   220
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
225   230   235   240
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
                245   250   255
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
            260   265   270
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
        275   280   285
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
    290   295   300
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
305   310   315   320
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
                325   330   335
Leu Ser Pro Gly Lys
            340

<210> 9
<211> 1839
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of Ck(YAE) Fc (N297A) 2E12
      (X0244)

<400> 9
actgtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 60
actgcctctg ttgtgtgcct gctgaattac ttctatccca gagaggccaa agtacagtgg 120

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aaggtggata acgccctcca atcgggtaac tcccaggaga gtgccacaga gcaggacagc 180
aaggacagca cctacagcct cagcagcgag ctgacgctga gcaaagcaga ctacgagaaa 240
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 300
ttcaacaggg gagagcgtac ggagcccaaa tcttctgaca aaactcacac atgcccaccg 360
tgcccatccg gagcacctga actcctgggt ggaccgtcag tcttcctctt cccccaaaa 420
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 480
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 540
gccaagacaa agccgcggga ggagcagtac gccagcacgt accgtgtggt cagcgtcctc 600
accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 660
gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 720
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 780
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 840
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 900
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 960
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1020
aactcattat tcaaccaaga agttcaaatt cccttgaccg aaagttacag cccgaattct 1080
caggtgcagc tgaaggagtc aggacctggc agcgtggcgc cctcacagag cctgtccatc 1140
acatgcaccg tctcagggtt ctcattaacc ggctatggtg taaactgggt tcgccagcct 1200
ccaggaaagg gtctggagtg gctgggaatg atatggggtg atggaagcac agactataat 1260
tcagctctca aatccagact atcgatcacc aaggacaact ccaagagcca agttttctta 1320
aaaatgaaca gtctgcaaac tgatgacaca gccagatact actgtgctcg ggatggttat 1380
agtaactttc attactatgt tatggactac tggggtcaag gaacctcagt caccgtctcc 1440
tctgggggtg gaggctctgg tggcggtgga tccggcggag gtgggtcggg tggcggcgga 1500
tctgacattg tgctcaccca atctccagct tctttggctg tgtctctagg tcagagagcc 1560
accatctcct gcagagccag tgaaagtgtt gaatattatg tcacaagttt aatgcagtgg 1620
taccaacaga aaccaggaca gccacccaaa ctcctcatct ctgctgctag caacgtagaa 1680
tctggggtcc ctgccaggtt tagtggcagt gggtctggga cagactttag cctcaacatc 1740
catcctgtgg aggaggatga tattgcaatg tatttctgtc agcaaagtag gaaggttcca 1800
tggacgttcg gtggaggcac caagctggaa atcaagtga                          1839
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<210> 10
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of Ck(YAE) Fc (N297A) 2E12 (X0244)

<400> 10

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Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1               5                  10                  15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr
            20                  25                  30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35                  40                  45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50                  55                  60
Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65                  70                  75                  80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85                  90                  95
Val Thr Lys Ser Phe Asn Arg Gly Glu Arg Thr Glu Pro Lys Ser Ser
            100                 105                 110
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ser Gly Ala Pro Glu Leu
        115                 120                 125
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
    130                 135                 140
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
145                 150                 155                 160
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
                165                 170                 175
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser
            180                 185                 190
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
        195                 200                 205
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
    210                 215                 220
```

```
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
225                 230                 235                 240
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
                245                 250                 255
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
            260                 265                 270
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
        275                 280                 285
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
    290                 295                 300
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
305                 310                 315                 320
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
                325                 330                 335
Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu
            340                 345                 350
Thr Glu Ser Tyr Ser Pro Asn Ser Gln Val Gln Leu Lys Glu Ser Gly
        355                 360                 365
Pro Gly Ser Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val
    370                 375                 380
Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp Val Arg Gln Pro
385                 390                 395                 400
Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile Trp Gly Asp Gly Ser
                405                 410                 415
Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser Ile Thr Lys Asp
            420                 425                 430
Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp
        435                 440                 445
Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Asp Gly Tyr Ser Asn Phe His
    450                 455                 460
Tyr Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
465                 470                 475                 480
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                485                 490                 495
Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu
            500                 505                 510
Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu
        515                 520                 525
Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys
    530                 535                 540
Pro Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala Ala Ser Asn Val Glu
545                 550                 555                 560
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                565                 570                 575
Ser Leu Asn Ile His Pro Val Glu Glu Asp Asp Ile Ala Met Tyr Phe
            580                 585                 590
Cys Gln Gln Ser Arg Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys
        595                 600                 605
Leu Glu Ile Lys
    610
```

<210> 11
<211> 1770
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of 2E12 CH1 Fc (N297A)
(X0245)

<400> 11

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acatgcaccg tctcagggtt ctcattaacc ggctatggtg taaactgggt tcgccagcct 120
ccaggaaagg gtctggagtg gctgggaatg atatggggtg atggaagcac agactataat 180
tcagctctca aatccagact atcgatcacc aaggacaact ccaagagcca agttttctta 240
aaaatgaaca gtctgcaaac tgatgacaca gccagatact actgtgctcg ggatggttat 300
agtaactttc attactatgt tatggactac tggggtcaag gaacctcagt caccgtctcc 360
```

tctgggggtg gaggctctgg tggcggtgga tccggcggag gtgggtcggg tggcggcgga 420
tctgacattg tgctcaccca atctccagct tctttggctg tgtctctagg tcagagagcc 480
accatctcct gcagagccag tgaaagtgtt gaatattatg tcacaagttt aatgcagtgg 540
taccaacaga aaccaggaca gccacccaaa ctcctcatct ctgctgctag caacgtagaa 600
tctggggtcc ctgccaggtt tagtggcagt gggtctggga cagactttag cctcaacatc 660
catcctgtgg aggaggatga tattgcaatg tatttctgtc agcaaagtag gaaggttcca 720
tggacgttcg gtggaggcac caagctggaa atcaagtcct cgagcgcctc caccaagggc 780
ccatcggtct tcccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 840
ggctgcctgg tcaaggacta cttccccgag ccggtgacgg tgtcgtggaa ctcaggcgcc 900
ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 960
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 1020
aatcacaagc ccagcaacac caaggtggac aagaaagttc gtacggagcc caaatcttct 1080
gacaaaactc acacatgccc accgtgccca tccggagcac ctgaactcct gggtggaccg 1140
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 1200
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 1260
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacgccagc 1320
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1380
tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1440
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1500
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatccaag cgacatcgcc 1560
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1620
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1680
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1740
aagagcctct ccctgtctcc gggtaaatga 1770

<210> 12
<211> 589
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of 2E12 CH1 Fc (N297A)
(X0245)

<400> 12
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Ser Val Ala Pro Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr
20 25 30
Gly Val Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Met Ile Trp Gly Asp Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys
50 55 60
Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala
85 90 95
Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr Val Met Asp Tyr Trp Gly
100 105 110
Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
130 135 140
Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala
145 150 155 160
Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser
165 170 175
Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
180 185 190
Ile Ser Ala Ala Ser Asn Val Glu Ser Gly Val Pro Ala Arg Phe Ser
195 200 205
Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His Pro Val Glu
210 215 220
Glu Asp Asp Ile Ala Met Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro
225 230 235 240
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Ser Ser Ala
245 250 255
Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser

```
            260                 265                 270
Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
        275                 280                 285
Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
    290                 295                 300
Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
305                 310                 315                 320
Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
                325                 330                 335
Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
            340                 345                 350
Val Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
        355                 360                 365
Cys Pro Ser Gly Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
    370                 375                 380
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
385                 390                 395                 400
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
                405                 410                 415
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
            420                 425                 430
Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu
        435                 440                 445
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
    450                 455                 460
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
465                 470                 475                 480
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
                485                 490                 495
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
            500                 505                 510
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
        515                 520                 525
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
    530                 535                 540
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
545                 550                 555                 560
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
                565                 570                 575
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            580                 585
```

<210> 13
<211> 1749
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of P2C2 Ck(YAE) Fc (N297A)
(X0246)

<400> 13

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gatattgtga tgatccagga tgaactctcc aatcctgtca gttctggaga atcagtttcc 60
atctcctgta ggtctagtaa gagtctccta gataaggaag ggaagacata cttgaattgg 120
tttctgcaga gaccaggaca atctcctcag ctcctgatct atctgatgtc catgcgtgaa 180
tcaggagtct cagaccggtt tagtggcagt gggtcaggaa cagatttcac cctggaaatc 240
agtagagtga aggctgagga tgtgggtgtg tattactgtc aacaacttgt agagtatccg 300
tggacgttcg gtggaggcac caagctggaa atcaaaggtg gcggtggctc tggcggaggt 360
ggatccggtg gcggcggctc tcagatccag ttggtgcagt ctggacctga gctgaagaag 420
cctggagaga cagtcaagat ctcctgcaag gcttctggtt ataccttcac agacttttca 480
atgcactggg tgaggcaggc tccaggaaag ggtttaaagt ggatgggctg gataaacact 540
gagactggtg agccaacata tgcagatgac ttcaggggac ggtttgcctt ctctttggaa 600
acttctgcca gcactgccta tttgcagatc aacaacctca aaaatgagga cacggctaca 660
tatttttgta cctggtctgc ttactggggc caagggactc tggtcactgt ctctgcctcg 720
agcactgtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 780
ggaactgcct ctgttgtgtg cctgctgaat tacttctatc ccagagaggc caaagtacag 840
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgccac agagcaggac 900
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agcaaggaca gcacctacag cctcagcagc gagctgacgc tgagcaaagc agactacgag 960
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 1020
agcttcaaca ggggagagcg tacggagccc aaatcttctg acaaaactca cacatgccca 1080
ccgtgcccat ccggagcacc tgaactcctg ggtggaccgt cagtcttcct cttcccccca 1140
aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 1200
gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1260
aatgccaaga caaagccgcg ggaggagcag tacgccagca cgtaccgtgt ggtcagcgtc 1320
ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 1380
aaagccctcc cagccccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1440
ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1500
acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1560
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1620
ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1680
tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1740
ggtaaatga                                                        1749
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<210> 14
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of P2C2 Ck(YAE) Fc (N297A)
(X0246)

<400> 14

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Asp Ile Val Met Ile Gln Asp Glu Leu Ser Asn Pro Val Ser Ser Gly
 1               5                  10                  15
Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asp Lys
            20                  25                  30
Glu Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser
        35                  40                  45
Pro Gln Leu Leu Ile Tyr Leu Met Ser Met Arg Glu Ser Gly Val Ser
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile
65                  70                  75                  80
Ser Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
                85                  90                  95
Val Glu Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
        115                 120                 125
Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Phe Ser
145                 150                 155                 160
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly
                165                 170                 175
Trp Ile Asn Thr Glu Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Arg
            180                 185                 190
Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu
        195                 200                 205
Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Thr
    210                 215                 220
Trp Ser Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser
225                 230                 235                 240
Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
                245                 250                 255
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe
            260                 265                 270
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        275                 280                 285
Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser
    290                 295                 300
Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu
305                 310                 315                 320
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                325                 330                 335
```

```
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Arg Thr Glu Pro Lys Ser
            340                 345                 350
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ser Gly Ala Pro Glu
        355                 360                 365
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    370                 375                 380
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
385                 390                 395                 400
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                405                 410                 415
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala
            420                 425                 430
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        435                 440                 445
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
    450                 455                 460
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
465                 470                 475                 480
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
                485                 490                 495
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            500                 505                 510
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        515                 520                 525
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
    530                 535                 540
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
545                 550                 555                 560
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                565                 570                 575
Ser Leu Ser Pro Gly Lys
            580
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<210> 15
<211> 2583
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of 2E12 CH1 Fc (N297A) H68
2E12 (X0247)

<400> 15

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gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacgccagc 1320
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tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1440
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<210> 16
<211> 860
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of 2E12 CH1 Fc (N297A) H68
2E12 (X0247)

<400> 16

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Gly Val Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
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Gly Met Ile Trp Gly Asp Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys
    50                  55                  60
Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala
                85                  90                  95
Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr Val Met Asp Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
    130                 135                 140
Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala
145                 150                 155                 160
Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser
                165                 170                 175
Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
            180                 185                 190
Ile Ser Ala Ala Ser Asn Val Glu Ser Gly Val Pro Ala Arg Phe Ser
        195                 200                 205
Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His Pro Val Glu
    210                 215                 220
Glu Asp Asp Ile Ala Met Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro
225                 230                 235                 240
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Ser Ser Ala
                245                 250                 255
Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
            260                 265                 270
Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
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Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
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Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
305                 310                 315                 320
Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
                325                 330                 335
Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
            340                 345                 350
Val Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
        355                 360                 365
Cys Pro Ser Gly Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
    370                 375                 380
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
385                 390                 395                 400
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
                405                 410                 415
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
            420                 425                 430
Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu
        435                 440                 445
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
    450                 455                 460
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
465                 470                 475                 480
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Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
            500                 505                 510
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
        515                 520                 525
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
    530                 535                 540
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
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Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
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His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe
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Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser
        595                 600                 605
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Ser Val Ala Pro Ser Gln
    610                 615                 620
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr
625                 630                 635                 640
Gly Val Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
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Gly Met Ile Trp Gly Asp Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys
            660                 665                 670
Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
        675                 680                 685
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala
    690                 695                 700
Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr Val Met Asp Tyr Trp Gly
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Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
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Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
            740                 745                 750
Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala
        755                 760                 765
Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser
    770                 775                 780
Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
785                 790                 795                 800
Ile Ser Ala Ala Ser Asn Val Glu Ser Gly Val Pro Ala Arg Phe Ser
                805                 810                 815
Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His Pro Val Glu
            820                 825                 830
Glu Asp Asp Ile Ala Met Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro
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Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
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<210> 17
<211> 2547
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of P2C2 CK(YAE) Fc (N297A) H68 A2 (X0248)

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tcaggagtct cagaccggtt tagtggcagt gggtcaggaa cagatttcac cctggaaatc 240
agtagagtga aggctgagga tgtgggtgtg tattactgtc aacaacttgt agagtatccg 300
tggacgttcg gtggaggcac caagctggaa atcaaaggtg gcggtggctc tggcggaggt 360
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<210> 18
<211> 848
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of P2C2 CK(YAE) Fc (N297A) H68 A2 (X0248)

<400> 18

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        35                  40                  45
Pro Gln Leu Leu Ile Tyr Leu Met Ser Met Arg Glu Ser Gly Val Ser
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile
65                  70                  75                  80
Ser Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
                85                  90                  95
Val Glu Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
        115                 120                 125
Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Phe Ser
145                 150                 155                 160
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly
                165                 170                 175
Trp Ile Asn Thr Glu Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Arg
            180                 185                 190
Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu
        195                 200                 205
Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Thr
    210                 215                 220
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225                 230                 235                 240
Ser Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
                245                 250                 255
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe
            260                 265                 270
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        275                 280                 285
Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser
    290                 295                 300
Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu
305                 310                 315                 320
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                325                 330                 335
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Arg Thr Glu Pro Lys Ser
            340                 345                 350
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ser Gly Ala Pro Glu
        355                 360                 365
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    370                 375                 380
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
385                 390                 395                 400
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                405                 410                 415
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala
            420                 425                 430
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        435                 440                 445
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
    450                 455                 460
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
465                 470                 475                 480
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
                485                 490                 495
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            500                 505                 510
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        515                 520                 525
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
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Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                565                 570                 575
Ser Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro
            580                 585                 590
Leu Thr Glu Ser Tyr Ser Pro Asn Ser Glu Val Gln Leu Leu Glu Ser
        595                 600                 605
Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
    610                 615                 620
Ala Ser Gly Phe Thr Phe Ser Phe Tyr Gln Met His Trp Val Arg Gln
625                 630                 635                 640
Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Tyr Pro Ser Gly
                645                 650                 655
Gly Tyr Thr Lys Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
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Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
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Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Leu Gly Tyr Gly
    690                 695                 700
Ser Ser Trp Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
705                 710                 715                 720
Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
                725                 730                 735
Gly Ser Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro
            740                 745                 750
Gly Gln Ser Ile Thr Ile Ser Cys Ser Gly Thr Asp Ser Asp Val Gly
        755                 760                 765
Gly Tyr Asn His Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro
    770                 775                 780
Lys Leu Ile Ile Tyr Asp Val Asp His Arg Pro Ser Gly Ile Ser Asn
785                 790                 795                 800
Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser
                805                 810                 815
Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Arg
            820                 825                 830
Ser Gly Ser Thr Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
        835                 840                 845
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<210> 19
<211> 2427
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of PDL2-CH1 Fc(N297A) H68 2E12
(X0249)

<400> 19

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<210> 20
<211> 808
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of PDL2-CH1 Fc(N297A) H68 2E12 (X0249)

<400> 20

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Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly
 1               5                  10                  15
Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn
            20                  25                  30
Leu Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser
        35                  40                  45
Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly
    50                  55                  60
Lys Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65                  70                  75                  80
Tyr Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
                85                  90                  95
Thr Leu Lys Val Lys Ala Ser Tyr Arg Lys Ile Asn Thr His Ile Leu
            100                 105                 110
Lys Val Pro Glu Thr Asp Glu Val Glu Leu Thr Cys Gln Ala Thr Gly
        115                 120                 125
Tyr Pro Leu Ala Glu Val Ser Trp Pro Asn Val Ser Val Pro Ala Asn
    130                 135                 140
Thr Ser His Ser Arg Thr Pro Glu Gly Leu Tyr Gln Val Thr Ser Val
145                 150                 155                 160
Leu Arg Leu Lys Pro Pro Pro Gly Arg Asn Phe Ser Cys Val Phe Trp
                165                 170                 175
Asn Thr His Val Arg Glu Leu Thr Leu Ala Ser Ile Asp Leu Gln Ser
            180                 185                 190
Gln Met Glu Pro Arg Thr His Pro Thr Ser Ser Ala Ser Thr Lys Gly
        195                 200                 205
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    210                 215                 220
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
225                 230                 235                 240
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                245                 250                 255
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
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            260                 265                 270
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        275                 280                 285
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Arg Thr Glu
    290                 295                 300
Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ser Gly
305                 310                 315                 320
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                325                 330                 335
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            340                 345                 350
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        355                 360                 365
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    370                 375                 380
Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
385                 390                 395                 400
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                405                 410                 415
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            420                 425                 430
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        435                 440                 445
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    450                 455                 460
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
465                 470                 475                 480
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                485                 490                 495
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            500                 505                 510
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        515                 520                 525
Lys Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe Asn Gln Glu Val
    530                 535                 540
Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser Gln Val Gln Leu
545                 550                 555                 560
Lys Glu Ser Gly Pro Gly Ser Val Ala Pro Ser Gln Ser Leu Ser Ile
                565                 570                 575
Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp
            580                 585                 590
Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile Trp
        595                 600                 605
Gly Asp Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser
    610                 615                 620
Ile Thr Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser
625                 630                 635                 640
Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Asp Gly Tyr
                645                 650                 655
Ser Asn Phe His Tyr Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Ser
            660                 665                 670
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        675                 680                 685
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser
    690                 695                 700
Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
705                 710                 715                 720
Arg Ala Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp
                725                 730                 735
Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala Ala
            740                 745                 750
Ser Asn Val Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
        755                 760                 765
Gly Thr Asp Phe Ser Leu Asn Ile His Pro Val Glu Glu Asp Asp Ile
    770                 775                 780
Ala Met Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro Trp Thr Phe Gly
785                 790                 795                 800
Gly Gly Thr Lys Leu Glu Ile Lys
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<210> 21
<211> 2331
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of monoIL10 Ck(YAE) Fc(N297A)
H68 3D1 (X0281)

<400> 21
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aacatgcttc gagatctccg agatgccttc agcagagtga agactttctt tcaaatgaag 120
gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacat caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacgg tggtggatcc 360
ggcggtaaga gcaaggccgt ggagcaggtg aagaatgcct ttaataagct ccaagagaaa 420
ggcatctaca aagccatgag tgagtttgac atcttcatca actacataga agcctacatt 480
acaatgaaga tacgaaactc gagcactgtg gctgcaccat ctgtcttcat cttcccgcca 540
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa ttacttctat 600
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 660
gagagtgcca cagagcagga cagcaaggac agcacctaca gcctcagcag cgagctgacg 720
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 780
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagc gtacggagcc caaatcttct 840
gacaaaactc acacatgccc accgtgccca tccggagcac ctgaactcct gggtggaccg 900
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 960
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 1020
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacgccagc 1080
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1140
tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1200
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1260
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatccaag cgacatcgcc 1320
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1380
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1440
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1500
aagagcctct ccctgtctcc gggtaactca ttattcaacc aagaagttca aattcccttg 1560
accgaaagtt acagcccgaa ttctcaggtc cagctgcagc agtctgggcc tgagctggtg 1620
aggcctgggg aatcagtgaa gatttcctgc aagggttccg gctacacatt cactgattat 1680
gctatacagt gggtgaagca gagtcatgca aagagtctag agtggattgg agttattaat 1740
atttactatg ataatacaaa ctacaaccag aagtttaagg gcaaggccac aatgactgta 1800
gacaaatcct ccagcacagc ctatatggaa cttgccagat tgacatctga ggattctgcc 1860
atctattact gtgcaagagc ggcctggtat atggactact ggggtcaagg aacctcagtc 1920
accgtctcct caggggtgg aggctctggt ggcggtggct ctggcggagg tggatccggt 1980
ggcggcggat ctgacattgt gctgtcacag tctccatcct ccctggctgt gtcagcagga 2040
gagaaggtca ctatgagctg caaatccagt cagagtctgc tcaacagtag aacccgagag 2100
aactacttgg cttggtacca gcagaaacca gggcagtctc ctaaactgct gatctactgg 2160
gcatccacta gggaatctgg ggtccctgat cgcttcacag gcagtggatc tgggacagat 2220
ttcactctca ccatcagcag tgtgcaggct gaagacctgg cagtttatta ctgcacgcaa 2280
tcttataatc tttacacgtt cggaggggg accaagctgg aaataaaata a 2331

<210> 22
<211> 776
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of monoIL10 Ck(YAE) Fc(N297A)
H68 3D1 (X0281)

<400> 22
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Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu

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        35                  40                  45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
    50                  55                  60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65                  70                  75                  80
Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
                85                  90                  95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
            100                 105                 110
Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu
        115                 120                 125
Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys
    130                 135                 140
Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Ile
145                 150                 155                 160
Thr Met Lys Ile Arg Asn Ser Ser Thr Val Ala Ala Pro Ser Val Phe
                165                 170                 175
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
            180                 185                 190
Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
        195                 200                 205
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Ala Thr
    210                 215                 220
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Glu Leu Thr
225                 230                 235                 240
Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
                245                 250                 255
Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
            260                 265                 270
Glu Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
        275                 280                 285
Cys Pro Ser Gly Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
    290                 295                 300
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
305                 310                 315                 320
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
                325                 330                 335
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
            340                 345                 350
Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu
        355                 360                 365
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
    370                 375                 380
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
385                 390                 395                 400
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
                405                 410                 415
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
            420                 425                 430
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
        435                 440                 445
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
    450                 455                 460
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
465                 470                 475                 480
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
                485                 490                 495
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe
            500                 505                 510
Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser
        515                 520                 525
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Glu
    530                 535                 540
Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
545                 550                 555                 560
Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile
                565                 570                 575
Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe
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            580                 585                 590
Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
        595                 600                 605
Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
    610                 615                 620
Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
625                 630                 635                 640
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                645                 650                 655
Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Ser Gln Ser Pro
            660                 665                 670
Ser Ser Leu Ala Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys
        675                 680                 685
Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala
    690                 695                 700
Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp
705                 710                 715                 720
Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly
                725                 730                 735
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp
            740                 745                 750
Leu Ala Val Tyr Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly
        755                 760                 765
Gly Gly Thr Lys Leu Glu Ile Lys
    770                 775
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<210> 23
<211> 2330
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of monoIl10CkwtFc(N297A)H68
3D1 (X0282)

<400> 23

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gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacat caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacgg tggtggatcc 360
ggcggtaaga gcaaggccgt ggagcaggtg aagaatgcct ttaataagct ccaagagaaa 420
ggcatctaca aagccatgag tgagtttgac atcttcatca actacataga agcctacatt 480
acaatgaaga tacgaaactc gagcactgtg gctgcaccat ctgtcttcat cttcccgcca 540
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 600
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 660
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 720
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 780
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagc gtacggagcc caaatcttct 840
gacaaaactc acacatgccc accgtgccca tccggagcac ctgaactcct gggtggaccg 900
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 960
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 1020
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacgccagc 1080
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1140
tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1200
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1260
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aagagcctct ccctgtctcc gggtaactca ttattcaacc aagaagttca aattcccttg 1560
accgaaagtt acagcccgaa ttctcaggtc cagctgcagc agtctgggcc tgagctggtg 1620
aggcctgggg aatcagtgaa gatttcctgc aagggttccg gctacacatt cactgattat 1680
gctatacagt gggtgaagca gagtcatgca aagagtctag agtggattgg agttattaat 1740
atttactatg ataatacaaa ctacaaccag aagtttaagg gcaaggccac aatgactgta 1800
gacaaatcct ccagcacagc ctatatggaa cttgccagat tgacatctga ggattctgcc 1860
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atctattact gtgcaagagc ggcctggtat atggactact ggggtcaagg aacctcagtc 1920
accgtctcct caggggtgg aggctctggt ggcggtggct ctggcggagg tggatccggt 1980
ggcggcggat ctgacattgt gctgtcacag tctccatcct ccctggctgt gtcagcagga 2040
gagaaggtca ctatgagctg caaatccagt cagagtctgc tcaacagtag aacccgagag 2100
aactacttgg cttggtacca gcagaaacca gggcagtctc ctaaactgct gatctactgg 2160
gcatccacta gggaatctgg ggtccctgat cgcttcacag gcagtggatc tgggacagat 2220
ttcactctca ccatcagcag tgtgcaggct gaagacctgg cagtttatta ctgcacgcaa 2280
tcttataatc tttacacgtt cggaggggg accaagctgg aaataaaata 2330

<210> 24
<211> 776
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of monoIl10CkwtFc(N297A)H68
3D1 (X0282)

<400> 24

Ser	Pro	Gly	Gln	Gly	Thr	Gln	Ser	Glu	Asn	Ser	Cys	Thr	His	Phe	Pro
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Gly	Asn	Leu	Pro	Asn	Met	Leu	Arg	Asp	Leu	Arg	Asp	Ala	Phe	Ser	Arg
			20					25					30		
Val	Lys	Thr	Phe	Phe	Gln	Met	Lys	Asp	Gln	Leu	Asp	Asn	Leu	Leu	Leu
		35					40					45			
Lys	Glu	Ser	Leu	Leu	Glu	Asp	Phe	Lys	Gly	Tyr	Leu	Gly	Cys	Gln	Ala
	50					55					60				
Leu	Ser	Glu	Met	Ile	Gln	Phe	Tyr	Leu	Glu	Glu	Val	Met	Pro	Gln	Ala
65					70					75					80
Glu	Asn	Gln	Asp	Pro	Asp	Ile	Lys	Ala	His	Val	Asn	Ser	Leu	Gly	Glu
				85					90					95	
Asn	Leu	Lys	Thr	Leu	Arg	Leu	Arg	Leu	Arg	Arg	Cys	His	Arg	Phe	Leu
			100					105					110		
Pro	Cys	Glu	Asn	Gly	Gly	Gly	Ser	Gly	Gly	Lys	Ser	Lys	Ala	Val	Glu
		115					120					125			
Gln	Val	Lys	Asn	Ala	Phe	Asn	Lys	Leu	Gln	Glu	Lys	Gly	Ile	Tyr	Lys
	130					135					140				
Ala	Met	Ser	Glu	Phe	Asp	Ile	Phe	Ile	Asn	Tyr	Ile	Glu	Ala	Tyr	Ile
145					150					155					160
Thr	Met	Lys	Ile	Arg	Asn	Ser	Ser	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe
				165					170					175	
Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val
			180					185					190		
Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp
		195					200					205			
Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr
	210					215					220				
Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr
225					230					235					240
Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val
				245					250					255	
Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly
			260					265					270		
Glu	Arg	Thr	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro
		275					280					285			
Cys	Pro	Ser	Gly	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu
	290					295					300				
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu
305					310					315					320
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys
				325					330					335	
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys
			340					345					350		
Pro	Arg	Glu	Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu
		355					360					365			
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys
	370					375					380				
Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys

385 390 395 400
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
405 410 415
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
420 425 430
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
435 440 445
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
450 455 460
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
465 470 475 480
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
485 490 495
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Asn Ser Leu Phe
500 505 510
Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser
515 520 525
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Glu
530 535 540
Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
545 550 555 560
Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile
565 570 575
Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe
580 585 590
Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
595 600 605
Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
610 615 620
Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
625 630 635 640
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
645 650 655
Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Ser Gln Ser Pro
660 665 670
Ser Ser Leu Ala Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys
675 680 685
Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala
690 695 700
Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp
705 710 715 720
Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly
725 730 735
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp
740 745 750
Leu Ala Val Tyr Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly
755 760 765
Gly Gly Thr Lys Leu Glu Ile Lys
770 775

<210> 25
<211> 1806
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for ORN116 comprising MET021 (anti-c-Met) scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3 and human CH1

<400> 25
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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 240
aggttcagtg gcagtggatc tgggacagac ttcattctca ccatcagcag tctgcagcct 300
gaagattttg caacttacta ctgtcaacag agttacgtta ccccgctcac tttcggcgga 360

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cctggtggtt ctttacgtct ttcttgcgct gcttccggat tcactttctc taagtacgat 540
atgctttggg ttcgccaagc tcctggtaaa ggtttggagt gggtttctta tatctatcct 600
tctggtggcc ttactgagta tgctgactcc gttaaaggtc gcttcactat ctctagagac 660
aactctaaga atactctcta cttgcagatg aacagcttaa gggctgagga cacggccgtg 720
tattactgtg cgagacgggc tccccggtcc ctttcttttg atatctgggg ccaagggaca 780
atggtcaccg tctcctcgag cgagcccaaa tcttctgaca aaactcacac atgcccaccg 840
tgcccatccg gagcacctga actcctgggt ggaccgtcag tcttcctctt cccccaaaa 900
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 960
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 1020
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 1080
accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 1140
gccctcccag ccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1200
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1260
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tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1440
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1500
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acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 1680
cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 1740
acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 1800
gtttga 1806

<210> 26
<211> 1797
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for ORN145 comprising : 4C04 (anti-RON) scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3 and human CH1

<400> 26
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atcacatgcc tggcaagtca gaccattggt acatggttag catggtatca gcagaaacca 180
gggaaatctc ctcagctcct gatttatgct gcaaccagct tggcagatgg ggtcccatca 240
aggttcagtg ctagtggatc tggcacaaaa ttttctttca agatcgacag cctacagtct 300
gaagattttg taagttatta ctgtcaacaa ctttacaata ctccgtggac gttcggtgga 360
ggcaccaagc tggaaatcaa aggtggcggt ggctctggcg gaggtggatc cggtggcggc 420
ggctctcaga tccagctgca gcagtctgga cctgagctgg tgaagcctgg gacttcagtg 480
aagatatcct gcaaggcttc tgactacaca ctcactgact tctatatgaa ctgggtgagg 540
cagaagcctg gacagggact tgagtggatt gggaggattt atcctggaac cgataaaact 600
agatacaatg agaaattcag ggacaaggcc atactgaccg tggacacgtc ctccagcaca 660
gcctacatgc agctcagcag cctgacatca gaggacactg ctgtctattt ctgtgcaaga 720
tccgcctact atggtaacta cgttgctatg gactactggg gtcaaggaac ctcagtcacc 780
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accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 960
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1020
aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 1080
caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1140
gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1200
accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc 1260
aaaggcttct atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1320
aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1380
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1440
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaatctaga 1500
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 1560
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgagccggt gacggtgtcg 1620
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 1680
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 1740
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agtttga 1797

<210> 27
<211> 1818
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for ORN146 comprising : 4C04 (anti-RON) scFv, human IgG1 SCC-P hinge, human CH2, human CH3, and human Ck(YAE)

<400> 27
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gacattcaga tgacccagtc tcctgcctcc cagtctgcat ctctgggaga aagtgtcacc 120
atcacatgcc tggcaagtca gaccattggt acatggttag catggtatca gcagaaacca 180
gggaaatctc ctcagctcct gatttatgct gcaaccagct tggcagatgg ggtcccatca 240
aggttcagtg ctagtggatc tggcacaaaa ttttctttca agatcgacag cctacagtct 300
gaagattttg taagttatta ctgtcaacaa ctttacaata ctccgtggac gttcggtgga 360
ggcaccaagc tggaaatcaa aggtggcggt ggctctggcg gaggtggatc cggtggcggc 420
ggctctcaga tccagctgca gcagtctgga cctgagctgg tgaagcctgg gacttcagtg 480
aagatatcct gcaaggcttc tgactacaca ctcactgact tctatatgaa ctgggtgagg 540
cagaagcctg gacagggact tgagtggatt gggaggattt atcctggaac cgataaaact 600
agatacaatg agaaattcag ggacaaggcc atactgaccg tggacacgtc ctccagcaca 660
gcctacatgc agctcagcag cctgacatca gaggacactg ctgtctattt ctgtgcaaga 720
tccgcctact atggtaacta cgttgctatg gactactggg gtcaaggaac ctcagtcacc 780
gtctcctcga gcgagcccaa atcttctgac aaaactcaca catgcccacc gtgcccatcc 840
ggagcacctg aactcctggg tggaccgtca gtcttcctct tccccccaaa acccaaggac 900
accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 960
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1020
aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 1080
caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1140
gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1200
accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc 1260
aaaggcttct atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1320
aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1380
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1440
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaatctaga 1500
actgtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 1560
actgcctctg ttgtgtgcct gctgaattac ttctatccca gagaggccaa agtacagtgg 1620
aaggtggata acgccctcca atcgggtaac tcccaggaga gtgccacaga gcaggacagc 1680
aaggacagca cctacagcct cagcagcgag ctgacgctga gcaaagcaga ctacgagaaa 1740
cacaaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt cacaaagagc 1800
ttcaacaggg gagagtga 1818

<210> 28
<211> 1806
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for ORN148 comprising : 11H09 (anti-RON) scFv, human IgG1 SCC-P hinge, human CH2, human CH3, and human Ck(YAE)

<400> 28
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gacatccaga tgacccagtc tccatcctcc ttatctgcct ctctgggaga aagagtcagt 120
ctcacttgtc gggcaagtca ggacattggt agtagcttaa gctggcttca gcaggaacca 180
gatggtacta ttaaacgcct gatctactcc acatccagtt tagattctgg tgtccccaaa 240
aggttcagtg gcagtaggtc ggggtcagat tattctctca ccatcagcag ccttgagtct 300
gaagattttg tagactatta ctgtctacaa tatgctagtt ctccgtggac gttcggtgga 360
ggcaccaagc tggaaatcaa aggtggcggt ggctctggcg gaggtggatc cggtggcggc 420
ggctctcagg tccagcttca gcagtctggg gctgaactgg caaaacctgg ggcctcagtg 480
aagatgtcct gcaagtcttc tggctacacc tttactagct actggataca ctgggtaaaa 540
gagaggcctg gacagggtct ggaatggatt ggatacattt atcctaccac tggttatact 600
gagtccaatc agaagttcaa ggacaaggcc acattgactg cagacaaatc ctccagcaca 660
gcctacatgc aactgagcag cctgacatct gaggactctg cagtctatta ctgtttccta 720
ctacggccct ggtacttcga tgtctggggc gcagggacca cggtcaccgt ctcctcgagc 780
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccatccgg agcacctgaa 840

ctcctgggtg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 900
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 960
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1020
gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1080
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 1140
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1200
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1260
ccaagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1320
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1380
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1440
aaccactaca cgcagaagag cctctccctg tctccgggta aatctagaac tgtggctgca 1500
ccatctgtct tcatcttccc gccatctgat gagcagttga aatctggaac tgcctctgtt 1560
gtgtgcctgc tgaattactt ctatcccaga gaggccaaag tacagtggaa ggtggataac 1620
gccctccaat cgggtaactc ccaggagagt gccacagagc aggacagcaa ggacagcacc 1680
tacagcctca gcagcgagct gacgctgagc aaagcagact acgagaaaca caaagtctac 1740
gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt caacagggga 1800
gagtga 1806

<210> 29
<211> 581
<212> PRT
<213> Artificial Sequence

<220>
<223> ORN116 mature protein comprising MET021
(anti-c-Met) scFv, human IgG1 SCC-P hinge, human
IgG1 CH2, human IgG1 CH3 and human CH1

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Asn Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Glu Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Val Thr Pro Leu
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
115 120 125
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
130 135 140
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr Asp
145 150 155 160
Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
165 170 175
Tyr Ile Tyr Pro Ser Gly Gly Leu Thr Glu Tyr Ala Asp Ser Val Lys
180 185 190
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
195 200 205
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
210 215 220
Arg Arg Ala Pro Arg Ser Leu Ser Phe Asp Ile Trp Gly Gln Gly Thr
225 230 235 240
Met Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His
245 250 255
Thr Cys Pro Pro Cys Pro Ser Gly Ala Pro Glu Leu Leu Gly Gly Pro
260 265 270
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
275 280 285
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
290 295 300
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn

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305                 310                 315                 320
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
                325                 330                 335
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
            340                 345                 350
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
        355                 360                 365
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
    370                 375                 380
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
385                 390                 395                 400
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                405                 410                 415
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
            420                 425                 430
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
        435                 440                 445
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
    450                 455                 460
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465                 470                 475                 480
Lys Ser Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
                485                 490                 495
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
            500                 505                 510
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
        515                 520                 525
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
    530                 535                 540
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
545                 550                 555                 560
Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
                565                 570                 575
Val Asp Lys Lys Val
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<210> 30
<211> 578
<212> PRT
<213> Artificial Sequence

<220>
<223> ORN145 mature protein comprising : 4C04 (anti-RON) scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3 and human CH1

<400> 30

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Glu Ser Val Thr Ile Thr Cys Leu Ala Ser Gln Thr Ile Gly Thr Trp
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Thr Ser Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Ala
    50                  55                  60
Ser Gly Ser Gly Thr Lys Phe Ser Phe Lys Ile Asp Ser Leu Gln Ser
65                  70                  75                  80
Glu Asp Phe Val Ser Tyr Tyr Cys Gln Gln Leu Tyr Asn Thr Pro Trp
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile Gln Leu Gln Gln
        115                 120                 125
Ser Gly Pro Glu Leu Val Lys Pro Gly Thr Ser Val Lys Ile Ser Cys
    130                 135                 140
Lys Ala Ser Asp Tyr Thr Leu Thr Asp Phe Tyr Met Asn Trp Val Arg
145                 150                 155                 160
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Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly
                165                 170                 175
Thr Asp Lys Thr Arg Tyr Asn Glu Lys Phe Arg Asp Lys Ala Ile Leu
            180                 185                 190
Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
        195                 200                 205
Thr Ser Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg Ser Ala Tyr Tyr
    210                 215                 220
Gly Asn Tyr Val Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
225                 230                 235                 240
Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
                245                 250                 255
Pro Cys Pro Ser Gly Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
            260                 265                 270
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
        275                 280                 285
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
    290                 295                 300
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305                 310                 315                 320
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
                325                 330                 335
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
            340                 345                 350
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
        355                 360                 365
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
    370                 375                 380
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385                 390                 395                 400
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                405                 410                 415
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            420                 425                 430
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
        435                 440                 445
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
    450                 455                 460
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg
465                 470                 475                 480
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
                485                 490                 495
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            500                 505                 510
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        515                 520                 525
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    530                 535                 540
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
545                 550                 555                 560
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                565                 570                 575
Lys Val
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<210> 31
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> ORN146 mature protein comprising : 4C04 (anti-RON) scFv, human IgG1 SCC-P hinge, human CH2, human CH3, and human Ck(YAE)

<400> 31

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 1               5                  10                  15
Glu Ser Val Thr Ile Thr Cys Leu Ala Ser Gln Thr Ile Gly Thr Trp
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Thr Ser Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Ala
    50                  55                  60
Ser Gly Ser Gly Thr Lys Phe Ser Phe Lys Ile Asp Ser Leu Gln Ser
65                  70                  75                  80
Glu Asp Phe Val Ser Tyr Tyr Cys Gln Gln Leu Tyr Asn Thr Pro Trp
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile Gln Leu Gln Gln
        115                 120                 125
Ser Gly Pro Glu Leu Val Lys Pro Gly Thr Ser Val Lys Ile Ser Cys
    130                 135                 140
Lys Ala Ser Asp Tyr Thr Leu Thr Asp Phe Tyr Met Asn Trp Val Arg
145                 150                 155                 160
Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly
                165                 170                 175
Thr Asp Lys Thr Arg Tyr Asn Glu Lys Phe Arg Asp Lys Ala Ile Leu
            180                 185                 190
Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
        195                 200                 205
Thr Ser Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg Ser Ala Tyr Tyr
    210                 215                 220
Gly Asn Tyr Val Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
225                 230                 235                 240
Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
                245                 250                 255
Pro Cys Pro Ser Gly Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
            260                 265                 270
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
        275                 280                 285
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
    290                 295                 300
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305                 310                 315                 320
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
                325                 330                 335
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
            340                 345                 350
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
        355                 360                 365
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
    370                 375                 380
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385                 390                 395                 400
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                405                 410                 415
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            420                 425                 430
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
        435                 440                 445
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
    450                 455                 460
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg
465                 470                 475                 480
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
                485                 490                 495
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr
            500                 505                 510
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        515                 520                 525
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    530                 535                 540
Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
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His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
565 570 575
Val Thr Lys Ser Phe Asn Arg Gly Glu
580 585

<210> 32
<211> 581
<212> PRT
<213> Artificial Sequence

<220>
<223> ORN148 mature protein comprising : 11H09 (anti-RON) scFv, human IgG1 SCC-P hinge, human CH2, human CH3, and human Ck(YAE)

<400> 32
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35 40 45
Tyr Ser Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
50 55 60
Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
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85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln
115 120 125
Ser Gly Ala Glu Leu Ala Lys Pro Gly Ala Ser Val Lys Met Ser Cys
130 135 140
Lys Ser Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Ile His Trp Val Lys
145 150 155 160
Glu Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Thr
165 170 175
Thr Gly Tyr Thr Glu Ser Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu
180 185 190
Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
195 200 205
Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Phe Leu Leu Arg Pro Trp
210 215 220
Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ser
225 230 235 240
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ser
245 250 255
Gly Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
260 265 270
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
275 280 285
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
290 295 300
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305 310 315 320
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
325 330 335
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
340 345 350
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
355 360 365
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
370 375 380
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385 390 395 400

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Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Thr Val Ala Ala
465                 470                 475                 480
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                485                 490                 495
Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu Ala
            500                 505                 510
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        515                 520                 525
Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    530                 535                 540
Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
545                 550                 555                 560
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
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Phe Asn Arg Gly Glu
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<210> 33
<211> 1809
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for ORN160 comprising : 5D5 (anti-c-Met) scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 33

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aggcctgggg cttcagtgaa gatgtcctgc agggcttcgg gctatacctt caccagctac 540
tggttgcact gggttaaaca gaggcctgga caaggccttg agtggattgg catgattgat 600
ccttccaata gtgacactag gtttaatccg aacttcaagg acaaggccac attgaatgta 660
gacagatctt ccaacacagc ctacatgctg ctcagcagcc tgacatctgc tgactctgca 720
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<210> 34
<211> 1821
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC001 comprising : HD37 (anti-CD39), human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3 and human CH1

<400> 34
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aaggtggaca agaaagtttg a 1821

<210> 35
<211> 1800
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC002 comprising : 2H7 (anti-CD20) scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3 and human CH1

<400> 35
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<210> 36
<211> 1851
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC003 comprising : G19-4 (anti-CD3) scFv, altered human IgA1 hinge, human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 36
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tcaagcggtg gcggagggtc tgggggtggc ggatccggag gtggtggctc tgcacaagac 480
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catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg a 1851

<210> 37
<211> 1812
<212> DNA
<213> Artificial Sequence

<220>

<223> Nucleotide sequence for TSC004 comprising : G19-4 (anti-CD3) scFv, altered human IgA2 hinge, human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 37

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cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1260
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aggggagagt ga 1812

<210> 38
<211> 1842
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC005 comprising : G19-4 (anti-CD3) scFv, altered human IgG3 hinge, human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 38

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<210> 39
<211> 1899
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC006 comprising : G19-4 (anti-CD3) scFv, altered human IgD hinge, human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 39
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gaggtccagc tgcaacagtc tggacctgaa ctggtgaagc ctggagcttc aatgaagatt 120
tcctgcaagg cctctggtta ctcattcact ggctacatcg tgaactggct gaagcagagc 180
catggaaaga accttgagtg gattggactt attaatccat acaaaggtct tactacctac 240
aaccagaaat tcaagggcaa ggccacatta actgtagaca agtcatccag cacagcctac 300
atggagctcc tcagtctgac atctgaagac tctgcagtct attactgtgc aagatctggg 360
tactatggtg actcggactg gtacttcgat gtctggggcg cagggaccac ggtcaccgtc 420
tcaagcggtg gcggagggtc tgggggtggc ggatccggag gtggtggctc tgcacaagac 480
atccagatga cacagactac atcctccctg tctgcctctc tgggagacag agtcaccatc 540
agttgcaggg caagtcagga cattcgcaat tatttaaact ggtatcagca gaaaccagat 600
ggaactgtta aactcctgat ctactacaca tcaagattac actcaggagt cccatcaagg 660
ttcagtggca gtgggtctgg aacagattat tctctcacca ttgccaacct gcaaccagaa 720
gatattgcca cttacttttg ccaacagggt aatacgcttc cgtggacgtt cggtggaggc 780
accaaactgg taaccaaacg ctcgagcgag tctccaaagg cacaggcctc ctccgtgccc 840
actgcacaac cccaagcaga gggcagcctc gccaaggcaa ccacagcccc agccaccacc 900
cgtaacacat gcccaccgtg cccagcacct gaactcctgg gtggaccgtc agtcttcctc 960
ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 1020
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1080
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 1140
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1200
gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag 1260
ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1320
gtcagcctga cctgcctggt caaaggcttc tatccaagcg acatcgccgt ggagtgggag 1380
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1440
tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1500
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1560
ctgtctccgg gtaaatctag aactgtggct gcaccatctg tcttcatctt cccgccatct 1620
gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaatta cttctatccc 1680
agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag 1740
agtgccacag agcaggacag caaggacagc acctacagcc tcagcagcga gctgacgctg 1800
agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 1860
agctcgcccg tcacaaagag cttcaacagg ggagagtga 1899

<210> 40
<211> 1842
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC007 comprising : G19-4 (anti-CD3) scFv, altered human IgG1 hinge, human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 40
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gaggtccagc tgcaacagtc tggacctgaa ctggtgaagc ctggagcttc aatgaagatt 120
tcctgcaagg cctctggtta ctcattcact ggctacatcg tgaactggct gaagcagagc 180
catggaaaga accttgagtg gattggactt attaatccat acaaaggtct tactacctac 240
aaccagaaat tcaagggcaa ggccacatta actgtagaca agtcatccag cacagcctac 300
atggagctcc tcagtctgac atctgaagac tctgcagtct attactgtgc aagatctggg 360
tactatggtg actcggactg gtacttcgat gtctggggcg cagggaccac ggtcaccgtc 420
tcaagcggtg gcggagggtc tgggggtggc ggatccggag gtggtggctc tgcacaagac 480
atccagatga cacagactac atcctccctg tctgcctctc tgggagacag agtcaccatc 540
agttgcaggg caagtcagga cattcgcaat tatttaaact ggtatcagca gaaaccagat 600
ggaactgtta aactcctgat ctactacaca tcaagattac actcaggagt cccatcaagg 660
ttcagtggca gtgggtctgg aacagattat tctctcacca ttgccaacct gcaaccagaa 720
gatattgcca cttacttttg ccaacagggt aatacgcttc cgtggacgtt cggtggaggc 780
accaaactgg taaccaaacg ctcgagcgag cccaaatctt ctgacaaaac tcacacaagc 840
ccaccgagcc catgcccacc gtgcccagca cctgaactcc tgggtggacc gtcagtcttc 900
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gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 1020
gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 1080
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1140
aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 1200
cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1260
caggtcagcc tgacctgcct ggtcaaaggc ttctatccaa gcgacatcgc cgtggagtgg 1320
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1380
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1440
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1500
tccctgtctc cgggtaaatc tagaactgtg gctgcaccat ctgtcttcat cttcccgcca 1560
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa ttacttctat 1620
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 1680
gagagtgcca cagagcagga cagcaaggac agcacctaca gcctcagcag cgagctgacg 1740
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 1800
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt ga 1842

<210> 41
<211> 2115
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC008 comprising : G19-4
(anti-CD3) scFv, altered human IgE CH2 hinge,
human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 41
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gaggtccagc tgcaacagtc tggacctgaa ctggtgaagc ctggagcttc aatgaagatt 120
tcctgcaagg cctctggtta ctcattcact ggctacatcg tgaactggct gaagcagagc 180
catggaaaga accttgagtg gattggactt attaatccat acaaaggtct tactacctac 240
aaccagaaat tcaagggcaa ggccacatta actgtagaca agtcatccag cacagcctac 300
atggagctcc tcagtctgac atctgaagac tctgcagtct attactgtgc aagatctggg 360
tactatggtg actcggactg gtacttcgat gtctggggcg cagggaccac ggtcaccgtc 420
tcaagcggtg gcggagggtc tgggggtggc ggatccggag gtggtggctc tgcacaagac 480
atccagatga cacagactac atcctccctg tctgcctctc tgggagacag agtcaccatc 540
agttgcaggg caagtcagga cattcgcaat tatttaaact ggtatcagca gaaaccagat 600
ggaactgtta aactcctgat ctactacaca tcaagattac actcaggagt cccatcaagg 660
ttcagtggca gtgggtctgg aacagattat tctctcacca ttgccaacct gcaaccagaa 720
gatattgcca cttacttttg ccaacagggt aatacgcttc cgtggacgtt cggtggaggc 780
accaaactgg taaccaaacg ctcgagctcc agggacttca ccccgcccac cgtgaagatc 840
ttacagtcgt ccagcgacgg cggcgggcac ttcccccccga ccatccagct cctgtgcctc 900
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gacgtggact tgtccaccgc ctctaccacg caggagggtg agctggcctc cacacaaagc 1020
gagctcaccc tcagccagaa gcactggctg tcagaccgca cctacacctg ccaggtcacc 1080
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gcacctgaac tcctgggtgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 1200
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 1260
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1320
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1380
caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1440
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1500
ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1560

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1620
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accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1740
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atctagaact 1800
gtggctgcac catctgtctt catcttcccg ccatctgatg agcagttgaa atctggaact 1860
gcctctgttg tgtgcctgct gaattacttc tatcccagag aggccaaagt acagtggaag 1920
gtggataacg ccctccaatc gggtaactcc caggagagtg ccacagagca ggacagcaag 1980
gacagcacct acagcctcag cagcgagctg acgctgagca aagcagacta cgagaaacac 2040
aaagtctacg cctgcgaagt cacccatcag ggcctgagct cgcccgtcac aaagagcttc 2100
aacaggggag agtga 2115

<210> 42
<211> 2136
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC009 comprising : G19-4 (anti-CD3) scFv, altered human IgM CH2 hinge, human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 42
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gaggtccagc tgcaacagtc tggacctgaa ctggtgaagc ctggagcttc aatgaagatt 120
tcctgcaagg cctctggtta ctcattcact ggctacatcg tgaactggct gaagcagagc 180
catggaaaga accttgagtg gattggactt attaatccat acaaaggtct tactacctac 240
aaccagaaat tcaagggcaa ggccacatta actgtagaca agtcatccag cacagcctac 300
atggagctcc tcagtctgac atctgaagac tctgcagtct attactgtgc aagatctggg 360
tactatggtg actcggactg gtacttcgat gtctggggcg cagggaccac ggtcaccgtc 420
tcaagcggtg gcggagggtc tgggggtggc ggatccggag gtggtggctc tgcacaagac 480
atccagatga cacagactac atcctccctg tctgcctctc tgggagacag agtcaccatc 540
agttgcaggg caagtcagga cattcgcaat tatttaaact ggtatcagca gaaaccagat 600
ggaactgtta aactcctgat ctactacaca tcaagattac actcaggagt cccatcaagg 660
ttcagtggca gtgggtctgg aacagattat tctctcacca ttgccaacct gcaaccagaa 720
gatattgcca cttacttttg ccaacagggt aatacgcttc cgtggacgtt cggtggaggc 780
accaaactgg taaccaaacg ctcgagcatt gccgagctgc ctcccaaagt gagcgtcttc 840
gtcccacccc gcgacggctt cttcggcaac ccccgcaagt ccaagctcat ctgccaggcc 900
acgggtttca gtccccggca gattcaggtg tcctggctgc gcgaggggaa gcaggtgggg 960
tctggcgtca ccacggacca ggtgcaggct gaggccaaag agtctgggcc cacgacctac 1020
aaggtgacca gcacactgac catcaaagag agcgactggc tcagccagag catgttcacc 1080
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tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1800
tctccgggta aatctagaac tgtggctgca ccatctgtct tcatcttccc gccatctgat 1860
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gaggccaaag tacagtggaa ggtggataac gccctccaat cgggtaactc ccaggagagt 1980
gccacagagc aggacagcaa ggacagcacc tacagcctca gcagcgagct gacgctgagc 2040
aaagcagact acgagaaaca caaagtctac gcctgcgaag tcacccatca gggcctgagc 2100
tcgcccgtca caaagagctt caacagggga gagtga 2136

<210> 43
<211> 1839
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC010 comprising : HD37 (anti-CD19) scFv, altered human IgA1 hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 43
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gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 180
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 240
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cctgtggaga aggtggatgc tgcaacctat cactgccagc aaagtactga ggatccgtgg 360
acgttcggtg gaggcaccaa gctggaaatc aaaggtggcg gtggttcggg cggtggtggg 420
tcgggtggcg gcggagctag ccaggttcag ctgcagcagt ctggggctga gctggtgagg 480
cctgggtcct cagtgaagat ttcctgcaag gcttctggct atgcattcag tagctactgg 540
atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct 600
ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac 660
gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc 720
tatttctgtg caagacggga gactacgacg gtaggccgtt attactatgc tatggactac 780
tggggtcaag gaacctcagt caccgtctcc tcgagcccct caactccacc taccccatct 840
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ggtggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 960
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1020
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1080
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1140
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atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1260
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cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1440
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tacacgcaga agagcctctc cctgtctccg ggtaaatcta gagcctccac caagggccca 1560
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tgcctggtca aggactactt ccccgagccg gtgacggtgt cgtggaactc aggcgccctg 1680
accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcagc 1740
agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 1800
cacaagccca gcaacaccaa ggtggacaag aaagtttga 1839

<210> 44
<211> 1800
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC011 comprising : HD37 (anti-CD19) scFv, altered human IgA2 hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 44
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gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 180
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 240
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 300
cctgtggaga aggtggatgc tgcaacctat cactgccagc aaagtactga ggatccgtgg 360
acgttcggtg gaggcaccaa gctggaaatc aaaggtggcg gtggttcggg cggtggtggg 420
tcgggtggcg gcggagctag ccaggttcag ctgcagcagt ctggggctga gctggtgagg 480
cctgggtcct cagtgaagat ttcctgcaag gcttctggct atgcattcag tagctactgg 540
atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct 600
ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac 660
gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc 720
tatttctgtg caagacggga gactacgacg gtaggccgtt attactatgc tatggactac 780
tggggtcaag gaacctcagt caccgtctcc tcgagccccc cacctccccc atgcccaccg 840
tgcccagcac ctgaactcct gggtggaccg tcagtcttcc tcttcccccc aaaacccaag 900
gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac 960
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 1020
acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 1080
ctgcaccagg actggctgaa tggcaaggag tacaagtgca aggtctccaa caaagccctc 1140
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tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 1260
gtcaaaggct tctatccaag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1320
aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1380

aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1440
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agagcctcca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 1560
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgagcc ggtgacggtg 1620
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 1680
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 1740
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagtttga 1800

<210> 45
<211> 1830
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC012 comprising : HD37 (anti-CD19) scFv, altered human IgG1 hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 45
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gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 180
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 240
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 300
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acgttcggtg gaggcaccaa gctggaaatc aaaggtggcg gtggttcggg cggtggtggg 420
tcgggtggcg gcggagctag ccaggttcag ctgcagcagt ctggggctga gctggtgagg 480
cctgggtcct cagtgaagat ttcctgcaag gcttctggct atgcattcag tagctactgg 540
atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct 600
ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac 660
gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc 720
tatttctgtg caagacggga gactacgacg gtaggccgtt attactatgc tatggactac 780
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cacacaagcc caccgagccc atgcccaccg tgcccagcac ctgaactcct gggtggaccg 900
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 960
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gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 1080
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1140
tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1200
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1260
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatccaag cgacatcgcc 1320
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1380
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1440
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1500
aagagcctct ccctgtctcc gggtaaatct agagcctcca ccaagggccc atcggtcttc 1560
cccctggcac cctcctccaa gagcacctct gggggcacag cggccctggg ctgcctggtc 1620
aaggactact tccccgagcc ggtgacggtg tcgtggaact caggcgccct gaccagcggc 1680
gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtggtg 1740
accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa tcacaagccc 1800
agcaacacca aggtggacaa gaaagtttga 1830

<210> 46
<211> 1830
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC013 comprising : HD37 (anti-CD19) scFv, altered human IgG3 hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 46
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 180
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 240
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 300

cctgtggaga aggtggatgc tgcaacctat cactgccagc aaagtactga ggatccgtgg 360
acgttcggtg gaggcaccaa gctggaaatc aaaggtggcg gtggttcggg cggtggtggg 420
tcgggtggcg gcggagctag ccaggttcag ctgcagcagt ctggggctga gctggtgagg 480
cctgggtcct cagtgaagat ttcctgcaag gcttctggct atgcattcag tagctactgg 540
atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct 600
ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac 660
gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc 720
tatttctgtg caagacggga gactacgacg gtaggccgtt attactatgc tatggactac 780
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gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 1020
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acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1140
tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1200
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1260
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatccaag cgacatcgcc 1320
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1380
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1440
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1500
aagagcctct ccctgtctcc gggtaaatct agagcctcca ccaagggccc atcggtcttc 1560
cccctggcac cctcctccaa gagcacctct gggggcacag cggccctggg ctgcctggtc 1620
aaggactact tccccgagcc ggtgacggtg tcgtggaact caggcgccct gaccagcggc 1680
gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtggtg 1740
accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa tcacaagccc 1800
agcaacacca aggtggacaa gaaagtttga 1830

<210> 47
<211> 1887
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC014 comprising : HD37 (anti-CD19) scFv, altered human IgD hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 47
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 180
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 240
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 300
cctgtggaga aggtggatgc tgcaacctat cactgccagc aaagtactga ggatccgtgg 360
acgttcggtg gaggcaccaa gctggaaatc aaaggtggcg gtggttcggg cggtggtggg 420
tcgggtggcg gcggagctag ccaggttcag ctgcagcagt ctggggctga gctggtgagg 480
cctgggtcct cagtgaagat ttcctgcaag gcttctggct atgcattcag tagctactgg 540
atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct 600
ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac 660
gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc 720
tatttctgtg caagacggga gactacgacg gtaggccgtt attactatgc tatggactac 780
tggggtcaag gaacctcagt caccgtctcc tcgagcgagt ctccaaaggc acaggcctcc 840
tccgtgccca ctgcacaacc ccaagcagag ggcagcctcg ccaaggcaac cacagcccca 900
gccaccaccc gtaacacatg cccaccgtgc ccagcacctg aactcctggg tggaccgtca 960
gtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 1020
acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 1080
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 1140
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1200
aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1260
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1320
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atccaagcga catcgccgtg 1380
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1440
tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1500
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1560
agcctctccc tgtctccggg taaatctaga gcctccacca agggcccatc ggtcttcccc 1620
ctggcaccct cctccaagag cacctctggg ggcacagcgg ccctgggctg cctggtcaag 1680
gactacttcc ccgagccggt gacggtgtcg tggaactcag gcgccctgac cagcggcgtg 1740
cacaccttcc cggctgtcct acagtcctca ggactctact ccctcagcag cgtggtgacc 1800

gtgccctcca gcagcttggg cacccagacc tacatctgca acgtgaatca caagcccagc 1860
aacaccaagg tggacaagaa agtttga 1887

<210> 48
<211> 2103
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC015 comprising : HD37 (anti-CD19) scFv, altered human IgE CH2 hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 48
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 180
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 240
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 300
cctgtggaga aggtggatgc tgcaacctat cactgccagc aaagtactga ggatccgtgg 360
acgttcggtg gaggcaccaa gctggaaatc aaaggtggcg gtggttcggg cggtggtggg 420
tcgggtggcg gcggagctag ccaggttcag ctgcagcagt ctggggctga gctggtgagg 480
cctgggtcct cagtgaagat ttcctgcaag gcttctggct atgcattcag tagctactgg 540
atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct 600
ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac 660
gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc 720
tatttctgtg caagacggga gactacgacg gtaggccgtt attactatgc tatggactac 780
tggggtcaag gaacctcagt caccgtctcc tcgagctcca gggacttcac cccgcccacc 840
gtgaagatct tacagtcgtc cagcgacggc ggcgggcact tccccccgac catccagctc 900
ctgtgcctcg tctctgggta caccccaggg actatcaaca tcacctggct ggaggacggg 960
caggtcatgg acgtggactt gtccaccgcc tctaccacgc aggagggtga gctggcctcc 1020
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caggtcacct atcaaggtca caccttgag gacagcacca agaagtctgc atgcccaccg 1140
tgctccggag cacctgaact cctgggtgga ccgtcagtct tcctcttccc cccaaaaccc 1200
aaggacaccc tcatgatctc ccggaccccct gaggtcacat gcgtggtggt ggacgtgagc 1260
cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 1320
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gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 1440
ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1500
gtgtacaccc tgcccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 1560
ctggtcaaag gcttctatcc aagcgacatc gccgtggagt gggagagcaa tgggcagccg 1620
gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1680
agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 1740
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa 1800
tctagagcct ccaccaaggg cccatcggtc ttcccctgg caccctcctc caagagcacc 1860
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga gccggtgacg 1920
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 1980
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 2040
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 2100
tga 2103

<210> 49
<211> 2124
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC016 comprising : HD37 (anti-CD19) scFv, altered human IgM CH2 hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 49
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 180
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 240
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 300
cctgtggaga aggtggatgc tgcaacctat cactgccagc aaagtactga ggatccgtgg 360

acgttcggtg gaggcaccaa gctggaaatc aaaggtggcg gtggttcggg cggtggtggg 420
tcgggtggcg gcggagctag ccaggttcag ctgcagcagt ctggggctga gctggtgagg 480
cctgggtcct cagtgaagat ttcctgcaag gcttctggct atgcattcag tagctactgg 540
atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct 600
ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac 660
gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc 720
tatttctgtg caagacggga gactacgacg gtaggccgtt attactatgc tatggactac 780
tggggtcaag gaacctcagt caccgtctcc tcgagcattg ccgagctgcc tcccaaagtg 840
agcgtcttcg tcccaccccg cgacggcttc ttcggcaacc cccgcaagtc caagctcatc 900
tgccaggcca cgggtttcag tccccggcag attcaggtgt cctggctgcg cgaggggaag 960
caggtggggt ctggcgtcac cacggaccag gtgcaggctg aggccaaaga gtctgggccc 1020
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tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 1320
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cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 1440
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gggcagcccc gagaaccaca ggtgtacacc ctgccccccat cccgggatga gctgaccaag 1560
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ctctccctgt ctccgggtaa atctagagcc tccaccaagg gcccatcggt cttccccctg 1860
gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac 1920
tacttccccg agccggtgac ggtgtcgtgg aactcaggcg ccctgaccag cggcgtgcac 1980
accttcccgg ctgtcctaca gtcctcagga ctctactccc tcagcagcgt ggtgaccgtg 2040
ccctccagca gcttgggcac ccagacctac atctgcaacg tgaatcacaa gcccagcaac 2100
accaaggtgg acaagaaagt ttga 2124

<210> 50
<211> 1788
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC017 comprising : P2C2 (anti-CD79b) scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3 and human CH1

<400> 50
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gatattgtga tgatccagga tgaactctcc aatcctgtca gttctggaga atcagtttcc 120
atctcctgta ggtctagtaa gagtctccta gataaggaag ggaagacata cttgaattgg 180
tttctgcaga gaccaggaca atctcctcag ctcctgatct atctgatgtc catgcgtgaa 240
tcaggagtct cagaccggtt tagtggcagt gggtcaggaa cagatttcac cctggaaatc 300
agtagagtga aggctgagga tgtgggtgtg tattactgtc aacaacttgt agagtatccg 360
tggacgttcg gtggaggcac caagctggaa atcaaaggtg gcggtggctc tggcggaggt 420
ggatccggtg gcggcggctc tcagatccag ttggtgcagt ctggacctga gctgaagaag 480
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atgcactggg tgaggcaggc tccaggaaag ggtttaaagt ggatgggctg gataaacact 600
gagactggtg agccaacata tgcagatgac ttcaggggac ggtttgcctt ctctttggaa 660
acttctgcca gcactgccta tttgcagatc aacaacctca aaaatgagga cacggctaca 720
tatttttgta cctggtctgc ttactggggc caagggactc tggtcactgt ctctgcctcg 780
agcgagccca aatcttctga caaaactcac acatgcccac cgtgcccatc cggagcacct 840
gaactcctgg gtggaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
atctcccgga ccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020
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tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc 1140
gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1200
ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260
tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1320
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gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatctag agcctccacc 1500
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gccctgggct gcctggtcaa ggactacttc cccgagccgg tgacggtgtc gtggaactca 1620
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 1680
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 1740
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagtttga 1788

<210> 51
<211> 1812
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC018 comprising : M0042 (anti-HLA-DR) scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 51
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 120
atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 180
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gaagattttg ccacttacta ctgtcaacag agttacagta ccccattcac tttcggccct 360
gggaccaaag tggatatcaa agggggtgga ggctctggtg gcggtggctc tggcggaggt 420
ggatccggtg gcggcggctc tgaagttcaa ttgttagagt ctggtggcgg tcttgttcag 480
cctggtggtt ctttacgtct ttcttgcgct gcttccggat tcactttctc tcattactat 540
atgtcttggg ttcgccaagc tcctggtaaa ggtttggagt gggtttctta tatcggtcct 600
tctggtggct ttactgctta tgctgactcc gttaaaggtc gcttcactat ctctagagac 660
aactctaaga atactctcta cttgcagatg aacagcttaa gggctgagga cacggccgtg 720
tattactgtg cgagagacgg gtgggttggt agcgagaact actccggtat ggacgtctgg 780
ggccaaggga ccacggtctc ctcgagcgag cccaaatctt ctgacaaaac tcacacatgc 840
ccaccgtgcc catccggagc acctgaactc ctgggtggac cgtcagtctt cctcttcccc 900
ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 960
gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1020
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1140
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gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260
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gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1380
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ccgggtaaat ctagagcctc caccaagggc ccatcggtct tcccccctggc accctcctcc 1560
aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgag 1620
ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 1680
gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 1740
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 1800
aagaaagttt ga 1812

<210> 52
<211> 1833
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for TSC019 comprising : G19-4 (anti-CD3) scFv, human IgG1 SCC-P hinge, human CH2, human CH3, and human Ck(YAE)

<400> 52
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gaggtccagc tgcaacagtc tggacctgaa ctggtgaagc ctggagcttc aatgaagatt 120
tcctgcaagg cctctggtta ctcattcact ggctacatcg tgaactggct gaagcagagc 180
catggaaaga accttgagtg gattggactt attaatccat acaaaggtct tactacctac 240
aaccagaaat tcaagggcaa ggccacatta actgtagaca agtcatccag cacagcctac 300
atggagctcc tcagtctgac atctgaagac tctgcagtct attactgtgc aagatctggg 360
tactatggtg actcggactg gtacttcgat gtctggggcg cagggaccac ggtcaccgtc 420
tcaagcggtg gcggagggtc tgggggtggc ggatccggag gtggtggctc tgcacaagac 480
atccagatga cacagactac atcctccctg tctgcctctc tgggagacag agtcaccatc 540

```
agttgcaggg caagtcagga cattcgcaat tatttaaact ggtatcagca gaaaccagat 600
ggaactgtta aactcctgat ctactacaca tcaagattac actcaggagt cccatcaagg 660
ttcagtggca gtgggtctgg aacagattat tctctcacca ttgccaacct gcaaccagaa 720
gatattgcca cttacttttg ccaacagggt aatacgcttc cgtggacgtt cggtggaggc 780
accaaactgg taaccaaacg ctcgagcgag cccaaatctt ctgacaaaac tcacacatgc 840
ccaccgtgcc catccggagc acctgaactc ctgggtggac cgtcagtctt cctcttcccc 900
ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 960
gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1020
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1140
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1200
gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260
ctgacctgcc tggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat 1320
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1380
ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1440
tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500
ccgggtaaat ctagaactgt ggctgcacca tctgtcttca tcttcccgcc atctgatgag 1560
cagttgaaat ctggaactgc ctctgttgtg tgcctgctga attacttcta tcccagagag 1620
gccaaagtac agtggaaggt ggataacgcc ctccaatcgg gtaactccca ggagagtgcc 1680
acagagcagg acagcaagga cagcacctac agcctcagca gcgagctgac gctgagcaaa 1740
gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 1800
cccgtcacaa agagcttcaa caggggagag tga                              1833
```

<210> 53
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> ORN160 mature protein comprising : 5D5 (anti-c-Met) scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 53

```
Asp Phe Met Met Ser Gln Ser Pro Ser Ser Leu Thr Val Ser Val Gly
 1               5                  10                  15
Glu Lys Val Thr Val Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Thr
            20                  25                  30
Ser Ser Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80
Ile Thr Ser Val Lys Ala Asp Asp Leu Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95
Tyr Tyr Ala Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu
            100                 105                 110
Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Ala
    130                 135                 140
Ser Val Lys Met Ser Cys Arg Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
145                 150                 155                 160
Trp Leu His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
                165                 170                 175
Gly Met Ile Asp Pro Ser Asn Ser Asp Thr Arg Phe Asn Pro Asn Phe
            180                 185                 190
Lys Asp Lys Ala Thr Leu Asn Val Asp Arg Ser Ser Asn Thr Ala Tyr
        195                 200                 205
Met Leu Leu Ser Ser Leu Thr Ser Ala Asp Ser Ala Val Tyr Tyr Cys
    210                 215                 220
Ala Thr Tyr Gly Ser Tyr Val Ser Pro Leu Asp Tyr Trp Gly Gln Gly
225                 230                 235                 240
Thr Ser Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr
                245                 250                 255
His Thr Cys Pro Pro Cys Pro Ser Gly Ala Pro Glu Leu Leu Gly Gly
            260                 265                 270
```

```
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
        275                 280                 285
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
385                 390                 395                 400
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480
Gly Lys Ser Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
                485                 490                 495
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
            500                 505                 510
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
        515                 520                 525
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
    530                 535                 540
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
545                 550                 555                 560
Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
                565                 570                 575
Lys Val Asp Lys Lys Val
            580
```

<210> 54
<211> 586
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC001 mature protein comprising : HD37 (anti-CD39), human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3 and human CH1

<400> 54

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1                 5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
```

```
        115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Glu Pro Lys Ser
                245                 250                 255
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ser Gly Ala Pro Glu
            260                 265                 270
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        275                 280                 285
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    290                 295                 300
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305                 310                 315                 320
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
                325                 330                 335
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
            340                 345                 350
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
        355                 360                 365
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
    370                 375                 380
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
385                 390                 395                 400
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                405                 410                 415
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            420                 425                 430
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        435                 440                 445
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    450                 455                 460
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465                 470                 475                 480
Ser Leu Ser Pro Gly Lys Ser Arg Ala Ser Thr Lys Gly Pro Ser Val
                485                 490                 495
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
            500                 505                 510
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
        515                 520                 525
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
    530                 535                 540
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
545                 550                 555                 560
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
                565                 570                 575
Pro Ser Asn Thr Lys Val Asp Lys Lys Val
            580                 585
```

<210> 55
<211> 579
<212> P&I
<213> Artificial Sequence

<220>
<223> TSC002 mature protein comprising : 2H7 (anti-CD20)

scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3 and human CH1

<400> 55

```
Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
 1               5                  10                  15
Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
        35                  40                  45
Ala Pro Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65                  70                  75                  80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe Asn Pro Pro Thr
                85                  90                  95
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Asp Gly Gly Gly Ser Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln Ala Tyr Leu Gln Gln
        115                 120                 125
Ser Gly Ala Glu Ser Val Arg Pro Gly Ala Ser Val Lys Met Ser Cys
    130                 135                 140
Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys
145                 150                 155                 160
Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly
                165                 170                 175
Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu
            180                 185                 190
Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
        195                 200                 205
Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Val Val Tyr Tyr
    210                 215                 220
Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp Gly Thr Gly Thr Thr Val
225                 230                 235                 240
Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
                245                 250                 255
Pro Pro Cys Pro Ser Gly Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
            260                 265                 270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275                 280                 285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    290                 295                 300
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
                325                 330                 335
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
            340                 345                 350
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        355                 360                 365
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        435                 440                 445
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    450                 455                 460
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser
465                 470                 475                 480
Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
                485                 490                 495
Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
            500                 505                 510
```

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
515 520 525
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
530 535 540
Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
545 550 555 560
Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
565 570 575
Lys Lys Val

<210> 56
<211> 596
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC003 mature protein comprising : G19-4 (anti-CD3) scFv, altered human IgA1 hinge, human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 56
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30
Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
35 40 45
Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
100 105 110
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr
130 135 140
Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
145 150 155 160
Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
165 170 175
Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
180 185 190
Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205
Asp Tyr Ser Leu Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr
210 215 220
Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly
225 230 235 240
Thr Lys Leu Val Thr Lys Arg Ser Ser Pro Ser Thr Pro Pro Thr Pro
245 250 255
Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Pro Pro Cys Pro
260 265 270
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
275 280 285
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
290 295 300
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
305 310 315 320
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
325 330 335
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
340 345 350
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

```
        355                 360                 365
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    370                 375                 380
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
385                 390                 395                 400
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                405                 410                 415
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            420                 425                 430
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        435                 440                 445
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    450                 455                 460
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
465                 470                 475                 480
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Thr Val Ala Ala Pro
                485                 490                 495
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
            500                 505                 510
Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu Ala Lys
        515                 520                 525
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
    530                 535                 540
Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
545                 550                 555                 560
Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
                565                 570                 575
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
            580                 585                 590
Asn Arg Gly Glu
        595
```

<210> 57
<211> 583
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC004 mature protein comprising : G19-4 (anti-CD3) scFv, altered human IgA2 hinge, human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 57

```
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1                5                  10                  15
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
            20                  25                  30
Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
        35                  40                  45
Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
            100                 105                 110
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr
    130                 135                 140
Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
145                 150                 155                 160
Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
                165                 170                 175
Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
            180                 185                 190
```

```
Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
Asp Tyr Ser Leu Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr
    210                 215                 220
Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly
225                 230                 235                 240
Thr Lys Leu Val Thr Lys Arg Ser Ser Pro Pro Pro Pro Pro Cys Pro
                245                 250                 255
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
            260                 265                 270
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
        275                 280                 285
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
    290                 295                 300
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
305                 310                 315                 320
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
                325                 330                 335
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
            340                 345                 350
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
        355                 360                 365
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
    370                 375                 380
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
385                 390                 395                 400
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
                405                 410                 415
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
            420                 425                 430
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
        435                 440                 445
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
    450                 455                 460
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Thr Val
465                 470                 475                 480
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
                485                 490                 495
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg
            500                 505                 510
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
        515                 520                 525
Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
    530                 535                 540
Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
545                 550                 555                 560
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
                565                 570                 575
Lys Ser Phe Asn Arg Gly Glu
            580
```

<210> 58
<211> 593
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC005 mature protein comprising : G19-4 (anti-CD3) scFv, altered human IgG3 hinge, human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 58

```
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1                  5                  10                  15
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
            20                  25                  30
Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
```

```
        35                  40                  45
Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
            100                 105                 110
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr
    130                 135                 140
Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
145                 150                 155                 160
Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
                165                 170                 175
Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
            180                 185                 190
Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
Asp Tyr Ser Leu Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr
    210                 215                 220
Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly
225                 230                 235                 240
Thr Lys Leu Val Thr Lys Arg Ser Ser Glu Pro Lys Ser Ser Asp Thr
                245                 250                 255
Pro Pro Pro Ser Pro Arg Ser Pro Cys Pro Pro Cys Pro Ala Pro Glu
            260                 265                 270
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        275                 280                 285
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    290                 295                 300
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305                 310                 315                 320
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
                325                 330                 335
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
            340                 345                 350
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
        355                 360                 365
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
    370                 375                 380
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
385                 390                 395                 400
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                405                 410                 415
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            420                 425                 430
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        435                 440                 445
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    450                 455                 460
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465                 470                 475                 480
Ser Leu Ser Pro Gly Lys Ser Arg Thr Val Ala Ala Pro Ser Val Phe
                485                 490                 495
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
            500                 505                 510
Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
        515                 520                 525
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Ala Thr
    530                 535                 540
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Glu Leu Thr
545                 550                 555                 560
Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
                565                 570                 575
Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
```

580 585 590
Glu

<210> 59
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC006 mature protein comprising : G19-4 (anti-CD3) scFv, altered human IgD hinge, human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<220>
<221> VARIANT
<222> 375
<223> Xaa = Any Amino Acid

<400> 59
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30
Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
35 40 45
Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
100 105 110
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr
130 135 140
Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
145 150 155 160
Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
165 170 175
Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
180 185 190
Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205
Asp Tyr Ser Leu Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr
210 215 220
Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly
225 230 235 240
Thr Lys Leu Val Thr Lys Arg Ser Ser Glu Ser Pro Lys Ala Gln Ala
245 250 255
Ser Ser Val Pro Thr Ala Gln Pro Gln Ala Glu Gly Ser Leu Ala Lys
260 265 270
Ala Thr Thr Ala Pro Ala Thr Thr Arg Asn Thr Cys Pro Pro Cys Pro
275 280 285
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
290 295 300
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
305 310 315 320
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
325 330 335
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
340 345 350
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
355 360 365
Gln Asp Trp Leu Asn Gly Xaa Glu Tyr Lys Cys Lys Val Ser Asn Lys

```
    370                 375                 380
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
385                 390                 395                 400
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
                405                 410                 415
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
            420                 425                 430
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        435                 440                 445
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
    450                 455                 460
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
465                 470                 475                 480
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
                485                 490                 495
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Thr Val Ala Ala Pro
            500                 505                 510
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        515                 520                 525
Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu Ala Lys
    530                 535                 540
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
545                 550                 555                 560
Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                565                 570                 575
Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            580                 585                 590
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        595                 600                 605
Asn Arg Gly Glu
    610
```

<210> 60
<211> 593
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC007 mature protein comprising : G19-4 (anti-CD3) scFv, altered human IgG1 hinge, human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 60

```
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1                5                  10                  15
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
            20                  25                  30
Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
        35                  40                  45
Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
            100                 105                 110
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr
    130                 135                 140
Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
145                 150                 155                 160
Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
                165                 170                 175
Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
            180                 185                 190
```

```
Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
Asp Tyr Ser Leu Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr
    210                 215                 220
Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly
225                 230                 235                 240
Thr Lys Leu Val Thr Lys Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys
                245                 250                 255
Thr His Thr Ser Pro Pro Ser Pro Cys Pro Pro Cys Pro Ala Pro Glu
            260                 265                 270
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        275                 280                 285
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    290                 295                 300
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305                 310                 315                 320
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
                325                 330                 335
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
            340                 345                 350
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
        355                 360                 365
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
    370                 375                 380
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
385                 390                 395                 400
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                405                 410                 415
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            420                 425                 430
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        435                 440                 445
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    450                 455                 460
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465                 470                 475                 480
Ser Leu Ser Pro Gly Lys Ser Arg Thr Val Ala Ala Pro Ser Val Phe
                485                 490                 495
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
            500                 505                 510
Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
        515                 520                 525
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Ala Thr
    530                 535                 540
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Glu Leu Thr
545                 550                 555                 560
Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
                565                 570                 575
Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
            580                 585                 590
Glu
```

<210> 61
<211> 684
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC008 mature protein comprising : G19-4 (anti-CD3) scFv, altered human IgE CH2 hinge (SEQ ID NO:757), human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 61

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

```
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
                20                  25                  30
Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
            35                  40                  45
Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
            100                 105                 110
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr
    130                 135                 140
Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
145                 150                 155                 160
Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
                165                 170                 175
Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
            180                 185                 190
Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
Asp Tyr Ser Leu Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr
    210                 215                 220
Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly
225                 230                 235                 240
Thr Lys Leu Val Thr Lys Arg Ser Ser Ser Arg Asp Phe Thr Pro Pro
                245                 250                 255
Thr Val Lys Ile Leu Gln Ser Ser Ser Asp Gly Gly Gly His Phe Pro
            260                 265                 270
Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr
        275                 280                 285
Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu
    290                 295                 300
Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser
305                 310                 315                 320
Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr
                325                 330                 335
Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys
            340                 345                 350
Ser Ala Cys Pro Pro Cys Ser Gly Ala Pro Glu Leu Leu Gly Gly Pro
        355                 360                 365
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
    370                 375                 380
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
385                 390                 395                 400
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
                405                 410                 415
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
            420                 425                 430
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
        435                 440                 445
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
    450                 455                 460
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
465                 470                 475                 480
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
                485                 490                 495
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
            500                 505                 510
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
        515                 520                 525
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
    530                 535                 540
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
545                 550                 555                 560
```

```
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                565                 570                 575
Lys Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
            580                 585                 590
Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
        595                 600                 605
Tyr Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
    610                 615                 620
Leu Gln Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys
625                 630                 635                 640
Asp Ser Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp
                645                 650                 655
Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
            660                 665                 670
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
        675                 680


<210> 62
<211> 691
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC009 mature protein comprising : G19-4
      (anti-CD3) scFv, altered human IgM CH2 hinge,
      human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 62
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1                5                  10                  15
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
            20                  25                  30
Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
        35                  40                  45
Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
            100                 105                 110
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr
    130                 135                 140
Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
145                 150                 155                 160
Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
                165                 170                 175
Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
            180                 185                 190
Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
Asp Tyr Ser Leu Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr
    210                 215                 220
Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly
225                 230                 235                 240
Thr Lys Leu Val Thr Lys Arg Ser Ser Ile Ala Glu Leu Pro Pro Lys
                245                 250                 255
Val Ser Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg
            260                 265                 270
Lys Ser Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile
        275                 280                 285
Gln Val Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr
    290                 295                 300
Thr Asp Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr
```

```
305                 310                 315                 320
Lys Val Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Ser Gln
                325                 330                 335
Ser Met Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln
            340                 345                 350
Asn Ala Ser Ser Met Ser Val Pro Cys Pro Pro Cys Pro Ser Gly Ala
        355                 360                 365
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    370                 375                 380
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
385                 390                 395                 400
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                405                 410                 415
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            420                 425                 430
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        435                 440                 445
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    450                 455                 460
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
465                 470                 475                 480
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
                485                 490                 495
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            500                 505                 510
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        515                 520                 525
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    530                 535                 540
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
545                 550                 555                 560
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                565                 570                 575
Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Thr Val Ala Ala Pro Ser
            580                 585                 590
Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
        595                 600                 605
Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu Ala Lys Val
    610                 615                 620
Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
625                 630                 635                 640
Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Glu
                645                 650                 655
Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
            660                 665                 670
Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
        675                 680                 685
Arg Gly Glu
    690
```

<210> 63
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC010 mature protein comprising : HD37 (anti-CD19) scFv, altered human IgA1 hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 63

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1                5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
```

```
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
        115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Pro Ser Thr Pro
                245                 250                 255
Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Pro
            260                 265                 270
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        275                 280                 285
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    290                 295                 300
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305                 310                 315                 320
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                325                 330                 335
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            340                 345                 350
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        355                 360                 365
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    370                 375                 380
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
385                 390                 395                 400
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                405                 410                 415
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            420                 425                 430
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        435                 440                 445
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    450                 455                 460
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
465                 470                 475                 480
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Ala Ser
                485                 490                 495
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
            500                 505                 510
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
        515                 520                 525
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
    530                 535                 540
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
545                 550                 555                 560
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
                565                 570                 575
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
            580                 585                 590
```

<210> 64
<211> 579
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC011 mature protein comprising : HD37 (anti-CD19) scFv, altered human IgA2 hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 64

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1               5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
        115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Pro Pro Pro Pro
                245                 250                 255
Pro Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
            260                 265                 270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275                 280                 285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    290                 295                 300
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
                325                 330                 335
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
            340                 345                 350
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        355                 360                 365
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
```

```
        435                 440                 445
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    450                 455                 460
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser
465                 470                 475                 480
Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
                485                 490                 495
Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
            500                 505                 510
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
        515                 520                 525
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
    530                 535                 540
Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
545                 550                 555                 560
Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
                565                 570                 575
Lys Lys Val
```

<210> 65
<211> 589
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC012 mature protein comprising : HD37 (anti-CD19) scFv, altered human IgG1 hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 65

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1                5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
        115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Glu Pro Lys Ser
                245                 250                 255
Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Cys Pro Pro Cys Pro
            260                 265                 270
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        275                 280                 285
```

```
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    290                 295                 300
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
305                 310                 315                 320
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
                325                 330                 335
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
            340                 345                 350
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        355                 360                 365
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    370                 375                 380
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
385                 390                 395                 400
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                405                 410                 415
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            420                 425                 430
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        435                 440                 445
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    450                 455                 460
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
465                 470                 475                 480
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Ala Ser Thr Lys Gly
                485                 490                 495
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
            500                 505                 510
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
        515                 520                 525
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
    530                 535                 540
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
545                 550                 555                 560
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
                565                 570                 575
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
            580                 585
```

<210> 66
<211> 589
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC013 mature protein comprising : HD37 (anti-CD19) scFv, altered human IgG3 hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 66

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1                   5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
        115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
```

```
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Glu Pro Lys Ser
                245                 250                 255
Ser Asp Thr Pro Pro Pro Ser Pro Arg Ser Pro Cys Pro Pro Cys Pro
            260                 265                 270
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        275                 280                 285
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    290                 295                 300
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
305                 310                 315                 320
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
                325                 330                 335
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
            340                 345                 350
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        355                 360                 365
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    370                 375                 380
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
385                 390                 395                 400
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                405                 410                 415
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            420                 425                 430
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        435                 440                 445
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    450                 455                 460
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
465                 470                 475                 480
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Ala Ser Thr Lys Gly
                485                 490                 495
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
            500                 505                 510
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
        515                 520                 525
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
    530                 535                 540
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
545                 550                 555                 560
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
                565                 570                 575
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
            580                 585
```

<210> 67
<211> 608
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC014 mature protein comprising : HD37 (anti-CD19) scFv, altered human IgD hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 67

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1               5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
        115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Glu Ser Pro Lys
                245                 250                 255
Ala Gln Ala Ser Ser Val Pro Thr Ala Gln Pro Gln Ala Glu Gly Ser
            260                 265                 270
Leu Ala Lys Ala Thr Thr Ala Pro Ala Thr Thr Arg Asn Thr Cys Pro
        275                 280                 285
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
    290                 295                 300
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
305                 310                 315                 320
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
                325                 330                 335
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
            340                 345                 350
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
        355                 360                 365
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
    370                 375                 380
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
385                 390                 395                 400
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
                405                 410                 415
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
            420                 425                 430
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
        435                 440                 445
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
    450                 455                 460
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
465                 470                 475                 480
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
                485                 490                 495
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Ala Ser
            500                 505                 510
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
        515                 520                 525
```

```
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
    530                 535                 540
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
545                 550                 555                 560
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
                565                 570                 575
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
            580                 585                 590
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
        595                 600                 605
```

<210> 68
<211> 680
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC015 mature protein comprising : HD37 (anti-CD19) scFv, altered human IgE CH2 hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 68

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1                   5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
        115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Ser Arg Asp Phe
                245                 250                 255
Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Ser Asp Gly Gly Gly
            260                 265                 270
His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr Thr
        275                 280                 285
Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met Asp
    290                 295                 300
Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala Ser
305                 310                 315                 320
Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp Arg
                325                 330                 335
Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp Ser
            340                 345                 350
Thr Lys Lys Ser Ala Cys Pro Pro Cys Ser Gly Ala Pro Glu Leu Leu
```

```
        355                 360                 365
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
    370                 375                 380
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
385                 390                 395                 400
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
                405                 410                 415
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
            420                 425                 430
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
        435                 440                 445
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
    450                 455                 460
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
465                 470                 475                 480
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
                485                 490                 495
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
            500                 505                 510
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
        515                 520                 525
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
    530                 535                 540
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
545                 550                 555                 560
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
                565                 570                 575
Ser Pro Gly Lys Ser Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
            580                 585                 590
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
        595                 600                 605
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
    610                 615                 620
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
625                 630                 635                 640
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
                645                 650                 655
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
            660                 665                 670
Asn Thr Lys Val Asp Lys Lys Val
        675                 680


<210> 69
<211> 687
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC016 mature protein comprising : HD37
      (anti-CD19) scFv, altered human IgM CH2 hinge,
      human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 69
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1                   5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
```

```
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
        115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Ile Ala Glu Leu
                245                 250                 255
Pro Pro Lys Val Ser Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly
            260                 265                 270
Asn Pro Arg Lys Ser Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro
        275                 280                 285
Arg Gln Ile Gln Val Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser
    290                 295                 300
Gly Val Thr Thr Asp Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro
305                 310                 315                 320
Thr Thr Tyr Lys Val Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp
                325                 330                 335
Leu Ser Gln Ser Met Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr
            340                 345                 350
Phe Gln Gln Asn Ala Ser Ser Met Ser Val Pro Cys Pro Pro Cys Pro
        355                 360                 365
Ser Gly Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
    370                 375                 380
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
385                 390                 395                 400
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
                405                 410                 415
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
            420                 425                 430
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
        435                 440                 445
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
    450                 455                 460
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
465                 470                 475                 480
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
                485                 490                 495
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            500                 505                 510
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        515                 520                 525
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    530                 535                 540
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
545                 550                 555                 560
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                565                 570                 575
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Ala Ser Thr
            580                 585                 590
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
        595                 600                 605
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
    610                 615                 620
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
625                 630                 635                 640
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
                645                 650                 655
```

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
660 665 670
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
675 680 685

<210> 70
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC017 mature protein comprising : P2C2 (anti-CD79b) scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3 and human CH1

<400> 70
Asp Ile Val Met Ile Gln Asp Glu Leu Ser Asn Pro Val Ser Ser Gly
1 5 10 15
Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asp Lys
20 25 30
Glu Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Leu Met Ser Met Arg Glu Ser Gly Val Ser
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile
65 70 75 80
Ser Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
85 90 95
Val Glu Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
115 120 125
Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr
130 135 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Phe Ser
145 150 155 160
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly
165 170 175
Trp Ile Asn Thr Glu Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Arg
180 185 190
Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu
195 200 205
Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Thr
210 215 220
Trp Ser Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser
225 230 235 240
Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
245 250 255
Ser Gly Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
260 265 270
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
275 280 285
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
290 295 300
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305 310 315 320
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
325 330 335
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
340 345 350
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
355 360 365
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
370 375 380
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385 390 395 400
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

```
                405                 410                 415
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
            420                 425                 430
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        435                 440                 445
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    450                 455                 460
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Ala Ser Thr
465                 470                 475                 480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
                485                 490                 495
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
            500                 505                 510
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
        515                 520                 525
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
    530                 535                 540
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
545                 550                 555                 560
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
                565                 570                 575
```

<210> 71
<211> 583
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC018 mature protein comprising : M0042 (anti-HLA-DR) scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3, and human CH1

<400> 71

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1                5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val
        35                  40                  45
Tyr Ser Val Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe
                85                  90                  95
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
        115                 120                 125
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
    130                 135                 140
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr Tyr
145                 150                 155                 160
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
                165                 170                 175
Tyr Ile Gly Pro Ser Gly Gly Phe Thr Ala Tyr Ala Asp Ser Val Lys
            180                 185                 190
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
        195                 200                 205
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
    210                 215                 220
Arg Asp Gly Trp Val Gly Ser Glu Asn Tyr Ser Gly Met Asp Val Trp
225                 230                 235                 240
Gly Gln Gly Thr Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys
                245                 250                 255
Thr His Thr Cys Pro Pro Cys Pro Ser Gly Ala Pro Glu Leu Leu Gly
            260                 265                 270
```

```
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
    290                 295                 300
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305                 310                 315                 320
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
                325                 330                 335
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
        355                 360                 365
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
    370                 375                 380
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
385                 390                 395                 400
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
        435                 440                 445
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480
Pro Gly Lys Ser Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
                485                 490                 495
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
            500                 505                 510
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
        515                 520                 525
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
    530                 535                 540
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
545                 550                 555                 560
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
                565                 570                 575
Thr Lys Val Asp Lys Lys Val
            580
```

<210> 72
<211> 590
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC019 mature protein comprising : G19-4 (anti-CD3) scFv, human IgG1 SCC-P hinge, human CH2, human CH3, and human Ck(YAE)

<400> 72

```
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1                 5                  10                  15
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
            20                  25                  30
Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
        35                  40                  45
Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
            100                 105                 110
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
```

```
        115                 120                 125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr
    130                 135                 140
Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
145                 150                 155                 160
Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
                165                 170                 175
Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
            180                 185                 190
Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
Asp Tyr Ser Leu Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr
    210                 215                 220
Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly
225                 230                 235                 240
Thr Lys Leu Val Thr Lys Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys
                245                 250                 255
Thr His Thr Cys Pro Pro Cys Pro Ser Gly Ala Pro Glu Leu Leu Gly
            260                 265                 270
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
    290                 295                 300
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305                 310                 315                 320
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
                325                 330                 335
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
        355                 360                 365
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
    370                 375                 380
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
385                 390                 395                 400
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
        435                 440                 445
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480
Pro Gly Lys Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                485                 490                 495
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
            500                 505                 510
Leu Asn Tyr Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
        515                 520                 525
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp
    530                 535                 540
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys
545                 550                 555                 560
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
                565                 570                 575
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
            580                 585                 590
```

<210> 73
<211> 2292
<212> DNA
<213> Artificial Sequence

<220>
<223> 4C04 (anti-RON) x G19-4 (anti-CD3) Scorpion DNA

sequence (SO266)

<400> 73
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gacattcaga tgacccagtc tcctgcctcc cagtctgcat ctctgggaga aagtgtcacc 120
atcacatgcc tggcaagtca gaccattggt acatggttag catggtatca gcagaaacca 180
gggaaatctc ctcagctcct gatttatgct gcaaccagct tggcagatgg ggtcccatca 240
aggttcagtg ctagtggatc tggcacaaaa ttttctttca agatcgacag cctacagtct 300
gaagattttg taagttatta ctgtcaacaa ctttacaata ctccgtggac gttcggtgga 360
ggcaccaagc tggaaatcaa aggtggcggt ggctctggcg gaggtggatc cggtggcggc 420
ggctctcaga tccagctgca gcagtctgga cctgagctgg tgaagcctgg gacttcagtg 480
aagatatcct gcaaggcttc tgactacaca ctcactgact tctatatgaa ctgggtgagg 540
cagaagcctg gacagggact tgagtggatt gggaggattt atcctggaac cgataaaact 600
agatacaatg agaaattcag ggacaaggcc atactgaccg tggacacgtc ctccagcaca 660
gcctacatgc agctcagcag cctgacatca gaggacactg ctgtctattt ctgtgcaaga 720
tccgcctact atggtaacta cgttgctatg gactactggg gtcaaggaac ctcagtcacc 780
gtctcctcga gcgagcccaa atcttctgac aaaactcaca catgcccacc gtgcccagca 840
cctgaactcc tgggtggacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 900
atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 960
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 1020
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 1080
gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 1140
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1200
cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1260
ttctatccaa gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1320
aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc 1380
gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1440
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtcagag gcacaacaat 1500
tcttccctga atacaggaac tcagatggca ggtcattctc cgaattctga ggtccagctg 1560
caacagtctg gacctgaact ggtgaagcct ggagcttcaa tgaagatttc ctgcaaggcc 1620
tctggttact cattcactgg ctacatcgtg aactggctga agcagagcca tggaaagaac 1680
cttgagtgga ttggacttat taatccatac aaaggtctta ctacctacaa ccagaaattc 1740
aagggcaagg ccacattaac tgtagacaag tcatccagca cagcctacat ggagctcctc 1800
agtctgacat ctgaagactc tgcagtctat tactgtgcaa gatctgggta ctatggtgac 1860
tcggactggt acttcgatgt ctggggcgca gggaccacgg tcaccgtctc aagcggtggc 1920
ggagggtctg ggggtggcgg atccggaggt ggtggctctg cacaagacat ccagatgaca 1980
cagactacat cctccctgtc tgcctctctg ggagacagag tcaccatcag ttgcagggca 2040
agtcaggaca ttcgcaatta tttaaactgg tatcagcaga aaccagatgg aactgttaaa 2100
ctcctgatct actacacatc aagattacac tcaggagtcc catcaaggtt cagtggcagt 2160
gggtctggaa cagattattc tctcaccatt gccaacctgc aaccagaaga tattgccact 2220
tacttttgcc aacagggtaa tacgcttccg tggacgttcg gtggaggcac caaactggta 2280
accaaacgat aa 2292

<210> 74
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> 4C04 (anti-RON) x G19-4 (anti-CD3) Scorpion mature protein sequence (SO266)

<400> 74
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Gln Ser Ala Ser Leu Gly
 1   5   10   15
Glu Ser Val Thr Ile Thr Cys Leu Ala Ser Gln Thr Ile Gly Thr Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile
        35   40   45
Tyr Ala Ala Thr Ser Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Ala
    50   55   60
Ser Gly Ser Gly Thr Lys Phe Ser Phe Lys Ile Asp Ser Leu Gln Ser
65   70   75   80
Glu Asp Phe Val Ser Tyr Tyr Cys Gln Gln Leu Tyr Asn Thr Pro Trp
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
            100   105   110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile Gln Leu Gln Gln

```
        115                 120                 125
Ser Gly Pro Glu Leu Val Lys Pro Gly Thr Ser Val Lys Ile Ser Cys
    130                 135                 140
Lys Ala Ser Asp Tyr Thr Leu Thr Asp Phe Tyr Met Asn Trp Val Arg
145                 150                 155                 160
Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly
                165                 170                 175
Thr Asp Lys Thr Arg Tyr Asn Glu Lys Phe Arg Asp Lys Ala Ile Leu
            180                 185                 190
Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
        195                 200                 205
Thr Ser Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg Ser Ala Tyr Tyr
    210                 215                 220
Gly Asn Tyr Val Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
225                 230                 235                 240
Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
                245                 250                 255
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
            260                 265                 270
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
        275                 280                 285
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
    290                 295                 300
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
305                 310                 315                 320
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
                325                 330                 335
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
            340                 345                 350
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
        355                 360                 365
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
    370                 375                 380
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
385                 390                 395                 400
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
                405                 410                 415
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
            420                 425                 430
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
        435                 440                 445
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
    450                 455                 460
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn
465                 470                 475                 480
Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser
                485                 490                 495
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
            500                 505                 510
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
        515                 520                 525
Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
    530                 535                 540
Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr Asn Gln Lys Phe
545                 550                 555                 560
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
                565                 570                 575
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
            580                 585                 590
Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
        595                 600                 605
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
    610                 615                 620
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr
625                 630                 635                 640
Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
                645                 650                 655
Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
```

660 665 670
Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
675 680 685
Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
690 695 700
Asp Tyr Ser Leu Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr
705 710 715 720
Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly
725 730 735
Thr Lys Leu Val Thr Lys Arg
740

<210> 75

<400> 75
000

<210> 76

<400> 76
000

<210> 77
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutated M0039

<220>
<221> SIGNAL
<222> (1)...(22)

<400> 77
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
-20 -15 -10
Val Ile Met Ser Arg Gly Val Gln Val Gln Leu Lys Glu Ser Gly Pro
-5 1 5 10
Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser
15 20 25
Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp Val Arg Gln Pro Pro
30 35 40
Gly Lys Gly Leu Glu Trp Leu Gly Met Ile Trp Gly Asp Gly Ser Thr
45 50 55
Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser Ile Thr Lys Asp Asn
60 65 70
Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp
75 80 85 90
Thr Ala Arg Tyr Tyr Cys Ala Arg Asp Gly Tyr Ser Asn Phe His Tyr
95 100 105
Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
110 115 120
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
125 130 135
Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
140 145 150
Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser
155 160 165 170
Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro
175 180 185
Gly Gln Pro Pro Lys Leu Leu Ile Ser Ala Ala Ser Asn Val Glu Ser
190 195 200
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser
205 210 215
Leu Asn Ile His Pro Val Glu Glu Asp Asp Ile Ala Met Tyr Phe Cys
220 225 230

```
Gln Gln Ser Arg Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
235                 240                 245                 250
Glu Ile Lys Arg Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr
                255                 260                 265
Ser Pro Pro Ser Pro Ala Pro Glu Leu Gly Gly Pro Ser Val Phe
            270                 275                 280
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
        285                 290                 295
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
    300                 305                 310
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
315                 320                 325                 330
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
                335                 340                 345
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
            350                 355                 360
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
        365                 370                 375
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
    380                 385                 390
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
395                 400                 405                 410
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                415                 420                 425
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            430                 435                 440
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
        445                 450                 455
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
    460                 465                 470
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
475                 480                 485
```

<210> 78
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H68 linker (scorpion linker derived from NKG2D)

<400> 78

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Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
 1               5                  10                  15
Ser Pro Asn Ser
            20
```

<210> 79
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> VH of A2

<400> 79

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gaagttcaat tgttagagtc tggtggcggt cttgttcagc ctggtggttc tttacgtctt 60
tcttgcgctg cttccggatt cactttctct ttttaccaga tgcattgggt tcgccaagct 120
cctggtaaag gtttggagtg ggtttctggt atctatcctt ctggtggcta tactaagtat 180
gctgactccg ttaaaggtcg cttcactatc tctagagaca actctaagaa tactctctac 240
ttgcagatga acagcttaag ggctgaggac actgcagtct actattgtgc gagagatcta 300
gggtacggca gtagctggta ctactttgac tactggggcc agggaaccct ggtcaccgtc 360
tcaagc                                                          366
```

<210> 80
<211> 122

<212> PRT
<213> Artificial Sequence

<220>
<223> VH of A2

<400> 80
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Phe Tyr
            20   25   30
Gln Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Tyr Pro Ser Gly Gly Tyr Thr Lys Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Asp Leu Gly Tyr Gly Ser Ser Trp Tyr Tyr Phe Asp Tyr Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 81
<400> 81
 000

<210> 82
<400> 82
 000

<210> 83
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> VL of A2

<400> 83
cagagcgctt tgactcagcc tgcctccgtg tctgggtctc ctggacagtc gatcaccatc 60
tcctgcagtg gaaccgacag tgacgttggt ggttataacc atgtctcctg gtaccaacaa 120
cacccaggca aggcccccaa actcataatt tatgatgtcg atcatcggcc ctcagggatc 180
tctaaccgtt tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240
caggctgagg acgaggctga ttattactgc agctcatata gaagcggtag cacttatgtc 300
ttcggaactg ggaccaaggt caccgtccta   330

<210> 84
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> VL of A2

<400> 84
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1   5   10   15
Ser Ile Thr Ile Ser Cys Ser Gly Thr Asp Ser Asp Val Gly Gly Tyr
            20   25   30
Asn His Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35   40   45
Ile Ile Tyr Asp Val Asp His Arg Pro Ser Gly Ile Ser Asn Arg Phe
    50   55   60
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65   70   75   80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Arg Ser Gly
85 90 95
Ser Thr Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 85
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> A2 scFv

<400> 85
gaagttcaat tgttagagtc tggtggcggt cttgttcagc ctggtggttc tttacgtctt 60
tcttgcgctg cttccggatt cactttctct ttttaccaga tgcattgggt tcgccaagct 120
cctggtaaag gtttggagtg ggtttctggt atctatcctt ctggtggcta tactaagtat 180
gctgactccg ttaaaggtcg cttcactatc tctagagaca actctaagaa tactctctac 240
ttgcagatga acagcttaag ggctgaggac actgcagtct actattgtgc gagagatcta 300
gggtacggca gtagctggta ctactttgac tactggggcc agggaaccct ggtcaccgtc 360
tcaagcggtg gcggcggttc gggggggtggc ggaagtggag gtggagggag tcagagcgct 420
ttgactcagc ctgcctccgt gtctgggtct cctggacagt cgatcaccat ctcctgcagt 480
ggaaccgaca gtgacgttgg tggttataac catgtctcct ggtaccaaca acacccaggc 540
aaggccccca aactcataat ttatgatgtc gatcatcggc cctcagggat ctctaaccgt 600
ttctctggct ccaagtctgg caacacggcc tccctgacca tctctgggct ccaggctgag 660
gacgaggctg attattactg cagctcatat agaagcggta gcacttatgt cttcggaact 720
gggaccaagg tcaccgtcct a 741

<210> 86
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> A2 scFv

<400> 86
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Phe Tyr
20 25 30
Gln Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Tyr Pro Ser Gly Gly Tyr Thr Lys Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp Leu Gly Tyr Gly Ser Ser Trp Tyr Tyr Phe Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Ala Leu Thr Gln Pro
130 135 140
Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Ser
145 150 155 160
Gly Thr Asp Ser Asp Val Gly Gly Tyr Asn His Val Ser Trp Tyr Gln
165 170 175
Gln His Pro Gly Lys Ala Pro Lys Leu Ile Ile Tyr Asp Val Asp His
180 185 190
Arg Pro Ser Gly Ile Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn
195 200 205
Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp
210 215 220
Tyr Tyr Cys Ser Ser Tyr Arg Ser Gly Ser Thr Tyr Val Phe Gly Thr
225 230 235 240

Gly Thr Lys Val Thr Val Leu
245

<210> 87
<211> 603
<212> DNA
<213> Artificial Sequence

<220>
<223> PLD ECD

<400> 87
ttattcacag tgacagtccc taaggaactg tacataatag agcatggcag caatgtgacc 60
ctggaatgca actttgacac tggaagtcat gtgaaccttg gagcaataac agccagtttg 120
caaaaggtgg aaaatgatac atccccacac cgtgaaagag ccactttgct ggaggagcag 180
ctgcccttag ggaaggcctc gttccacata cctcaagtcc aagtgaggga cgaaggacag 240
taccaatgca taatcatcta tggggtcgcc tgggactaca agtacctgac tctgaaagtc 300
aaagcttcct acaggaaaat aaacactcac atcctaaagg ttccagaaac agatgaggta 360
gagctcacct gccaggctac aggttatcct ctggcagaag tatcctggcc aaacgtcagc 420
gttcctgcca acaccagcca ctccaggacc cctgaaggcc tctaccaggt caccagtgtt 480
ctgcgcctaa agccaccccc tggcagaaac ttcagctgtg tgttctggaa tactcacgtg 540
agggaactta ctttggccag cattgacctt caaagtcaga tggaacccag gacccatcca 600
acc 603

<210> 88
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> PLD ECD

<400> 88
Leu Phe Thr Val Thr Val Pro Lys Glu Leu Tyr Ile Ile Glu His Gly
 1   5   10   15
Ser Asn Val Thr Leu Glu Cys Asn Phe Asp Thr Gly Ser His Val Asn
            20   25   30
Leu Gly Ala Ile Thr Ala Ser Leu Gln Lys Val Glu Asn Asp Thr Ser
        35   40   45
Pro His Arg Glu Arg Ala Thr Leu Leu Glu Glu Gln Leu Pro Leu Gly
    50   55   60
Lys Ala Ser Phe His Ile Pro Gln Val Gln Val Arg Asp Glu Gly Gln
65   70   75   80
Tyr Gln Cys Ile Ile Ile Tyr Gly Val Ala Trp Asp Tyr Lys Tyr Leu
                85   90   95
Thr Leu Lys Val Lys Ala Ser Tyr Arg Lys Ile Asn Thr His Ile Leu
            100   105   110
Lys Val Pro Glu Thr Asp Glu Val Glu Leu Thr Cys Gln Ala Thr Gly
        115   120   125
Tyr Pro Leu Ala Glu Val Ser Trp Pro Asn Val Ser Val Pro Ala Asn
    130   135   140
Thr Ser His Ser Arg Thr Pro Glu Gly Leu Tyr Gln Val Thr Ser Val
145   150   155   160
Leu Arg Leu Lys Pro Pro Pro Gly Arg Asn Phe Ser Cys Val Phe Trp
                165   170   175
Asn Thr His Val Arg Glu Leu Thr Leu Ala Ser Ile Asp Leu Gln Ser
            180   185   190
Gln Met Glu Pro Arg Thr His Pro Thr
        195   200

<210> 89
<211> 498
<212> DNA
<213> Artificial Sequence

<220>

<223> monoIL10

<400> 89
agcccaggcc agggcaccca gtctgagaac agctgcaccc acttcccagg caacctgcct 60
aacatgcttc gagatctccg agatgccttc agcagagtga agactttctt tcaaatgaag 120
gatcagctgg acaacttgtt gttaaaggag tccttgctgg aggactttaa gggttacctg 180
ggttgccaag ccttgtctga gatgatccag ttttacctgg aggaggtgat gccccaagct 240
gagaaccaag acccagacat caaggcgcat gtgaactccc tgggggagaa cctgaagacc 300
ctcaggctga ggctacggcg ctgtcatcga tttcttccct gtgaaaacgg tggtggatcc 360
ggcggtaaga gcaaggccgt ggagcaggtg aagaatgcct ttaataagct ccaagagaaa 420
ggcatctaca aagccatgag tgagtttgac atcttcatca actacataga agcctacatt 480
acaatgaaga tacgaaac 498

<210> 90
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> monoIL10

<400> 90
Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15
Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30
Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45
Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
50 55 60
Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
65 70 75 80
Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
85 90 95
Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110
Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu
115 120 125
Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys
130 135 140
Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Ile
145 150 155 160
Thr Met Lys Ile Arg Asn
165

<210> 91
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> VH of 3D1

<400> 91
caggtccagc tgcagcagtc tgggcctgag ctggtgaggc ctggggaatc agtgaagatt 60
tcctgcaagg gttccggcta cacattcact gattatgcta tacagtgggt gaagcagagt 120
catgcaaaga gtctagagtg gattggagtt attaatattt actatgataa tacaaactac 180
aaccagaagt ttaagggcaa ggccacaatg actgtagaca aatcctccag cacagcctat 240
atggaacttg ccagattgac atctgaggat tctgccatct attactgtgc aagagcggcc 300
tggtatatgg actactgggg tcaaggaacc tcagtcaccg tctcctca 348

<210> 92
<211> 116
<212> PRT
<213> Artificial Sequence

<220>

<223> VH of 3D1

<400> 92

```
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Glu
 1               5                  10                  15
Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30
Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile
        35                  40                  45
Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
                85                  90                  95
Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
            100                 105                 110
Thr Val Ser Ser
        115
```

<210> 93
<400> 93
000

<210> 94
<400> 94
000

<210> 95
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> VL of 3D1

<400> 95

```
gacattgtgc tgtcacagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60
atgagctgca aatccagtca gagtctgctc aacagtagaa cccgagagaa ctacttggct 120
tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180
gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240
atcagcagtg tgcaggctga agacctggca gtttattact gcacgcaatc ttataatctt 300
tacacgttcg gaggggggac caagctggaa ataaaa                           336
```

<210> 96
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> VL of 3D1

<400> 96

```
Asp Ile Val Leu Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
 1               5                  10                  15
Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
            20                  25                  30
Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Thr Gln
                85                  90                  95
Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 97
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> 3D1 scFv

<400> 97
caggtccagc tgcagcagtc tgggcctgag ctggtgaggc ctggggaatc agtgaagatt 60
tcctgcaagg gttccggcta cacattcact gattatgcta tacagtgggt gaagcagagt 120
catgcaaaga gtctagagtg gattggagtt attaatattt actatgataa tacaaactac 180
aaccagaagt ttaagggcaa ggccacaatg actgtagaca aatcctccag cacagcctat 240
atggaacttg ccagattgac atctgaggat tctgccatct attactgtgc aagagcggcc 300
tggtatatgg actactgggg tcaaggaacc tcagtcaccg tctcctcagg gggtggaggc 360
tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctga cattgtgctg 420
tcacagtctc catcctccct ggctgtgtca gcaggagaga aggtcactat gagctgcaaa 480
tccagtcaga gtctgctcaa cagtagaacc cgagagaact acttggcttg gtaccagcag 540
aaaccagggc agtctcctaa actgctgatc tactgggcat ccactaggga atctggggtc 600
cctgatcgct tcacaggcag tggatctggg acagatttca ctctcaccat cagcagtgtg 660
caggctgaag acctggcagt ttattactgc acgcaatctt ataatcttta cacgttcgga 720
gggggggacca agctggaaat aaaa 744

<210> 98
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D1 scFv

<400> 98
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Glu
 1   5   10   15
Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30
Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile
        35   40   45
Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
                85   90   95
Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
            100   105   110
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        115   120   125
Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Ser Gln Ser Pro
    130   135   140
Ser Ser Leu Ala Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys
145   150   155   160
Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala
                165   170   175
Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp
            180   185   190
Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly
        195   200   205
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp
    210   215   220
Leu Ala Val Tyr Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly
225   230   235   240
Gly Gly Thr Lys Leu Glu Ile Lys
                245

<210> 99
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> MET021 scFv

<400> 99
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Asn Tyr
            20   25   30
Leu Asn Trp Tyr Gln Gln Glu Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Val Thr Pro Leu
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
            100   105   110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
        115   120   125
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
    130   135   140
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr Asp
145   150   155   160
Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
                165   170   175
Tyr Ile Tyr Pro Ser Gly Gly Leu Thr Glu Tyr Ala Asp Ser Val Lys
            180   185   190
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
        195   200   205
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
    210   215   220
Arg Arg Ala Pro Arg Ser Leu Ser Phe Asp Ile Trp Gly Gln Gly Thr
225   230   235   240
Met Val Thr Val Ser Ser Ser
                245

<210> 100
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> VH of MET021 scFv

<400> 100
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
            20   25   30
Asp Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Tyr Ile Tyr Pro Ser Gly Gly Leu Thr Glu Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Arg Ala Pro Arg Ser Leu Ser Phe Asp Ile Trp Gly Gln Gly
            100   105   110
Thr Met Val Thr Val Ser Ser Ser
        115   120

<210> 101
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL of MET021 scFv

<400> 101
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Asn Tyr
            20   25   30
Leu Asn Trp Tyr Gln Gln Glu Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Val Thr Pro Leu
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 102
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> G19-4 scFv

<400> 102
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1   5   10   15
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
            20   25   30
Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
        35   40   45
Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr Asn Gln Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
            100   105   110
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115   120   125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr
    130   135   140
Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
145   150   155   160
Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
                165   170   175
Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
            180   185   190
Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195   200   205
Asp Tyr Ser Leu Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr
    210   215   220
Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly
225   230   235   240
Thr Lys Leu Val Thr Lys Arg Ser Ser
                245

<210> 103
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> VH of G19-4

<400> 103
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1   5   10   15
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
            20   25   30
Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
        35   40   45
Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr Asn Gln Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
            100   105   110
Gly Ala Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 104
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> VL of G19-4

<400> 104
Ala Gln Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser
 1   5   10   15
Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Arg
            20   25   30
Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu
        35   40   45
Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe
    50   55   60
Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ala Asn Leu
65   70   75   80
Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
                85   90   95
Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Val Thr Lys Arg Ser Ser
            100   105   110

<210> 105
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> HD37 scFv

<400> 105
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20   25   30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro

```
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
        115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser
                245                 250
```

<210> 106
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> VH of 2E12 scFv

<400> 106

```
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Ser Val Ala Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr
            20                  25                  30
Gly Val Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Met Ile Trp Gly Asp Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys
    50                  55                  60
Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala
                85                  90                  95
Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr Val Met Asp Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Ser Val Thr Val Ser Ser
        115                 120
```

<210> 107
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> VL of 2E12 scFv

<400> 107

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1               5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr
```

```
            20                  25                  30
Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Ser Ala Ala Ser Asn Val Glu Ser Gly Val Pro Ala
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Glu Asp Asp Ile Ala Met Tyr Phe Cys Gln Gln Ser Arg
                85                  90                  95
Lys Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210> 108
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker of 2E12 scFv

<400> 108
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1               5                  10                  15
Gly Gly Gly Ser
            20


<210> 109
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> full length 2E12 scFv

<400> 109
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Ser Val Ala Pro Ser Gln
 1               5                  10                  15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr
            20                  25                  30
Gly Val Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
Gly Met Ile Trp Gly Asp Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys
    50                  55                  60
Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala
                85                  90                  95
Arg Asp Gly Tyr Ser Asn Phe His Tyr Tyr Val Met Asp Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
    130                 135                 140
Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala
145                 150                 155                 160
Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser
                165                 170                 175
Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
            180                 185                 190
Ile Ser Ala Ala Ser Asn Val Glu Ser Gly Val Pro Ala Arg Phe Ser
        195                 200                 205
Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Asn Ile His Pro Val Glu
    210                 215                 220
Glu Asp Asp Ile Ala Met Tyr Phe Cys Gln Gln Ser Arg Lys Val Pro
225                 230                 235                 240
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
```

245 250

<210> 110
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal peptide of 2E12 scFv

<400> 110
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly
20

<210> 111
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal peptide in various signle chain fusion proteins (X01xx)

<400> 111
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15
Asp Thr Thr Gly
20

<210> 112
<211> 107
<212> PRT
<213> Homo sapiens

<400> 112
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 113
<211> 106
<212> PRT
<213> Homo sapiens

<400> 113
Gly Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser
1 5 10 15
Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
20 25 30
Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro
35 40 45

```
Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn
    50                  55                  60
Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65                  70                  75                  80
Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
                85                  90                  95
Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
            100                 105
```

<210> 114
<211> 98
<212> PRT
<213> Homo sapiens

<400> 114

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1               5                  10                  15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
Lys Val
```

<210> 115
<211> 110
<212> PRT
<213> Homo sapiens

<400> 115

```
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1               5                  10                  15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        35                  40                  45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100                 105                 110
```

<210> 116
<211> 107
<212> PRT
<213> Homo sapiens

<400> 116

```
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 1               5                  10                  15
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            20                  25                  30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        35                  40                  45
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    50                  55                  60
```

```
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65                  70                  75                  80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                85                  90                  95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            100                 105
```

<210> 117
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> VH of HD37

<400> 117

```
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
 1               5                  10                  15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
            20                  25                  30
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95
Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
            100                 105                 110
Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser
        115                 120                 125
```

<210> 118
<400> 118
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<210> 119
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> VL of HD37

<400> 119

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1               5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 120
<211> 249
<212> PRT

<213> Artificial Sequence

<220>
<223> M0042 scFv (VL-VH)

<400> 120

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val
        35                  40                  45
Tyr Ser Val Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe
                85                  90                  95
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
        115                 120                 125
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
    130                 135                 140
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr Tyr
145                 150                 155                 160
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
                165                 170                 175
Tyr Ile Gly Pro Ser Gly Gly Phe Thr Ala Tyr Ala Asp Ser Val Lys
            180                 185                 190
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
        195                 200                 205
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
    210                 215                 220
Arg Asp Gly Trp Val Gly Ser Glu Asn Tyr Ser Gly Met Asp Val Trp
225                 230                 235                 240
Gly Gln Gly Thr Thr Val Ser Ser Ser
                245
```

<210> 121
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> VH of M0042

<400> 121

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
            20                  25                  30
Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Ser Tyr Ile Gly Pro Ser Gly Gly Phe Thr Ala Tyr Ala Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Asp Gly Trp Val Gly Ser Glu Asn Tyr Ser Gly Met Asp Val
            100                 105                 110
Trp Gly Gln Gly Thr Thr Val Ser Ser Ser
        115                 120
```

<210> 122

<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL of M0042

<400> 122
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val
        35   40   45
Tyr Ser Val Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe
                85   90   95
Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 123
<400> 123
 000

<210> 124
<400> 124
 000

<210> 125
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> NKG2D Linker

<400> 125
Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
 1   5   10   15
Ser Pro Asn Ser
            20

<210> 126
<400> 126
 000

<210> 127
<400> 127
 000

<210> 128
<400> 128
 000

<210> 129
<400> 129
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<210> 130
<400> 130
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<210> 131
<400> 131
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<210> 132
<400> 132
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<210> 133
<400> 133
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<210> 134
<400> 134
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<210> 135
<400> 135
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<210> 136
<400> 136
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<210> 137
<400> 137
000

<210> 138
<400> 138
000

<210> 139
<400> 139
000

<210> 140
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Cl sequence used in constructing Interceptors

<400> 140

Gln	Pro	Lys	Ala	Asn	Pro	Thr	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu
1				5				10						15	
Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	Phe
			20					25					30		
Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Gly	Ser	Pro	Val
		35					40					45			
Lys	Ala	Gly	Val	Glu	Thr	Thr	Lys	Pro	Ser	Lys	Gln	Ser	Asn	Asn	Lys
	50					55					60				
Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser
65					70					75					80
His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	Glu
				85					90					95	
Lys	Thr	Val	Ala	Pro	Thr	Glu	Ser	Ser							
			100					105							

<210> 141
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck sequence used in constructing Interceptors

<400> 141
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 142
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with N29A substitution

<400> 142
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Ala Asn Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 143
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with N30A substitution

<400> 143
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Ala Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 144
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with Q52A substitution

<400> 144
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Ala Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 145
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with V55A substitution

<400> 145
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 146
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with T56A substitution

<400> 146
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Val Ala Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys

65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 147
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with S68A substitution

<400> 147
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ala Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 148
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with T70A substitution

<400> 148
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Ala Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 149
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with V55A N29A substitution

<400> 149
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15

```
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Ala Asn Phe Tyr
            20                  25                  30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35                  40                  45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50                  55                  60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65                  70                  75                  80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85                  90                  95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100                 105
```

<210> 150
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with V55A N30A substitution

<400> 150

```
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1               5                  10                  15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Ala Phe Tyr
            20                  25                  30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35                  40                  45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50                  55                  60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65                  70                  75                  80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85                  90                  95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100                 105
```

<210> 151
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with V55A Q52A substitution

<400> 151

```
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1               5                  10                  15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20                  25                  30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35                  40                  45
Gly Asn Ser Ala Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50                  55                  60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65                  70                  75                  80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85                  90                  95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100                 105
```

<210> 152
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with V55A S68A substitution

<400> 152
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ala Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 153
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with V55A T70A substitution

<400> 153
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Ala Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 154
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with V55A N29A N30A substitution

<400> 154
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Ala Ala Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu

100 105

<210> 155
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with V55A N29A S68A substitution

<400> 155
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Ala Asn Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ala Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 156
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with V55A S68A T70A substitution

<400> 156
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ala Ser Ala Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 157
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with V55A Q52A S68A substitution

<400> 157
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45

Gly Asn Ser Ala Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ala Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 158
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with N29R V55A T70A substitution

<400> 158
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Arg Asn Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Ala Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 159
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with N29AK V55A T70A substitution

<400> 159
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Lys Asn Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Ala Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 160
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with N29W V55A T70A substitution

<400> 160
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Trp Asn Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Ala Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 161
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with N29Y V55A T70A substitution

<400> 161
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Tyr Asn Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Ala Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 162
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with S68K V55A substitution

<400> 162
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Lys Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 163

<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with S68E V55A substitution

<400> 163
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Glu Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 164
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with S68Q V55A substitution

<400> 164
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Gln Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 165
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with T70E V55A substitution

<400> 165
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 166
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with Q52L N29A N30A substitution

<400> 166
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Ala Ala Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Leu Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 167
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with N30R V55A T70A substitution

<400> 167
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Arg Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Ala Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 168
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with N30K V55A T70A substitution

<400> 168
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Lys Phe Tyr

20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Ala Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 169
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with N30W V55A T70A substitution

<400> 169
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Trp Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Ala Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 170
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with N30E V55A T70A substitution

<400> 170
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Glu Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Ala Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 171
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with N30G V55A T70A substitution

<400> 171
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Gly Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Ala Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 172
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with V55R N29A N30A substitution

<400> 172
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Ala Ala Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Arg Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 173
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with V55W N29A N30A substitution

<400> 173
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Ala Ala Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Trp Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 174
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with V55E N29A N30A substitution

<400> 174
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Ala Ala Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Glu Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 175
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with N29W N30Y V55A T70E (WYAE)
      substitution

<400> 175
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Trp Tyr Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35   40   45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50   55   60
Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65   70   75   80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85   90   95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100   105

<210> 176
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with N29Y N30Y V55A T70E (YYAE)
      substitution

<400> 176
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1   5   10   15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Tyr Tyr Phe Tyr
            20   25   30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser

```
        35                  40                  45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50                  55                  60
Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65                  70                  75                  80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85                  90                  95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100                 105
```

<210> 177
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with N30E V55A T70E (EAE)
substitution

<400> 177

```
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1               5                  10                  15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Glu Phe Tyr
            20                  25                  30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35                  40                  45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50                  55                  60
Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65                  70                  75                  80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85                  90                  95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100                 105
```

<210> 178
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck with N30Y V55A T70E (YAE)
substitution

<400> 178

```
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1               5                  10                  15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr
            20                  25                  30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35                  40                  45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50                  55                  60
Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65                  70                  75                  80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                85                  90                  95
Val Thr Lys Ser Phe Asn Arg Gly Glu
            100                 105
```

<210> 179
<400> 179
000

<210> 180

<400> 180
000

<210> 181
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Portion of human IgG1 hinge

<400> 181
Cys Pro Pro Cys
1

<210> 182
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> VL of P2C2 scFv

<400> 182
Asp Ile Val Met Ile Gln Asp Glu Leu Ser Asn Pro Val Ser Ser Gly
1 5 10 15
Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asp Lys
20 25 30
Glu Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Leu Met Ser Met Arg Glu Ser Gly Val Ser
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile
65 70 75 80
Ser Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
85 90 95
Val Glu Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 183
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker of P2C2 scFv

<400> 183
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 184
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> VH of P2C2 scFv

<400> 184
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Phe
20 25 30

```
Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
        35                  40                  45
Gly Trp Ile Asn Thr Glu Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
    50                  55                  60
Arg Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
                85                  90                  95
Thr Trp Ser Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
            100                 105                 110
```

<210> 185
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> full length of P2C2 scFv

<400> 185

```
Asp Ile Val Met Ile Gln Asp Glu Leu Ser Asn Pro Val Ser Ser Gly
 1               5                  10                  15
Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asp Lys
            20                  25                  30
Glu Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser
        35                  40                  45
Pro Gln Leu Leu Ile Tyr Leu Met Ser Met Arg Glu Ser Gly Val Ser
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile
65                  70                  75                  80
Ser Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
                85                  90                  95
Val Glu Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
        115                 120                 125
Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Phe Ser
145                 150                 155                 160
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly
                165                 170                 175
Trp Ile Asn Thr Glu Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Arg
            180                 185                 190
Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu
        195                 200                 205
Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Thr
    210                 215                 220
Trp Ser Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
225                 230                 235
```

<210> 186
<211> 102
<212> PRT
<213> Homo sapiens

<400> 186

```
Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr
 1               5                  10                  15
Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe
            20                  25                  30
Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val
        35                  40                  45
Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr
    50                  55                  60
Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly
```

65 70 75 80
Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp
85 90 95
Val Thr Val Pro Cys Pro
100

<210> 187
<211> 102
<212> PRT
<213> Homo sapiens

<400> 187
Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Asp Ser Thr
1 5 10 15
Pro Gln Asp Gly Asn Val Val Val Ala Cys Leu Val Gln Gly Phe Phe
20 25 30
Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Asn Val
35 40 45
Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr
50 55 60
Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Pro Asp Gly
65 70 75 80
Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp
85 90 95
Val Thr Val Pro Cys Pro
100

<210> 188
<211> 101
<212> PRT
<213> Homo sapiens

<400> 188
Ala Pro Thr Lys Ala Pro Asp Val Phe Pro Ile Ile Ser Gly Cys Arg
1 5 10 15
His Pro Lys Asp Asn Ser Pro Val Val Leu Ala Cys Leu Ile Thr Gly
20 25 30
Tyr His Pro Thr Ser Val Thr Val Thr Trp Tyr Met Gly Thr Gln Ser
35 40 45
Gln Pro Gln Arg Thr Phe Pro Glu Ile Gln Arg Arg Asp Ser Tyr Tyr
50 55 60
Met Thr Ser Ser Gln Leu Ser Thr Pro Leu Gln Gln Trp Arg Gln Gly
65 70 75 80
Glu Tyr Lys Cys Val Val Gln His Thr Ala Ser Lys Ser Lys Lys Glu
85 90 95
Ile Phe Arg Trp Pro
100

<210> 189
<211> 103
<212> PRT
<213> Homo sapiens

<400> 189
Ala Ser Thr Gln Ser Pro Ser Val Phe Pro Leu Thr Arg Cys Cys Lys
1 5 10 15
Asn Ile Pro Ser Asn Ala Thr Ser Val Thr Leu Gly Cys Leu Ala Thr
20 25 30
Gly Tyr Phe Pro Glu Pro Val Met Val Thr Cys Asp Thr Gly Ser Leu
35 40 45
Asn Gly Thr Thr Met Thr Leu Pro Ala Thr Thr Leu Thr Leu Ser Gly
50 55 60
His Tyr Ala Thr Ile Ser Leu Leu Thr Val Ser Gly Ala Trp Ala Lys
65 70 75 80
Gln Met Phe Thr Cys Arg Val Ala His Thr Pro Ser Ser Thr Asp Trp

85 90 95
Val Asp Asn Lys Thr Phe Ser
100

<210> 190
<211> 98
<212> PRT
<213> Homo sapiens

<400> 190
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65 70 75 80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95
Thr Val

<210> 191
<211> 98
<212> PRT
<213> Homo sapiens

<400> 191
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80
Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95
Arg Val

<210> 192
<211> 98
<212> PRT
<213> Homo sapiens

<400> 192
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15
Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95
Arg Val

<210> 193
<400> 193
000

<210> 194
<211> 104
<212> PRT
<213> Homo sapiens

<400> 194
Gly Ser Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn
1 5 10 15
Ser Pro Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp
20 25 30
Phe Leu Pro Asp Ser Ile Thr Leu Ser Trp Lys Tyr Lys Asn Asn Ser
35 40 45
Asp Ile Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys
50 55 60
Tyr Ala Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln
65 70 75 80
Gly Thr Asp Glu His Val Val Cys Lys Val Gln His Pro Asn Gly Asn
85 90 95
Lys Glu Lys Asn Val Pro Leu Pro
100

<210> 195
<211> 101
<212> PRT
<213> Homo sapiens

<400> 195
Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu
1 5 10 15
Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr Gly Leu Arg
20 25 30
Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser
35 40 45
Ala Val Gln Gly Pro Pro Glu Arg Asp Leu Cys Gly Cys Tyr Ser Val
50 55 60
Ser Ser Val Leu Pro Gly Cys Ala Glu Pro Trp Asn His Gly Lys Thr
65 70 75 80
Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys Thr Pro Leu Thr Ala
85 90 95
Thr Leu Ser Lys Ser
100

<210> 196
<211> 101
<212> PRT
<213> Homo sapiens

<400> 196
Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu
1 5 10 15
Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr Gly Leu Arg
20 25 30
Asp Ala Ser Gly Ala Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser
35 40 45
Ala Val Gln Gly Pro Pro Glu Arg Asp Leu Cys Gly Cys Tyr Ser Val
50 55 60
Ser Ser Val Leu Pro Gly Cys Ala Gln Pro Trp Asn His Gly Glu Thr
65 70 75 80
Phe Thr Cys Thr Ala Ala His Pro Glu Leu Lys Thr Pro Leu Thr Ala

85 90 95
Asn Ile Thr Lys Ser
100

<210> 197
<211> 108
<212> PRT
<213> Homo sapiens

<400> 197
Glu Cys Pro Ser His Thr Gln Pro Leu Gly Val Tyr Leu Leu Thr Pro
1 5 10 15
Ala Val Gln Asp Leu Trp Leu Arg Asp Lys Ala Thr Phe Thr Cys Phe
20 25 30
Val Val Gly Ser Asp Leu Lys Asp Ala His Leu Thr Trp Glu Val Ala
35 40 45
Gly Lys Val Pro Thr Gly Gly Val Glu Glu Gly Leu Leu Glu Arg His
50 55 60
Ser Asn Gly Ser Gln Ser Gln His Ser Arg Leu Thr Leu Pro Arg Ser
65 70 75 80
Leu Trp Asn Ala Gly Thr Ser Val Thr Cys Thr Leu Asn His Pro Ser
85 90 95
Leu Pro Pro Gln Arg Leu Met Ala Leu Arg Glu Pro
100 105

<210> 198
<211> 107
<212> PRT
<213> Homo sapiens

<400> 198
Val Cys Ser Arg Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser
1 5 10 15
Ser Cys Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys
20 25 30
Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu
35 40 45
Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln
50 55 60
Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys
65 70 75 80
His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly
85 90 95
His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala
100 105

<210> 199
<211> 109
<212> PRT
<213> Homo sapiens

<400> 199
Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
1 5 10 15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
20 25 30
Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
35 40 45
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
50 55 60
Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
65 70 75 80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
85 90 95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys

100 105

<210> 200
<211> 110
<212> PRT
<213> Homo sapiens

<400> 200
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
35 40 45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60
Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
100 105 110

<210> 201
<211> 110
<212> PRT
<213> Homo sapiens

<400> 201
Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
35 40 45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 202
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human Ck region + T70E, N29A, N30A, V55A

<400> 202
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Ala Ala Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95

Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 203
<211> 112
<212> PRT
<213> Homo sapiens

<400> 203
Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val Pro Pro Arg
1 5 10 15
Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile Cys Gln Ala
20 25 30
Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu Arg Glu Gly
35 40 45
Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln Ala Glu Ala
50 55 60
Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr Leu Thr Ile
65 70 75 80
Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys Arg Val Asp
85 90 95
His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met Cys Val Pro
100 105 110

<210> 204
<211> 131
<212> PRT
<213> Homo sapiens

<400> 204
Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu
1 5 10 15
Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly
20 25 30
Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu
35 40 45
Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser
50 55 60
Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala
65 70 75 80
Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu
85 90 95
Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly
100 105 110
Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly
115 120 125
Thr Cys Tyr
130

<210> 205
<211> 131
<212> PRT
<213> Homo sapiens

<400> 205
Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu
1 5 10 15
Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly
20 25 30
Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu
35 40 45
Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser
50 55 60
Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala
65 70 75 80

```
Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu
                85                  90                  95
Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly
            100                 105                 110
Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly
        115                 120                 125
Thr Cys Tyr
    130
```

<210> 206
<211> 117
<212> PRT
<213> Homo sapiens

<400> 206

```
Ala Ala Gln Ala Pro Val Lys Leu Ser Leu Asn Leu Leu Ala Ser Ser
 1               5                  10                  15
Asp Pro Pro Glu Ala Ala Ser Trp Leu Leu Cys Glu Val Ser Gly Phe
            20                  25                  30
Ser Pro Pro Asn Ile Leu Leu Met Trp Leu Glu Asp Gln Arg Glu Val
        35                  40                  45
Asn Thr Ser Gly Phe Ala Pro Ala Arg Pro Pro Pro Gln Pro Arg Ser
    50                  55                  60
Thr Thr Phe Trp Ala Trp Ser Val Leu Arg Val Pro Ala Pro Pro Ser
65                  70                  75                  80
Pro Gln Pro Ala Thr Tyr Thr Cys Val Val Ser His Glu Asp Ser Arg
                85                  90                  95
Thr Leu Leu Asn Ala Ser Arg Ser Leu Glu Val Ser Tyr Val Thr Asp
            100                 105                 110
His Gly Pro Met Lys
        115
```

<210> 207
<211> 108
<212> PRT
<213> Homo sapiens

<400> 207

```
Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro Ser Pro
 1               5                  10                  15
Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr Cys Leu Val Val
            20                  25                  30
Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr Trp Ser Arg Ala
        35                  40                  45
Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys Gln Arg
    50                  55                  60
Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr Arg Asp
65                  70                  75                  80
Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro His Leu
                85                  90                  95
Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser
            100                 105
```

<210> 208
<211> 107
<212> PRT
<213> Homo sapiens

<400> 208

```
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 1               5                  10                  15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            20                  25                  30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        35                  40                  45
```

```
Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
    50                  55                  60
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65                  70                  75                  80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                85                  90                  95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            100                 105
```

<210> 209
<211> 107
<212> PRT
<213> Homo sapiens

<400> 209

```
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 1               5                  10                  15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            20                  25                  30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu
        35                  40                  45
Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
    50                  55                  60
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65                  70                  75                  80
Asn Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe
                85                  90                  95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            100                 105
```

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

<400> 210

```
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
 1               5                  10                  15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            20                  25                  30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        35                  40                  45
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    50                  55                  60
Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
65                  70                  75                  80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                85                  90                  95
Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
            100                 105
```

<210> 211
<211> 7
<212> PRT
<213> Homo sapiens

<400> 211

```
Glu Arg Lys Cys Cys Val Glu
 1               5
```

<210> 212
<211> 106
<212> PRT
<213> Homo sapiens

<400> 212
Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro Ser Phe Ala
1 5 10 15
Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu Val Thr Asp
20 25 30
Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg Gln Asn Gly
35 40 45
Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His Pro Asn Ala
50 55 60
Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp Asp Trp Asn
65 70 75 80
Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp Leu Pro Ser
85 90 95
Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys
100 105

<210> 213
<211> 110
<212> PRT
<213> Homo sapiens

<400> 213
Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp
1 5 10 15
Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn Phe
20 25 30
Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln Leu
35 40 45
Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser
50 55 60
Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu
65 70 75 80
Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro
85 90 95
Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys
100 105 110

<210> 214
<211> 131
<212> PRT
<213> Homo sapiens

<400> 214
Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg
1 5 10 15
Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr
20 25 30
Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln
35 40 45
Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro
50 55 60
Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu
65 70 75 80
Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu
85 90 95
Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly
100 105 110
Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly
115 120 125
Thr Cys Tyr
130

<210> 215
<211> 19

<212> PRT
<213> Homo sapiens

<400> 215
Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro
 1   5   10   15
Ser Pro Ser

<210> 216
<211> 6
<212> PRT
<213> Homo sapiens

<400> 216
Val Pro Pro Pro Pro Pro
 1   5

<210> 217
<211> 58
<212> PRT
<213> Homo sapiens

<400> 217
Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala Gln Pro Gln
 1   5   10   15
Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro Ala Thr Thr Arg
            20   25   30
Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Lys Glu Lys Glu Lys Glu
        35   40   45
Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro
    50   55

<210> 218
<400> 218
 000

<210> 219
<211> 12
<212> PRT
<213> Homo sapiens

<400> 219
Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
 1   5   10

<210> 220
<211> 62
<212> PRT
<213> Homo sapiens

<400> 220
Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys
 1   5   10   15
Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
            20   25   30
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu
        35   40   45
Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
    50   55   60

<210> 221

<211> 12
<212> PRT
<213> Homo sapiens

<400> 221
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
 1   5   10

<210> 222
<211> 34
<212> PRT
<213> Homo sapiens

<400> 222
Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala Gln Pro Gln
 1   5   10   15
Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro Ala Thr Thr Arg
            20   25   30
Asn Thr

<210> 223
<211> 106
<212> PRT
<213> Homo sapiens

<400> 223
Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 1   5   10   15
Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
            20   25   30
Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
        35   40   45
Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
    50   55   60
Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65   70   75   80
Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
                85   90   95
Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
            100   105

<210> 224
<211> 106
<212> PRT
<213> Homo sapiens

<400> 224
Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 1   5   10   15
Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
            20   25   30
Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
        35   40   45
Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
    50   55   60
Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65   70   75   80
Ser His Lys Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
                85   90   95
Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
            100   105

<210> 225

<211> 106
<212> PRT
<213> Homo sapiens

<400> 225
Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 1   5   10   15
Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
            20   25   30
Phe Tyr Pro Gly Ala Val Lys Val Ala Trp Lys Ala Asp Gly Ser Pro
        35   40   45
Val Asn Thr Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
    50   55   60
Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65   70   75   80
Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
                85   90   95
Glu Lys Thr Val Ala Pro Ala Glu Cys Ser
            100   105

<210> 226
<211> 106
<212> PRT
<213> Homo sapiens

<400> 226
Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 1   5   10   15
Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp
            20   25   30
Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro
        35   40   45
Val Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn
    50   55   60
Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65   70   75   80
Ser His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val
                85   90   95
Glu Lys Thr Val Ala Pro Ala Glu Cys Ser
            100   105

<210> 227
<211> 10
<212> PRT
<213> Homo sapiens

<400> 227
Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 1   5   10

<210> 228
<211> 5
<212> PRT
<213> Homo sapiens

<400> 228
Cys Pro Pro Cys Pro
 1   5

<210> 229
<400> 229
 000

<210> 230
<400> 230
000

<210> 231
<400> 231
000

<210> 232
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human IgG1 hinge (CSC-P)

<400> 232
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
1 5 10 15

<210> 233
<400> 233
000

<210> 234
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human IgG1 hinge (CCS-P)

<400> 234
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Ser Pro
1 5 10 15

<210> 235
<400> 235
000

<210> 236
<400> 236
000

<210> 237
<400> 237
000

<210> 238
<400> 238
000

<210> 239
<400> 239
000

<210> 240
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human IgG1 hinge (CCS-S)

<400> 240
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Ser Ser
 1   5   10   15

<210> 241
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Stalk region of CD69

<400> 241
Gln Tyr Asn Cys Pro Gly Gln Tyr Thr Phe Ser Met
 1   5   10

<210> 242
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Stalk region of CD72

<400> 242
Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys
 1   5   10

<210> 243
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Stalk region of CD94

<400> 243
Glu Pro Ala Phe Thr Pro Gly Pro Asn Ile Glu Leu Gln Lys Asp Ser
 1   5   10   15
Asp Cys

<210> 244
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Stalk region of NKG2A

<400> 244
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg
 1   5   10   15
His Cys

<210> 245

<211> 12
<212> PRT
<213> Homo sapiens

<400> 245
Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr
 1   5   10

<210> 246
<211> 10
<212> PRT
<213> Homo sapiens

<400> 246
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro
 1   5   10

<210> 247
<211> 7
<212> PRT
<213> Homo sapiens

<400> 247
Glu Ser Lys Tyr Gly Pro Pro
 1   5

<210> 248
<211> 5
<212> PRT
<213> Homo sapiens

<400> 248
Cys Pro Arg Cys Pro
 1   5

<210> 249
<211> 5
<212> PRT
<213> Homo sapiens

<400> 249
Cys Pro Ser Cys Pro
 1   5

<210> 250
<211> 17
<212> PRT
<213> Homo sapiens

<400> 250
Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys
 1   5   10   15
Pro

<210> 251
<211> 15
<212> PRT
<213> Homo sapiens

<400> 251
Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro

1 5 10 15

<210> 252
<211> 24
<212> PRT
<213> Homo sapiens

<400> 252
Gly Arg Gly Gly Glu Glu Lys Lys Lys Glu Lys Glu Lys Glu Glu Gln
1 5 10 15
Glu Glu Arg Glu Thr Lys Thr Pro
20

<210> 253
<211> 107
<212> PRT
<213> Homo sapiens

<400> 253
Val Cys Ser Arg Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser
1 5 10 15
Ser Ser Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys
20 25 30
Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu
35 40 45
Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln
50 55 60
Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys
65 70 75 80
His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly
85 90 95
His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala
100 105

<210> 254
<211> 112
<212> PRT
<213> Homo sapiens

<400> 254
Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val Pro Pro Arg
1 5 10 15
Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile Cys Gln Ala
20 25 30
Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu Arg Glu Gly
35 40 45
Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln Ala Glu Ala
50 55 60
Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr Leu Thr Ile
65 70 75 80
Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys Arg Val Asp
85 90 95
His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met Cys Val Pro
100 105 110

<210> 255
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered human CH2 upper hinge like sequence of IgE

<400> 255

```
Val Cys Ser Arg Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser
 1               5                  10                  15
Ser Ser Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys
            20                  25                  30
Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu
        35                  40                  45
Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln
    50                  55                  60
Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys
65                  70                  75                  80
His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly
                85                  90                  95
His Thr Phe Glu Asp Ser Thr Lys Lys Ser Ala
            100                 105


<210> 256
<211> 268
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D5 scFv (VLVH)

<220>
<221> SIGNAL
<222> (10)...(20)

<400> 256
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
-20                 -15                 -10                  -5
Asp Thr Thr Gly Asp Phe Met Met Ser Gln Ser Pro Ser Ser Leu Thr
                 1               5                  10
Val Ser Val Gly Glu Lys Val Thr Val Ser Cys Lys Ser Ser Gln Ser
        15                  20                  25
Leu Leu Tyr Thr Ser Ser Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
    30                  35                  40
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
45                  50                  55                  60
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
                65                  70                  75
Phe Thr Leu Thr Ile Thr Ser Val Lys Ala Asp Asp Leu Ala Val Tyr
            80                  85                  90
Tyr Cys Gln Gln Tyr Tyr Ala Tyr Pro Trp Thr Phe Gly Gly Gly Thr
        95                  100                 105
Lys Leu Glu Leu Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    110                 115                 120
Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val
125                 130                 135                 140
Arg Pro Gly Ala Ser Val Lys Met Ser Cys Arg Ala Ser Gly Tyr Thr
                145                 150                 155
Phe Thr Ser Tyr Trp Leu His Trp Val Lys Gln Arg Pro Gly Gln Gly
            160                 165                 170
Leu Glu Trp Ile Gly Met Ile Asp Pro Ser Asn Ser Asp Thr Arg Phe
        175                 180                 185
Asn Pro Asn Phe Lys Asp Lys Ala Thr Leu Asn Val Asp Arg Ser Ser
    190                 195                 200
Asn Thr Ala Tyr Met Leu Leu Ser Ser Leu Thr Ser Ala Asp Ser Ala
205                 210                 215                 220
Val Tyr Tyr Cys Ala Thr Tyr Gly Ser Tyr Val Ser Pro Leu Asp Tyr
                225                 230                 235
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser
            240                 245

<210> 257
<211> 248
<212> PRT
<213> Artificial Sequence
```

<220>
<223> 5D5 scFv (VLVH) mature protein without the signal peptide

<400> 257
Asp Phe Met Met Ser Gln Ser Pro Ser Ser Leu Thr Val Ser Val Gly
1 5 10 15
Glu Lys Val Thr Val Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Thr
20 25 30
Ser Ser Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Thr Ser Val Lys Ala Asp Asp Leu Ala Val Tyr Tyr Cys Gln Gln
85 90 95
Tyr Tyr Ala Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu
100 105 110
Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Ala
130 135 140
Ser Val Lys Met Ser Cys Arg Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
145 150 155 160
Trp Leu His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
165 170 175
Gly Met Ile Asp Pro Ser Asn Ser Asp Thr Arg Phe Asn Pro Asn Phe
180 185 190
Lys Asp Lys Ala Thr Leu Asn Val Asp Arg Ser Ser Asn Thr Ala Tyr
195 200 205
Met Leu Leu Ser Ser Leu Thr Ser Ala Asp Ser Ala Val Tyr Tyr Cys
210 215 220
Ala Thr Tyr Gly Ser Tyr Val Ser Pro Leu Asp Tyr Trp Gly Gln Gly
225 230 235 240
Thr Ser Val Thr Val Ser Ser Ser
245

<210> 258
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D5 VH

<400> 258
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Arg Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Trp Leu His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Met Ile Asp Pro Ser Asn Ser Asp Thr Arg Phe Asn Pro Asn Phe
50 55 60
Lys Asp Lys Ala Thr Leu Asn Val Asp Arg Ser Ser Asn Thr Ala Tyr
65 70 75 80
Met Leu Leu Ser Ser Leu Thr Ser Ala Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Thr Tyr Gly Ser Tyr Val Ser Pro Leu Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Ser Val Thr Val Ser Ser Ser
115 120

<210> 259

<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> 5D5 VL

<400> 259
Asp Phe Met Met Ser Gln Ser Pro Ser Ser Leu Thr Val Ser Val Gly
 1   5   10   15
Glu Lys Val Thr Val Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Thr
            20   25   30
Ser Ser Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80
Ile Thr Ser Val Lys Ala Asp Asp Leu Ala Val Tyr Tyr Cys Gln Gln
                85   90   95
Tyr Tyr Ala Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu
            100   105   110
Lys

<210> 260
<211> 792
<212> DNA
<213> Artificial Sequence

<220>
<223> 4C04 anti-Ron scFv with signal peptide and
junction amino acids SSS at carboxy-terminus

<400> 260
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gacattcaga tgacccagtc tcctgcctcc cagtctgcat ctctgggaga aagtgtcacc 120
atcacatgcc tggcaagtca gaccattggt acatggttag catggtatca gcagaaacca 180
gggaaatctc ctcagctcct gatttatgct gcaaccagct tggcagatgg ggtcccatca 240
aggttcagtg ctagtggatc tggcacaaaa ttttctttca agatcgacag cctacagtct 300
gaagattttg taagttatta ctgtcaacaa ctttacaata ctccgtggac gttcggtgga 360
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ggctctcaga tccagctgca gcagtctgga cctgagctgg tgaagcctgg gacttcagtg 480
aagatatcct gcaaggcttc tgactacaca ctcactgact tctatatgaa ctgggtgagg 540
cagaagcctg gacagggact tgagtggatt gggaggattt atcctggaac cgataaaact 600
agatacaatg agaaattcag ggacaaggcc atactgaccg tggacacgtc ctccagcaca 660
gcctacatgc agctcagcag cctgacatca gaggacactg ctgtctattt ctgtgcaaga 720
tccgcctact atggtaacta cgttgctatg gactactggg gtcaaggaac ctcagtcacc 780
gtctcctcga gc 792

<210> 261
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> 4C04 anti-Ron scFv with signal peptide and
junction amino acids SSS at carboxy-terminus

<400> 261
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Gln Ser Ala Ser Leu Gly
 1   5   10   15
Glu Ser Val Thr Ile Thr Cys Leu Ala Ser Gln Thr Ile Gly Thr Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile
        35   40   45
Tyr Ala Ala Thr Ser Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Ala

```
    50                  55                  60
Ser Gly Ser Gly Thr Lys Phe Ser Phe Lys Ile Asp Ser Leu Gln Ser
65                  70                  75                  80
Glu Asp Phe Val Ser Tyr Tyr Cys Gln Gln Leu Tyr Asn Thr Pro Trp
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile Gln Leu Gln Gln
        115                 120                 125
Ser Gly Pro Glu Leu Val Lys Pro Gly Thr Ser Val Lys Ile Ser Cys
    130                 135                 140
Lys Ala Ser Asp Tyr Thr Leu Thr Asp Phe Tyr Met Asn Trp Val Arg
145                 150                 155                 160
Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly
                165                 170                 175
Thr Asp Lys Thr Arg Tyr Asn Glu Lys Phe Arg Asp Lys Ala Ile Leu
            180                 185                 190
Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
        195                 200                 205
Thr Ser Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg Ser Ala Tyr Tyr
    210                 215                 220
Gly Asn Tyr Val Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
225                 230                 235                 240
Val Ser Ser Ser
```

<210> 262
<211> 2115
<212> DNA
<213> Artificial Sequence

<220>
<223> 4C04 anti-Ron single chain polypeptide (4C04 scFv-CH1-CH2-CH3-Ck with signal peptide)

<400> 262

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gacattcaga tgacccagtc tcctgcctcc cagtctgcat ctctgggaga aagtgtcacc 120
atcacatgcc tggcaagtca gaccattggt acatggttag catggtatca gcagaaacca 180
gggaaatctc ctcagctcct gatttatgct gcaaccagct tggcagatgg ggtcccatca 240
aggttcagtg ctagtggatc tggcacaaaa ttttctttca agatcgacag cctacagtct 300
gaagattttg taagttatta ctgtcaacaa ctttacaata ctccgtggac gttcggtgga 360
ggcaccaagc tggaaatcaa aggtggcggt ggctctggcg gaggtggatc cggtggcggc 420
ggctctcaga tccagctgca gcagtctgga cctgagctgg tgaagcctgg gacttcagtg 480
aagatatcct gcaaggcttc tgactacaca ctcactgact tctatatgaa ctgggtgagg 540
cagaagcctg gacagggact tgagtggatt gggaggattt atcctggaac cgataaaact 600
agatacaatg agaaattcag ggacaaggcc atactgaccg tggacacgtc ctccagcaca 660
gcctacatgc agctcagcag cctgacatca gaggacactg ctgtctattt ctgtgcaaga 720
tccgcctact atggtaacta cgttgctatg gactactggg gtcaaggaac ctcagtcacc 780
gtctcctcga gcgcctccac caagggccca tcggtcttcc ccctggcacc ctcctccaag 840
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gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1500
accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc 1560
aaaggcttct atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1620
aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1680
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aaggacagca cctacagcct cagcagcacc ctgacgctga gcaaagcaga ctacgagaaa 2040
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<210> 263
<400> 263
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<210> 264
<400> 264
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<210> 265
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> 11H09 anti-RON scFv mature protein without the signal peptide but with junction amino acids SSS at carboxy-terminus

<400> 265

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly
1				5				10					15		
Glu	Arg	Val	Ser	Leu	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Gly	Ser	Ser
		20					25					30			
Leu	Ser	Trp	Leu	Gln	Gln	Glu	Pro	Asp	Gly	Thr	Ile	Lys	Arg	Leu	Ile
	35					40					45				
Tyr	Ser	Thr	Ser	Ser	Leu	Asp	Ser	Gly	Val	Pro	Lys	Arg	Phe	Ser	Gly
50					55					60					
Ser	Arg	Ser	Gly	Ser	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Ser
65				70					75					80	
Glu	Asp	Phe	Val	Asp	Tyr	Tyr	Cys	Leu	Gln	Tyr	Ala	Ser	Ser	Pro	Trp
			85					90					95		
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser
		100					105					110			
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Gln	Gln
	115					120					125				
Ser	Gly	Ala	Glu	Leu	Ala	Lys	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys
130					135					140					
Lys	Ser	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Trp	Ile	His	Trp	Val	Lys
145				150					155					160	
Glu	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Pro	Thr
			165					170					175		
Thr	Gly	Tyr	Thr	Glu	Ser	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu
		180					185					190			
Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu
	195					200					205				
Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Phe	Leu	Leu	Arg	Pro	Trp
210					215					220					
Tyr	Phe	Asp	Val	Trp	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ser
225				230					235					240	

<210> 266
<400> 266
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<210> 296
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-c-Met Light Chain Complementarity Determining Region

<400> 296
Arg Ala Ser Gln Ser Ile Arg Asn Tyr Leu Asn
1 5 10

<210> 297
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-c-Met Light Chain Complementarity Determining Region

<400> 297
Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 298
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-c-Met Light Chain Complementarity Determining Region

<400> 298
Gln Gln Ser Tyr Val Thr Pro Leu Thr
1 5

<210> 299
<400> 299
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<210> 300
<400> 300
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<210> 301
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 VH amino acid sequence

<400> 301
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

```
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Thr Val Thr Val Ser Ser
        115
```

<210> 302
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3 VL amino acid sequence

<400> 302

```
Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 1               5                  10                  15
Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            20                  25                  30
Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        35                  40                  45
Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser
    50                  55                  60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu
65                  70                  75                  80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr
                85                  90                  95
Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn
            100                 105
```

<210> 303
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 VH amino acid sequence

<400> 303

```
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20                  25                  30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
    50                  55                  60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
            100                 105                 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
        115                 120
```

<210> 304
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3 VL amino acid sequence

<400> 304
Gln Ile Ile Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 1   5   10   15
Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            20   25   30
His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        35   40   45
Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65   70   75   80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
                85   90   95
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 305
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> G1 N297A CH2-CH3 (N297ST - A297ST)

<400> 305
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1   5   10   15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20   25   30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        35   40   45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50   55   60
Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65   70   75   80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85   90   95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            100   105   110
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        115   120   125
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130   135   140
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145   150   155   160
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                165   170   175
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            180   185   190
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        195   200   205
Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210   215

<210> 306
<211> 216
<212> PRT

<213> Artificial Sequence

<220>
<223> IgG1 AA N297A CH2CH3 (Ala substitutions at 234, 235, 237 and 297; 236 deleted)

<400> 306

```
Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 1               5                  10                  15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            20                  25                  30
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
        35                  40                  45
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    50                  55                  60
Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
65                  70                  75                  80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
                85                  90                  95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
            100                 105                 110
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
        115                 120                 125
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
    130                 135                 140
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
145                 150                 155                 160
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
                165                 170                 175
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
            180                 185                 190
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        195                 200                 205
Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215
```

<210> 307
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> G2 AA N297A CH2CH3 (Ala substitution at 234, 236 and 297)

<400> 307

```
Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 1               5                  10                  15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            20                  25                  30
Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
        35                  40                  45
Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    50                  55                  60
Phe Ala Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
65                  70                  75                  80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
                85                  90                  95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
            100                 105                 110
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
        115                 120                 125
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
    130                 135                 140
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
145                 150                 155                 160
Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
```

```
                165                 170                 175
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
            180                 185                 190
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        195                 200                 205
Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215
```

<210> 308
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> G4 AA N297A CH2CH3 (Ala substitutions at 234, 235, 237 and 297; 236 deleted)

<400> 308

```
Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 1               5                  10                  15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            20                  25                  30
Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
        35                  40                  45
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    50                  55                  60
Phe Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
65                  70                  75                  80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
                85                  90                  95
Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
            100                 105                 110
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr
        115                 120                 125
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
    130                 135                 140
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
145                 150                 155                 160
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
                165                 170                 175
Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
            180                 185                 190
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        195                 200                 205
Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215
```

<210> 309
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> DeltaCH2 (g1CH3 only)

<400> 309

```
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 1               5                  10                  15
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            20                  25                  30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        35                  40                  45
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    50                  55                  60
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
```

65 70 75 80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Thr Gly Leu Asn Asp
100 105 110
Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu Asp Tyr Lys Asp Asp
115 120 125
Asp Asp Lys Asp Tyr Lys Asp Asp Asp Asp Lys Asp Tyr Lys Asp Asp
130 135 140
Asp Asp Lys His His His His His His
145 150

<210> 310
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> BC3-VH-VL amino acid sequence (includes g4s linker)

<400> 310
Gln Val Gln Leu Gln Gln Ser Ala Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30
Thr Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ile Gly Tyr Ser Gln Lys Phe
50 55 60
Lys Asp Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Lys Val Tyr Tyr Asp Tyr Asp Val Tyr Ser Met Asp Tyr
100 105 110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Ile Leu
130 135 140
Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr
145 150 155 160
Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln
165 170 175
Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys
180 185 190
Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205
Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr
210 215 220
Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly
225 230 235 240
Thr Lys Leu Glu Leu Lys
245

<210> 311
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3-VH-VL amino acid sequence (includes g4s linker)

<400> 311
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15

```
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20                  25                  30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125
Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Val Leu Thr Gln Ser Pro
    130                 135                 140
Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser
145                 150                 155                 160
Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly
                165                 170                 175
Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly
            180                 185                 190
Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
        195                 200                 205
Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
    210                 215                 220
Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu
225                 230                 235                 240
Ile Asn
```

<210> 312
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> H57 VH-Linker-VL (without leader)

<400> 312

```
Glu Val Tyr Leu Val Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Ser
 1               5                  10                  15
Ser Leu Lys Val Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Phe
            20                  25                  30
Trp Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
Gly Arg Ile Lys Asn Lys Pro Asn Asn Tyr Ala Thr Glu Tyr Ala Asp
    50                  55                  60
Ser Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Arg Asn Ser
65                  70                  75                  80
Ile Tyr Leu Gln Met Asn Arg Leu Arg Val Asp Asp Thr Ala Ile Tyr
                85                  90                  95
Tyr Cys Thr Arg Ala Gly Arg Phe Asp His Phe Asp Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125
Gly Ser Gly Gly Gly Gly Ser Ala Gln Tyr Glu Leu Ile Gln Pro Ser
    130                 135                 140
Ser Ala Ser Val Thr Val Gly Glu Thr Val Lys Ile Thr Cys Ser Gly
145                 150                 155                 160
Asp Gln Leu Pro Lys Asn Phe Ala Tyr Trp Phe Gln Gln Lys Ser Asp
                165                 170                 175
Lys Asn Ile Leu Leu Leu Ile Tyr Met Asp Asn Lys Arg Pro Ser Gly
            180                 185                 190
Ile Pro Glu Arg Phe Ser Gly Ser Thr Ser Gly Thr Thr Ala Thr Leu
        195                 200                 205
Thr Ile Ser Gly Ala Gln Pro Glu Asp Glu Ala Ala Tyr Tyr Cys Leu
    210                 215                 220
```

Ser Ser Tyr Gly Asp Asn Asn Asp Leu Val Phe Gly Ser Gly Thr Gln
225 230 235 240
Leu Thr Val Leu

<210> 313
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> H57 Null2 SMIP - VH amino acid

<400> 313
Glu Val Tyr Leu Val Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Ser
1 5 10 15
Ser Leu Lys Val Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Phe
20 25 30
Trp Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Gly Arg Ile Lys Asn Lys Pro Asn Asn Tyr Ala Thr Glu Tyr Ala Asp
50 55 60
Ser Val Arg Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Arg Asn Ser
65 70 75 80
Ile Tyr Leu Gln Met Asn Arg Leu Arg Val Asp Asp Thr Ala Ile Tyr
85 90 95
Tyr Cys Thr Arg Ala Gly Arg Phe Asp His Phe Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 314
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse IGHG2c mutated CH2 (alanine substitutions at positions L234, L235, G237, E318, K320 and K322)

<400> 314
Ala Pro Asp Ala Ala Gly Ala Pro Ser Val Phe Ile Phe Pro Pro Lys
1 5 10 15
Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Met Val Thr Cys Val
20 25 30
Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
35 40 45
Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
50 55 60
Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
65 70 75 80
Gln Asp Trp Met Ser Gly Lys Ala Phe Ala Cys Ala Val Asn Asn Arg
85 90 95
Ala Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro Arg
100 105 110

<210> 315
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> H57 Null2 SMIP - VL amino acid sequence

<400> 315

```
Tyr Glu Leu Ile Gln Pro Ser Ser Ala Ser Val Thr Val Gly Glu Thr
 1               5                  10                  15
Val Lys Ile Thr Cys Ser Gly Asp Gln Leu Pro Lys Asn Phe Ala Tyr
            20                  25                  30
Trp Phe Gln Gln Lys Ser Asp Lys Asn Ile Leu Leu Leu Ile Tyr Met
        35                  40                  45
Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Thr
    50                  55                  60
Ser Gly Thr Thr Ala Thr Leu Thr Ile Ser Gly Ala Gln Pro Glu Asp
65                  70                  75                  80
Glu Ala Ala Tyr Tyr Cys Leu Ser Ser Tyr Gly Asp Asn Asn Asp Leu
                85                  90                  95
Val Phe Gly Ser Gly Thr Gln Leu Thr Val Leu
            100                 105
```

<210> 316
<400> 316
000

<210> 317
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C11 Null2 SMIP - VH amino acid

<400> 317

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
 1               5                  10                  15
Ser Leu Lys Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe Ser Gly Tyr
            20                  25                  30
Gly Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Ser Val
        35                  40                  45
Ala Tyr Ile Thr Ser Ser Ser Ile Asn Ile Lys Tyr Ala Asp Ala Val
    50                  55                  60
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Leu Leu Phe
65                  70                  75                  80
Leu Gln Met Asn Ile Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95
Ala Arg Phe Asp Trp Asp Lys Asn Tyr Trp Gly Gln Gly Thr Met Val
            100                 105                 110
Thr Val Ser Ser
        115
```

<210> 318
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C11 Null2 SMIP - VL amino acid

<400> 318

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Pro Ala Ser Leu Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Tyr Thr Asn Lys Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Arg Asp Ser Ser Phe Thr Ile Ser Ser Leu Glu Ser
65                  70                  75                  80
```

Glu Asp Ile Gly Ser Tyr Tyr Cys Gln Gln Tyr Tyr Asn Tyr Pro Trp
85 90 95
Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 319
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C11 VH-Linker-VL (without leader)

<400> 319
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15
Ser Leu Lys Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe Ser Gly Tyr
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Ser Val
35 40 45
Ala Tyr Ile Thr Ser Ser Ser Ile Asn Ile Lys Tyr Ala Asp Ala Val
50 55 60
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Leu Leu Phe
65 70 75 80
Leu Gln Met Asn Ile Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Phe Asp Trp Asp Lys Asn Tyr Trp Gly Gln Gly Thr Met Val
100 105 110
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
130 135 140
Pro Ala Ser Leu Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln
145 150 155 160
Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
165 170 175
Pro Lys Leu Leu Ile Tyr Tyr Thr Asn Lys Leu Ala Asp Gly Val Pro
180 185 190
Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Ser Ser Phe Thr Ile
195 200 205
Ser Ser Leu Glu Ser Glu Asp Ile Gly Ser Tyr Tyr Cys Gln Gln Tyr
210 215 220
Tyr Asn Tyr Pro Trp Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys
225 230 235 240

<210> 320
<211> 110
<212> PRT
<213> Mus musculus

<220>
<223> Human IGHG2c CH2 domain

<400> 320
Ala Pro Asp Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
1 5 10 15
Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Met Val Thr Cys Val
20 25 30
Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
35 40 45
Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
50 55 60
Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His

65 70 75 80
Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Arg
85 90 95
Ala Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro Arg
100 105 110

<210> 321
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> HM1 (IgM CH3:IgG1 CH3) without C-terminal tail

<400> 321
Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro Ser Phe Ala
1 5 10 15
Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu Val Thr Asp
20 25 30
Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg Gln Asn Gly
35 40 45
Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His Pro Asn Ala
50 55 60
Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp Asp Trp Asn
65 70 75 80
Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp Leu Pro Ser
85 90 95
Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Gln Pro Arg Glu Pro
100 105 110
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
115 120 125
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
130 135 140
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
145 150 155 160
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
165 170 175
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
180 185 190
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
195 200 205
Leu Ser Pro Gly Lys
210

<210> 322
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG4 AA CH2

<400> 322
Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
1 5 10 15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
20 25 30
Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
35 40 45
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
50 55 60
Phe Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
65 70 75 80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
85 90 95
Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys

100 105

<210> 323
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 CH2 CH3 Null2

<400> 323
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
85 90 95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
115 120 125
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
165 170 175
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205
Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215

<210> 324
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1 N297A CH2

<400> 324
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60
Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 325
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1 AA CH2

<400> 325
Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 1   5   10   15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            20   25   30
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
        35   40   45
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    50   55   60
Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
65   70   75   80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
                85   90   95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100   105

<210> 326
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG2 AA CH2

<400> 326
Ala Pro Glu Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 1   5   10   15
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            20   25   30
Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
        35   40   45
Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    50   55   60
Phe Ala Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
65   70   75   80
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
                85   90   95
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
            100   105

<210> 327
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7-VH murine hybridoma Amino Acid

<220>
<221> ACT_SITE
<222> (31)...(35)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (50)...(66)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (100)...(110)
<223> complementarity-determining region

<400> 327
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1   5   10   15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Ser Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ala
        115   120

<210> 328
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7-VL murine hybridoma Amino Acid

<220>
<221> ACT_SITE
<222> (24)...(33)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (49)...(55)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (88)...(96)
<223> complementarity-determining region

<400> 328
Gln Val Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Phe Pro Gly
 1   5   10   15
Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            20   25   30
Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        35   40   45
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Thr Glu
65   70   75   80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Arg
            100   105

<210> 329
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> HuCris7 VL.1

<220>
<221> ACT_SITE
<222> (24)...(33)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (49)...(55)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (88)...(96)
<223> complementarity-determining region

<400> 329
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            20   25   30
Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
        35   40   45
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65   70   75   80
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Arg
            100   105

<210> 330
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7 VL.2

<400> 330
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            20   25   30
Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
        35   40   45
Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
    50   55   60
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65   70   75   80
Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
                85   90   95
Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg
            100   105

<210> 331
<211> 121
<212> PRT
<213> Artificial Sequence

<220>

<223> HuCris7 VH.1

<220>
<221> ACT_SITE
<222> (31)...(35)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (50)...(66)
<223> complementarity-determining region

<220>
<221> ACT_SITE
<222> (100)...(110)
<223> complementarity-determining region

<400> 331
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 332
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7 VH.2

<400> 332
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Lys Asn Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 333
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCRIS7 VH.3

<400> 333
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65   70   75   80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Pro Val Thr Val Ser Ser
        115   120

<210> 334
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7-(VH-VL)

<220>
<221> SITE
<222> (122)...(138)
<223> Linker

<400> 334
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1   5   10   15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95
Ala Ser Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly
        115   120   125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Gln Val Val Leu Thr Gln
    130   135   140
Ser Pro Ala Ile Met Ser Ala Phe Pro Gly Glu Lys Val Thr Met Thr
145   150   155   160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165   170   175
Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180   185   190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr
        195   200   205
Ser Leu Thr Ile Ser Ser Met Glu Thr Glu Asp Ala Ala Thr Tyr Tyr
    210   215   220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225   230   235   240
Leu Gln Ile Thr Arg

245

<210> 335
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH1-VL1)

<220>
<221> SITE
<222> (122)...(138)
<223> Linker

<400> 335
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
130 135 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
165 170 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
180 185 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225 230 235 240
Leu Gln Ile Thr Arg
245

<210> 336
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH1-VL2)

<220>
<221> SITE
<222> (122)...(138)
<223> Linker

<400> 336
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser

```
            20                  25                  30
Thr Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg
                245


<210> 337
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH2-VL1)

<220>
<221> SITE
<222> (122)...(138)
<223> Linker

<400> 337
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1                  5                  10                  15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Lys Asn Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
```

180 185 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225 230 235 240
Leu Gln Ile Thr Arg
245

<210> 338
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH2-VL2)

<220>
<221> SITE
<222> (122)...(138)
<223> Linker

<400> 338
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
20 25 30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Lys Asn Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
130 135 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
165 170 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
180 185 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
210 215 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225 230 235 240
Leu Gln Ile Thr Arg
245

<210> 339
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH3-VL1)

<220>

<221> SITE
<222> (122)...(138)
<223> Liniker

<400> 339
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65   70   75   80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115   120   125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130   135   140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145   150   155   160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165   170   175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180   185   190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195   200   205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210   215   220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225   230   235   240
Leu Gln Ile Thr Arg
                245

<210> 340
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> HuCris7-(VH3-VL2)

<220>
<221> SITE
<222> (122)...(138)
<223> Linker

<400> 340
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20   25   30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65   70   75   80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85   90   95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100   105   110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

```
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg
                245
```

<210> 341
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Half null CH2-CH3 regions

<400> 341

```
Pro Asp Ala Ala Gly Ala Pro Ser Val Phe Ile Phe Pro Pro Lys Ile
 1               5                  10                  15
Lys Asp Val Leu Met Ile Ser Leu Ser Pro Met Val Thr Cys Val Val
            20                  25                  30
Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val
        35                  40                  45
Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp
    50                  55                  60
Tyr Ala Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln
65                  70                  75                  80
Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Arg Ala
                85                  90                  95
Leu Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro Arg Gly Pro Val
            100                 105                 110
Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Ala Glu Glu Met Thr
        115                 120                 125
Lys Lys Glu Phe Ser Leu Thr Cys Met Ile Thr Gly Phe Leu Pro Ala
    130                 135                 140
Glu Ile Ala Val Asp Trp Thr Ser Asn Gly Arg Thr Glu Gln Asn Tyr
145                 150                 155                 160
Lys Asn Thr Ala Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr
                165                 170                 175
Ser Lys Leu Arg Val Gln Lys Ser Thr Trp Glu Arg Gly Ser Leu Phe
            180                 185                 190
Ala Cys Ser Val Val His Glu Gly Leu His Asn His Leu Thr Thr Lys
        195                 200                 205
Thr Ile Ser Arg Ser Leu Gly Lys
    210                 215
```

<210> 342
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> HM2 (mouse CH3mu-CH3gamma) without C-termial tail

<400> 342
Ser Pro Ser Thr Asp Ile Leu Thr Phe Thr Ile Pro Pro Ser Phe Ala
 1   5   10   15
Asp Ile Phe Leu Ser Lys Ser Ala Asn Leu Thr Cys Leu Val Ser Asn
            20   25   30
Leu Ala Thr Tyr Glu Thr Leu Asn Ile Ser Trp Ala Ser Gln Ser Gly
        35   40   45
Glu Pro Leu Glu Thr Lys Ile Lys Ile Met Glu Ser His Pro Asn Gly
    50   55   60
Thr Phe Ser Ala Lys Gly Val Ala Ser Val Cys Val Glu Asp Trp Asn
65   70   75   80
Asn Arg Lys Glu Phe Val Cys Thr Val Thr His Arg Asp Leu Pro Ser
                85   90   95
Pro Gln Lys Lys Phe Ile Ser Lys Pro Asn Gly Pro Val Arg Ala Pro
            100   105   110
Gln Val Tyr Val Leu Pro Pro Pro Ala Glu Glu Met Thr Lys Lys Glu
        115   120   125
Phe Ser Leu Thr Cys Met Ile Thr Gly Phe Leu Pro Ala Glu Ile Ala
    130   135   140
Val Asp Trp Thr Ser Asn Gly Arg Thr Glu Gln Asn Tyr Lys Asn Thr
145   150   155   160
Ala Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu
                165   170   175
Arg Val Gln Lys Ser Thr Trp Glu Arg Gly Ser Leu Phe Ala Cys Ser
            180   185   190
Val Val His Glu Gly Leu His Asn His Leu Thr Thr Lys Thr Ile Ser
        195   200   205
Arg Ser Leu Gly Lys
    210

<210> 343
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> huamn IgG4 AA CH2 with alanine substitutions at
      F234 and N297

<400> 343
Ala Pro Glu Ala Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1   5   10   15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20   25   30
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        35   40   45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50   55   60
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65   70   75   80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85   90   95
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100   105   110

<210> 344
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG4 AA CH2 with alanine substitutions at
      L235 and N297

<400> 344

```
Ala Pro Glu Phe Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1               5                  10                  15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        35                  40                  45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100                 105                 110
```

<210> 345
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG4 AA CH2 with alanine substitutions at G236 and N297

<400> 345

```
Ala Pro Glu Phe Leu Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1               5                  10                  15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        35                  40                  45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100                 105                 110
```

<210> 346
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG4 AA CH2 with alanine substitutions at G237 and N297

<400> 346

```
Ala Pro Glu Phe Leu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
 1               5                  10                  15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        35                  40                  45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100                 105                 110
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<210> 347
<400> 347
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<210> 348
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<210> 379
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 134

<400> 379
Glu Pro Met Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 380
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 135

<400> 380
Glu Pro Met Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 381
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 136

<400> 381
Glu Pro Met Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
1 5 10 15

<210> 382
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 137

<400> 382
Glu Pro Met Ser Cys Asp Lys Thr His Thr Cys Pro Pro Ser Pro
1 5 10 15

<210> 383
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 138

<400> 383
Glu Pro Met Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
1 5 10 15

<210> 384
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 139

<400> 384
Glu Pro Met Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Pro

1 5 10 15

<210> 385
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 140

<400> 385
Glu Pro Met Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Pro
1 5 10 15

<210> 386
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 141

<400> 386
Glu Pro Met Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Ser
1 5 10 15

<210> 387
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 142

<400> 387
Glu Pro Met Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Ser
1 5 10 15

<210> 388
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 143

<400> 388
Glu Pro Met Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Ser
1 5 10 15

<210> 389
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 144

<400> 389
Glu Pro Met Ser Cys Asp Lys Thr His Thr Cys Pro Pro Ser Ser
1 5 10 15

<210> 390
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 145

<400> 390
Glu Pro Met Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Ser
1 5 10 15

<210> 391
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 146

<400> 391
Glu Pro Met Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Pro
1 5 10 15

<210> 392
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 147

<400> 392
Glu Pro Met Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Ser
1 5 10 15

<210> 393
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 148

<400> 393
Glu Pro Thr Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 394
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 149

<400> 394
Glu Pro Thr Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 395
<211> 15
<212> PRT

<213> Artificial Sequence

<220>
<223> Linker 150

<400> 395
Glu Pro Thr Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
 1   5   10   15

<210> 396
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 151

<400> 396
Glu Pro Thr Ser Cys Asp Lys Thr His Thr Cys Pro Pro Ser Pro
 1   5   10   15

<210> 397
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 152

<400> 397
Glu Pro Thr Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
 1   5   10   15

<210> 398
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 153

<400> 398
Glu Pro Thr Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Pro
 1   5   10   15

<210> 399
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 154

<400> 399
Glu Pro Thr Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Pro
 1   5   10   15

<210> 400
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Linker 155

<400> 400
Glu Pro Thr Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Ser
 1   5   10   15

<210> 401
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 156

<400> 401
Glu Pro Thr Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Ser
 1   5   10   15

<210> 402
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 157

<400> 402
Glu Pro Thr Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Ser
 1   5   10   15

<210> 403
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 158

<400> 403
Glu Pro Thr Ser Cys Asp Lys Thr His Thr Cys Pro Pro Ser Ser
 1   5   10   15

<210> 404
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 159

<400> 404
Glu Pro Thr Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Ser
 1   5   10   15

<210> 405
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 160

<400> 405

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

<210> 406
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 161

<400> 406
Glu Pro Thr Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Ser
1 5 10 15

<210> 407
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 162

<400> 407
Glu Pro Ala Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 408
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 163

<400> 408
Glu Pro Ala Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 409
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 164

<400> 409
Glu Pro Ala Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
1 5 10 15

<210> 410
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 165

<400> 410
Glu Pro Ala Ser Cys Asp Lys Thr His Thr Cys Pro Pro Ser Pro
1 5 10 15

<210> 411
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 166

<400> 411
Glu Pro Ala Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
 1   5   10   15

<210> 412
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 167

<400> 412
Glu Pro Ala Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Pro
 1   5   10   15

<210> 413
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 168

<400> 413
Glu Pro Ala Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Pro
 1   5   10   15

<210> 414
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 169

<400> 414
Glu Pro Ala Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Ser
 1   5   10   15

<210> 415
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 170

<400> 415
Glu Pro Ala Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Ser
 1   5   10   15

<210> 416
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 171

<400> 416
Glu Pro Ala Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Ser
 1   5   10   15

<210> 417
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 172

<400> 417
Glu Pro Ala Ser Cys Asp Lys Thr His Thr Cys Pro Pro Ser Ser
 1   5   10   15

<210> 418
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 173

<400> 418
Glu Pro Ala Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Ser
 1   5   10   15

<210> 419
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 174

<400> 419
Glu Pro Ala Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Ser
 1   5   10   15

<210> 420
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 175

<400> 420
Glu Pro Ala Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Ser
 1   5   10   15

<210> 421
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 176

<400> 421
Glu Pro Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10

<210> 422
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 177

<400> 422
Glu Pro Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10

<210> 423
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 178

<400> 423
Glu Pro Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
 1   5   10

<210> 424
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 179

<400> 424
Glu Pro Ser Cys Asp Lys Thr His Thr Cys Pro Pro Ser Pro
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<400> 425
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<223> Anti-c-Met Heavy Chain Complementarity Determining Region

<400> 464
Lys Tyr Asp Met Leu
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<223> Anti-c-Met Heavy Chain Complementarity Determining Region

<400> 465
Tyr Ile Tyr Pro Ser Gly Gly Leu Thr Glu Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 466
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<223> Anti-c-Met Heavy Chain Complementarity Determining Region

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Arg Ala Pro Arg Ser Leu Ser Phe Asp Ile
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<220>
<223> Human IgG1 CH2 with L235A, E318A, K320A and K322A substitutions

<400> 595
Ala Pro Glu Leu Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
85 90 95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 596
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 CH2 with L234A, L235A, G237A, E318A, K320A and K322A

<400> 596
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
85 90 95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 597
<400> 597
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<210> 598
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<220>
<223> Junction amino acids

<400> 598
Arg Asp Gln
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<210> 599

<211> 4
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<213> Artificial Sequence

<220>
<223> Junction amino acids

<400> 599
Ser Ala Ser Ser
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<210> 600
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<220>
<223> Junction amino acids

<400> 600
Ser Ser Ser
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<210> 601
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<220>
<223> NKG2D Linker

<400> 601
Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
 1   5   10   15
Ser

<210> 602
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-RON mAb 4C04 light chain

<400> 602
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Gln Ser Ala Ser Leu Gly
 1   5   10   15
Glu Ser Val Thr Ile Thr Cys Leu Ala Ser Gln Thr Ile Gly Thr Trp
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile
        35   40   45
Tyr Ala Ala Thr Ser Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Ala
    50   55   60
Ser Gly Ser Gly Thr Lys Phe Ser Phe Lys Ile Asp Ser Leu Gln Ser
65   70   75   80
Glu Asp Phe Val Ser Tyr Tyr Cys Gln Gln Leu Tyr Asn Thr Pro Trp
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 603
<211> 121
<212> PRT

<213> Artificial Sequence

<220>
<223> Anti-RON mAb 4C04 heavy chain

<400> 603
Gln Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Thr
 1   5   10   15
Ser Val Lys Ile Ser Cys Lys Ala Ser Asp Tyr Thr Leu Thr Asp Phe
            20   25   30
Tyr Met Asn Trp Val Arg Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Arg Ile Tyr Pro Gly Thr Asp Lys Thr Arg Tyr Asn Glu Lys Phe
    50   55   60
Arg Asp Lys Ala Ile Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Phe Cys
                85   90   95
Ala Arg Ser Ala Tyr Tyr Gly Asn Tyr Val Ala Met Asp Tyr Trp Gly
            100   105   110
Gln Gly Thr Ser Val Thr Val Ser Ser
        115   120

<210> 604
<211> 6
<212> PRT
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<220>
<223> Anti-RON mAb 4C04 light chain CDR1

<400> 604
Gln Thr Ile Gly Thr Trp
 1   5

<210> 605
<211> 3
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<220>
<223> Anti-RON mAb 4C04 light chain CDR2

<400> 605
Ala Ala Thr
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<210> 606
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-RON mAb 4C04 light chain CDR3

<400> 606
Gln Gln Leu Tyr Asn Thr Pro Trp Thr
 1   5

<210> 607
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-RON mAb 4C04 heavy chain CDR1

<400> 607
Asp Tyr Thr Leu Thr Asp Phe Tyr
 1   5

<210> 608
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-RON mAb 4C04 heavy chain CDR2

<400> 608
Ile Tyr Pro Gly Thr Asp Lys Thr
 1   5

<210> 609
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<212> PRT
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<220>
<223> Anti-RON mAb 4C04 heavy chain CDR3

<400> 609
Ala Arg Ser Ala Tyr Tyr Gly Asn Tyr Val Ala Met Asp Tyr
 1   5   10

<210> 610
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-RON mAb 11H09 light chain

<400> 610
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
 1   5   10   15
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly Ser Ser
            20   25   30
Leu Ser Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile Lys Arg Leu Ile
        35   40   45
Tyr Ser Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
    50   55   60
Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65   70   75   80
Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser Pro Trp
                85   90   95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 611
<211> 117
<212> PRT
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<220>
<223> Anti-RON mAb 11H09 heavy chain

<400> 611

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Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Met Ser Cys Lys Ser Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30
Trp Ile His Trp Val Lys Glu Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Tyr Pro Thr Thr Gly Tyr Thr Glu Ser Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Phe Leu Leu Arg Pro Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr
            100                 105                 110
Val Thr Val Ser Ser
        115
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<210> 612
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<220>
<223> Anti-RON mAb 11H09 light chain CDR1

<400> 612
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Gln Asp Ile Gly Ser Ser
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<210> 613
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<220>
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Ser Thr Ser
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<400> 614
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Leu Gln Tyr Ala Ser Ser Pro Trp Thr
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<210> 615
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<220>
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<400> 615
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Gly Tyr Thr Phe Thr Ser Tyr Trp
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<210> 616
<211> 8
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<220>
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<400> 616
Ile Tyr Pro Thr Thr Gly Tyr Thr
 1   5

<210> 617
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<220>
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<400> 617
Phe Leu Leu Arg Pro Trp Tyr Phe Asp Val
 1   5   10

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<220>
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<400> 618
Asn Ser
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<210> 619
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<220>
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<400> 619
Ser Cys Pro Pro Cys Pro
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<210> 620
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<220>
<223> Made in a lab

<400> 620
Gly Gly Gly Gly Ser Gly Asn Ser
 1   5

<210> 621
<211> 8
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<220>
<223> Made in a lab

<400> 621
Gly Cys Pro Pro Cys Pro Asn Ser
 1   5

<210> 622
<211> 8
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<220>
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<400> 622
Gly Ser Pro Pro Ser Pro Asn Ser
 1   5

<210> 623
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<220>
<223> Made in a lab

<400> 623
Gly Ser Pro Pro Ser Pro Asn Ser
 1   5

<210> 624
<211> 8
<212> PRT
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<223> Made in a lab

<400> 624
Gly Cys Pro Pro Cys Pro Asn Ser
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<210> 625
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<223> Made in a lab

<400> 625
Gly Cys Pro Pro Cys Pro Asn Ser
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<210> 626
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<212> PRT
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<220>
<223> Made in a lab

<400> 626
Gly Cys Pro Pro Cys Pro Gly Asn Ser
 1   5

<210> 627

<211> 9
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<220>
<223> Made in a lab

<400> 627
Gly Cys Pro Pro Cys Pro Ala Asn Ser
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<210> 628
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 628
Gly Cys Pro Pro Cys Pro Ala Asn Ser
 1   5

<210> 629
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 629
Glu Glu Glu Glu Asp Glu Gly Asn Ser
 1   5

<210> 630
<211> 10
<212> PRT
<213> Artificial Sequence

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<223> Made in a lab

<400> 630
Asn Tyr Gly Gly Gly Gly Ser Gly Asn Ser
 1   5   10

<210> 631
<211> 10
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<220>
<223> Made in a lab

<400> 631
Val Ser Glu Arg Pro Phe Pro Pro Asn Ser
 1   5   10

<210> 632
<211> 11
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<220>
<223> Made in a lab

<400> 632

Glu Pro Lys Ser Cys Asp Lys Thr Cys Cys Pro
1 5 10

<210> 633
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 633
Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ser
1 5 10

<210> 634
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<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 634
Gly Gly Gly Gly Ser Cys Pro Pro Cys Pro Asn Ser
1 5 10

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<220>
<223> Made in a lab

<400> 635
Lys Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
1 5 10

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<223> Made in a lab

<400> 636
Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
1 5 10

<210> 637
<211> 13
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<223> Made in a lab

<400> 637
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Cys Pro
1 5 10

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<220>
<223> Made in a lab

<400> 638
Glu Pro Lys Ser Cys Asp Lys Thr Cys Pro Pro Cys Pro
 1   5   10

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<220>
<223> Made in a lab

<400> 639
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser
 1   5   10

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<400> 640
Gly Cys Pro Pro Cys Pro Gly Gly Gly Gly Ser Asn Ser
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<400> 641
Gly Gly Gly Gly Ser Cys Pro Pro Cys Pro Gly Asn Ser
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<400> 642
Gly Cys Pro Pro Cys Pro Gly Gly Gly Gly Ser Asn Ser
 1   5   10

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<223> Made in a lab

<400> 643
Gly Gly Gly Ala Ser Cys Pro Pro Cys Pro Gly Asn Ser
 1   5   10

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<400> 644
Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Gly Asn Ser
 1   5   10

<210> 645
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<223> Made in a lab

<400> 645
Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Gly Asn Ser
 1   5   10

<210> 646
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<223> Made in a lab

<400> 646
Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser
 1   5   10   15

<210> 647
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<220>
<223> Made in a lab

<400> 647
Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
 1   5   10   15

<210> 648
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<223> Made in a lab

<400> 648
Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
 1   5   10   15

<210> 649
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 649

Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Asn Ser
1 5 10 15

<210> 650
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 650
Leu Asp Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Asn Ser
1 5 10 15

<210> 651
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 651
Arg Glu Gln Leu Ala Glu Val Thr Leu Ser Leu Lys Ala Asn Ser
1 5 10 15

<210> 652
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 652
Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
1 5 10 15

<210> 653
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 653
Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Ser Asn Ser
1 5 10 15

<210> 654
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 654
Leu Pro Pro Glu Thr Gln Glu Ser Gln Glu Val Thr Leu Asn Ser
1 5 10 15

<210> 655
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 655
Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro Asn Ser
 1   5   10   15

<210> 656
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 656
Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
 1   5   10   15

<210> 657
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 657
Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
 1   5   10   15

<210> 658
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 658
Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
 1   5   10   15

<210> 659
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 659
Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
 1   5   10   15

<210> 660
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 660
Lys Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys Pro Asn Ser
 1   5   10   15

<210> 661

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

<220>
<223> Made in a lab

<400> 661
Lys Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys Pro Asn Ser
 1   5   10   15

<210> 662
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 662
Gln Tyr Asn Cys Pro Gly Gln Tyr Thr Phe Ser Met Pro Asn Ser
 1   5   10   15

<210> 663
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 663
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10   15

<210> 664
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 664
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 665
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 665
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Ser
 1   5   10   15

<210> 666
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 666

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

<210> 667
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 667
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 668
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 668
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Ser
1 5 10 15

<210> 669
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 669
Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro
1 5 10 15

<210> 670
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 670
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Ser
1 5 10 15

<210> 671
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 671
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Ser
1 5 10 15

<210> 672
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 672
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Ser
 1   5   10   15

<210> 673
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 673
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
 1   5   10   15

<210> 674
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 674
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
 1   5   10   15

<210> 675
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 675
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
 1   5   10   15

<210> 676
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 676
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Pro
 1   5   10   15

<210> 677
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 677
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Pro
 1   5   10   15

<210> 678

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

<220>
<223> Made in a lab

<400> 678
Gly Gly Gly Gly Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 679
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 679
Glu Pro Lys Ser Cys Gly Gly Gly Gly Gly Cys Pro Pro Cys Pro
 1   5   10   15

<210> 680
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 680
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Gly Gly Cys Pro
 1   5   10   15

<210> 681
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 681
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Gly
 1   5   10   15

<210> 682
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 682
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Ser Pro
 1   5   10   15

<210> 683
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 683

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

<210> 684
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 684
Glu Pro Lys Ser Cys Asp Lys Thr Cys Cys Cys Pro Pro Cys Pro
1 5 10 15

<210> 685
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 685
Glu Pro Lys Ser Cys Pro Pro Pro Pro Pro Cys Pro Pro Cys Pro
1 5 10 15

<210> 686
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 686
Pro Pro Pro Pro Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 687
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 687
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Trp Trp Cys Pro
1 5 10 15

<210> 688
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 688
Glu Pro Lys Ser Cys Asp Trp Trp His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 689
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 689
Glu Pro Lys Cys Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 690
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 690
Glu Pro Lys Ser Asp Cys Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 691
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 691
Glu Pro Lys Ser Asp Cys Trp Trp His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 692
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 692
Glu Pro Lys Ser Cys Asp Phe Phe His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 693
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 693
Glu Pro Lys Ser Cys Asp Trp Trp Trp Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 694
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 694
Glu Pro Lys Ser Cys Trp Trp Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 695

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

<220>
<223> Made in a lab

<400> 695
Glu Pro Trp Trp Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 696
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 696
Ser Gln Pro Glu Ile Val Pro Ile Ser Cys Pro Pro Cys Pro Asn Ser
 1   5   10   15

<210> 697
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 697
Thr Gly Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 1   5   10   15
Pro

<210> 698
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 698
Glu Pro Lys Ser Thr Asp Lys Thr His Thr Cys Pro Pro Cys Pro Asn
 1   5   10   15
Ser

<210> 699
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 699
Glu Pro Lys Ser Thr Asp Lys Thr His Thr Ser Pro Pro Ser Pro Asn
 1   5   10   15
Ser

<210> 700
<211> 17
<212> PRT

<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 700
Glu Pro Lys Ser Thr Asp Lys Thr His Thr Cys Pro Pro Cys Pro Asn
 1   5   10   15
Ser

<210> 701
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 701
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Asn
 1   5   10   15
Ser

<210> 702
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 702
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Gly Gly Gly Pro
 1   5   10   15
Cys Pro

<210> 703
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 703
Glu Pro Lys Ser Cys Asp Gly Gly Gly Lys Thr His Thr Cys Pro Pro
 1   5   10   15
Cys Pro

<210> 704
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 704
Glu Pro Lys Ser Cys Asp Pro Pro Pro Lys Thr His Thr Cys Pro Pro
 1   5   10   15
Cys Pro

<210> 705

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

<220>
<223> Made in a lab

<400> 705
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Pro Pro Pro
 1   5   10   15
Cys Pro

<210> 706
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 706
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1   5   10   15
Asn Ser

<210> 707
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 707
Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1   5   10   15
Ser Asn Ser

<210> 708
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 708
Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Ser Pro Pro Cys
 1   5   10   15
Pro Asn Ser

<210> 709
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 709
Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Ser Cys Pro Pro Cys
 1   5   10   15
Pro Asn Ser

<210> 710
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 710
Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala
 1   5   10   15
Arg His Ser Pro
            20

<210> 711
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 711
Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Ser Cys Pro Pro
 1   5   10   15
Cys Pro Asn Ser
            20

<210> 712
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 712
Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Cys Pro Pro
 1   5   10   15
Cys Pro Asn Ser
            20

<210> 713
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 713
Arg Glu Gln Leu Ala Glu Val Thr Leu Ser Leu Lys Ala Cys Pro Pro
 1   5   10   15
Cys Pro Asn Ser
            20

<210> 714
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 714
Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Cys Pro Pro
 1   5   10   15

Cys Pro Asn Ser
20

<210> 715
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 715
Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro Cys Pro Pro
1 5 10 15
Cys Pro Asn Ser
20

<210> 716
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 716
Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
1 5 10 15
Cys Pro Asn Ser
20

<210> 717
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 717
Glu Glu Glu Glu Asp Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu
1 5 10 15
Asp Gly Asn Ser
20

<210> 718
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 718
Leu Asp Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Ser Cys Pro
1 5 10 15
Pro Cys Pro Asn Ser
20

<210> 719
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 719

Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Ser Cys Pro
1 5 10 15
Pro Cys Pro Asn Ser
20

<210> 720
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 720
Leu Pro Pro Glu Thr Gln Glu Ser Gln Glu Val Thr Leu Ser Cys Pro
1 5 10 15
Pro Cys Pro Asn Ser
20

<210> 721
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 721
Glu Pro Ala Phe Thr Pro Gly Pro Asn Ile Glu Leu Gln Lys Asp Ser
1 5 10 15
Asp Cys Pro Asn Ser
20

<210> 722
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 722
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg
1 5 10 15
His Cys Pro Asn Ser
20

<210> 723
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 723
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Arg
1 5 10 15
His Ser Pro Asn Ser
20

<210> 724
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 724
Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1   5   10   15
Ser Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            20   25   30
Gly Ser Asn Ser
        35

<210> 725
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 725
Arg Thr Arg Tyr Leu Gln Val Ser Gln Gln Leu Gln Gln Thr Asn Arg
 1   5   10   15
Val Leu Glu Val Thr Asn Ser Ser Leu Arg Gln Gln Leu Arg Leu Lys
            20   25   30
Ile Thr Gln Leu Gly Gln Ser Ala Glu Asp Leu Gln Gly Ser Arg Arg
        35   40   45
Glu Leu Ala Gln Ser Gln Glu Ala Leu Gln Val Glu Gln Arg Ala His
    50   55   60
Gln Ala Ala Glu Gly Gln Leu Gln Ala Cys Gln Ala Asp Arg Gln Lys
65   70   75   80
Thr Lys Glu Thr Leu Gln Ser Glu Glu Gln Gln Arg Arg Ala Leu Glu
                85   90   95
Gln Lys Leu Ser Asn Met Glu Asn Arg Leu Lys Pro Phe Phe Thr Cys
            100   105   110
Gly Ser Ala Asp Thr Cys Cys Pro Asn Ser
        115   120

<210> 726
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 726
Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Gly Asn Ser
 1   5   10

<210> 727
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 727
Asn Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 1   5   10   15
Gly Ser Gly Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            20   25   30
Gly Gly Gly Ser Gly Asn Ser
        35

<210> 728
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 728
Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1   5   10   15
Ser Gly Asn Ser
            20

<210> 729
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 729
Ser Pro Pro Ser Pro Asn Ser
 1   5

<210> 730
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 730
Glu Pro Thr Ser Thr Asp Lys Thr His Thr Ser Pro Pro Ser Pro Asn
 1   5   10   15
Ser

<210> 731
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 731
Glu Pro Thr Ser Thr Asp Lys Thr His Thr Cys Pro Pro Cys Pro Asn
 1   5   10   15
Ser

<210> 732
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 732
Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Ser Pro Pro Cys
 1   5   10   15
Pro Asn Ser

<210> 733
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 733
Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Asn Ser
 1   5   10

<210> 734
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 734
Arg Thr Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys
 1   5   10   15
Ala Arg His Ser Gly His
            20

<210> 735
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 735
Arg Thr Arg Tyr Leu Gln Val Ser Gln Gln Leu Gln Gln Thr Asn Arg
 1   5   10   15
Val Leu Glu Val Thr Asn Ser Ser Leu Arg Gln Gln Leu Arg Leu Lys
            20   25   30
Ile Thr Gln Leu Gly Gln Ser Ala Glu Asp Leu Gln Gly Ser Arg Arg
        35   40   45
Glu Leu Ala Gln Ser Gln Glu Ala Leu Gln Val Glu Gln Arg Ala His
    50   55   60
Gln Ala Ala Glu Gly Gln Leu Gln Ala Cys Gln Ala Asp Arg Gln Lys
65   70   75   80
Thr Lys Glu Thr Leu Gln Ser Glu Glu Gln Gln Arg Arg Ala Leu Glu
                85   90   95
Gln Lys Leu Ser Asn Met Glu Asn Arg Leu Lys Pro Phe Phe Thr Cys
            100   105   110
Gly Ser Ala Asp Thr Cys
        115

<210> 736
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 736
Arg Thr Gln Ser Glu Glu Gln Gln Arg Arg Ala Leu Glu Gln Lys Leu
 1   5   10   15
Ser Asn Met Glu Asn Arg Leu Lys Pro Phe Phe Thr Cys Gly Ser Ala
            20   25   30
Asp Thr Cys
        35

<210> 737
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 737
Arg Thr Glu Gln Lys Leu Ser Asn Met Glu Asn Arg Leu Lys Pro Phe
 1   5   10   15
Phe Thr Cys Gly Ser Ala Asp Thr Cys
            20   25

<210> 738
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 738
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10   15
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            20   25

<210> 739
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 739
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser
 1   5   10   15

<210> 740
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 740
Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 741
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 741
Gly Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro
 1   5   10   15
Cys Pro

<210> 742
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 742
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 743
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 743
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Lys Ala Arg
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 744
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 744
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Arg
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 745
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 745
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Gly
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 746
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 746
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Met Ala Gly
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 747
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 747
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Arg Thr Gln Met Ala Arg
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 748
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 748
Pro Pro Pro Pro Pro Cys Pro Pro Cys Pro
 1   5   10

<210> 749
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 749
Thr Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1   5   10   15

<210> 750
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 750
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Cys
 1   5   10   15
Pro Pro Cys Pro
            20

<210> 751
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 751
Glu Pro Lys Ser Ser Asp Thr Pro Pro Pro Ser Pro Arg Ser Pro Cys
 1   5   10   15
Pro Pro Cys Pro
            20

<210> 752
<211> 23
<212> PRT

<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 752
Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser
 1   5   10   15
Pro Ser Cys Pro Pro Cys Pro
            20

<210> 753
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 753
Arg Thr Glu Pro Arg Val Pro Ile Thr Gln Asn Pro Cys Pro Pro Leu
 1   5   10   15
Lys Glu Cys Pro Pro Cys Ala
            20

<210> 754
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 754
Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala Gln Pro Gln
 1   5   10   15
Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro Ala Thr Thr Arg
            20   25   30
Asn Thr Cys Pro Pro Cys Pro
        35

<210> 755
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 755
Gln Glu Lys Glu Ala Ile Glu Arg Leu Lys Ala Ala Gly Ala Pro Glu
 1   5   10   15
Ser Leu Val Ile Gln Ala Tyr Phe Ala Ser Glu Lys Asn Glu Asn Leu
            20   25   30
Ala Ala Asn Phe Leu Leu Ser Gln Asn Phe Asp Asp Glu Cys Pro Pro
        35   40   45
Cys Pro
    50

<210> 756
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 756
Gln Glu Lys Glu Ala Ile Glu Arg Leu Lys Ala Ala Gly Ala Pro Glu
1 5 10 15
Ser Leu Val Ile Gln Ala Tyr Phe Ala Ser Glu Lys Asn Glu Asn Leu
20 25 30
Ala Ala Asn Phe Leu Leu Ser Gln Asn Phe Asp Asp Glu Cys Pro Pro
35 40 45
Cys Pro Ser Gly
50

<210> 757
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 757
Ser Arg Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Ser
1 5 10 15
Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val
20 25 30
Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly
35 40 45
Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly
50 55 60
Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp
65 70 75 80
Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr
85 90 95
Phe Glu Asp Ser Thr Lys Lys Ser Ala Cys Pro Pro Cys Pro
100 105 110

<210> 758
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 758
Ser Arg Asp Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Ser
1 5 10 15
Asp Gly Gly Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val
20 25 30
Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly
35 40 45
Gln Val Met Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly
50 55 60
Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp
65 70 75 80
Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr
85 90 95
Phe Glu Asp Ser Thr Lys Lys Ser Ala Cys Pro Pro Cys Ser Gly
100 105 110

<210> 759
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge sequence

<400> 759
Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val Pro Pro Arg Asp
 1   5   10   15
Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile Cys Gln Ala Thr
            20   25   30
Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu Arg Glu Gly Lys
        35   40   45
Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln Ala Glu Ala Lys
    50   55   60
Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr Leu Thr Ile Lys
65   70   75   80
Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys Arg Val Asp His
                85   90   95
Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met Ser Val Pro Cys
            100   105   110
Pro Pro Cys Pro
        115

<210> 760
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> linker sequence of monoIL-10

<400> 760
Gly Gly Gly Ser Gly Gly
 1   5

<210> 761
<211> 106
<212> PRT
<213> Homo sapiens

<400> 761
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 1   5   10   15
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            20   25   30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        35   40   45
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    50   55   60
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65   70   75   80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                85   90   95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
            100   105

<210> 762
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1 CH2 CH3 Null2 desLys

<400> 762
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
 1   5   10   15
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

```
            20                  25                  30
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        35                  40                  45
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
                85                  90                  95
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            100                 105                 110
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        115                 120                 125
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130                 135                 140
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145                 150                 155                 160
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                165                 170                 175
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            180                 185                 190
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        195                 200                 205
Lys Ser Leu Ser Leu Ser Pro Gly
    210                 215
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<210> 763
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 763
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Ser Pro Pro Ser Pro Asn Ser
 1               5
```

<210> 764
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 764
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Glu Pro Thr Ser Thr Asp Lys Thr His Thr Ser Pro Pro Ser Pro Asn
 1               5                   10                  15
Ser
```

<210> 765
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 765
```
Glu Pro Thr Ser Thr Asp Lys Thr His Thr Cys Pro Pro Cys Pro Asn
 1               5                   10                  15
Ser
```

<210> 766
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 766
Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser
 1   5   10   15

<210> 767
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 767
Asn Ser Gly Ala Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
 1   5   10   15
Ser Pro Asn Ser
            20

<210> 768
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 768
Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser
 1   5   10

<210> 769
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 769
Asn Ser Gly Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
 1   5   10   15
Ser Pro Asn Ser
            20

<210> 770
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 770
Asn Ser Leu Ala Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr

1 5 10 15
Ser Pro Asn Ser
20

<210> 771
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 771
Asn Ser Leu Phe Ser Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
1 5 10 15
Ser Pro Asn Ser
20

<210> 772
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 772
Asn Ser Leu Ala Ser Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
1 5 10 15
Ser Pro Asn Ser
20

<210> 773
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 773
Glu Gln Lys Leu Ser Asn Met Glu Asn Arg Leu Lys Pro Phe Phe Thr
1 5 10 15
Ser Gly Ser Ala Asp Thr Ser Pro Asn Ser
20 25

<210> 774
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 774
Gln Arg His Ala Asn Ser Ala Leu Asn Thr Gly Thr Gln Met Ala Gly
1 5 10 15
His Ser Pro Asn Ser
20

<210> 775
<211> 21
<212> PRT

<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 775
Gln Arg His Asn Ala Ala Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 776
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 776
Gln Arg His Ala Ala Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 777
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 777
Gln Arg His Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser
 1   5   10   15
Pro Asn Ser

<210> 778
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 778
Gln Arg His Gly Gly Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
 1   5   10   15
His Ser Pro Asn Ser
            20

<210> 779
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 779
His Asp Gly Ser Ser Leu Asn Thr Pro Asn Ser
 1   5   10

<210> 780
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 780
Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser
1 5 10 15

<210> 781
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 781
Ser Ser Leu Asn Thr Arg Thr Gln Met Ala Gly His Ser Pro Asn Ser
1 5 10 15

<210> 782
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 782
Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Arg His Ser Pro Asn Ser
1 5 10 15

<210> 783
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 783
Ser Ser Leu Asn Thr Gly Thr Gln Lys Ala Gly His Ser Pro Asn Ser
1 5 10 15

<210> 784
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 784
Ser Ser Leu Asn Thr Gly Thr Gln Lys Ala Arg His Ser Pro Asn Ser
1 5 10 15

<210> 785

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

<220>
<223> Peptide linker

<400> 785
Ser Ser Leu Asn Thr Arg Thr Gln Met Ala Arg His Ser Pro Asn Ser
1 5 10 15

<210> 786
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 786
Ser Ser Leu Asn Thr Arg Thr Gln Lys Ala Gly His Ser Pro Asn Ser
1 5 10 15

<210> 787
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 787
Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Pro Asn
1 5 10 15
Ser

<210> 788
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 788
Asn Ser Leu Phe Asn Gln Glu Val Gln Ile Pro Pro Asn Ser
1 5 10

<210> 789
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 789
Asn Ser Leu Phe Asn Gln Glu Val Pro Asn Ser
1 5 10

<210> 790
<211> 13

<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 790
Gln Arg His Asn Asn Ser Ser Leu Asn Thr Pro Asn Ser
 1   5   10

<210> 791
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker

<400> 791
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1   5   10   15
Pro Asn Ser

<210> 792
<211> 2730
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC038 comprises: G19-4 (anti-CD3) scFv, human
      IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3,
      human Ck(YAE), H75 linker and 3D1 (anti-CD86) scFv

<400> 792
acgactcact atagggagac ccaagcttgc cgccatggaa gcaccagcgc agcttctctt 60
cctcctgcta ctctggctcc cagataccac cggtgaggtc cagctgcaac agtctggacc 120
tgaactggtg aagcctggag cttcaatgaa gatttcctgc aaggcctctg gttactcatt 180
cactggctac atcgtgaact ggctgaagca gagccatgga aagaaccttg agtggattgg 240
acttattaat ccatacaaag gtcttactac ctacaaccag aaattcaagg gcaaggccac 300
attaactgta gacaagtcat ccagcacagc ctacatggag ctcctcagtc tgacatctga 360
agactctgca gtctattact gtgcaagatc tgggtactat ggtgactcgg actggtactt 420
cgatgtctgg ggcgcaggga ccacggtcac cgtctcaagc ggtggcggag ggtctggggg 480
tggcggatcc ggaggtggtg gctctgcaca agacatccag atgacacaga ctacatcctc 540
cctgtctgcc tctctgggag acagagtcac catcagttgc agggcaagtc aggacattcg 600
caattattta aactggtatc agcagaaacc agatggaact gttaaactcc tgatctacta 660
cacatcaaga ttacactcag gagtcccatc aaggttcagt ggcagtgggt ctggaacaga 720
ttattctctc accattgcca acctgcaacc agaagatatt gccacttact tttgccaaca 780
gggtaatacg cttccgtgga cgttcggtgg aggcaccaaa ctggtaacca aacgctcgag 840
cgagcccaaa tcttctgaca aaactcacac atgcccaccg tgcccatccg gagcacctga 900
actcctgggt ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat 960
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caagttcaac tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga 1080
ggagcagtac aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg 1140
gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga 1200
gaaaaccatc tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc 1260
atcccgggat gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta 1320
tccaagcgac atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac 1380
cacgcctccc gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga 1440
caagagcagg tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca 1500
caaccactac acgcagaaga gcctctccct gtctccgggt aaatctagaa ctgtggctgc 1560
accatctgtc ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt 1620
tgtgtgcctg ctgaattact tctatcccag agaggccaaa gtacagtgga aggtggataa 1680
cgccctccaa tcgggtaact cccaggagag tgccacagag caggacagca aggacagcac 1740
ctacagcctc agcagcgagc tgacgctgag caaagcagac tacgagaaac acaaagtcta 1800
cgcctgcgaa gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg 1860
agagcagagg cacaacaatt cttccctgaa tacaggaact cagatggcag gtcattctcc 1920

gaattctcag gtccagctgc agcagtctgg gcctgagctg gtgaggcctg gggaatcagt 1980
gaagatttcc tgcaagggtt ccggctacac attcactgat tatgctatac agtgggtgaa 2040
gcagagtcat gcaaagagtc tagagtggat tggagttatt aatatttact atgataatac 2100
aaactacaac cagaagttta agggcaaggc cacaatgact gtagacaaat cctccagcac 2160
agcctatatg gaacttgcca gattgacatc tgaggattct gccatctatt actgtgcaag 2220
agcggcctgg tatatggact actggggtca aggaacctca gtcaccgtct cctcaggggg 2280
tggaggctct ggtggcggtg gctctggcgg aggtggatcc ggtggcggcg gatctgacat 2340
tgtgctgtca cagtctccat cctccctggc tgtgtcagca ggagagaagg tcactatgag 2400
ctgcaaatcc agtcagagtc tgctcaacag tagaacccga gagaactact tggcttggta 2460
ccagcagaaa ccagggcagt ctcctaaact gctgatctac tgggcatcca ctagggaatc 2520
tggggtccct gatcgcttca caggcagtgg atctgggaca gatttcactc tcaccatcag 2580
cagtgtgcag gctgaagacc tggcagttta ttactgcacg caatcttata atctttacac 2640
gttcggaggg gggaccaagc tggaaataaa ataatctaga gcggccgctc tagagggccc 2700
tattctatag tgtcacctaa atgctagagg 2730

<210> 793
<211> 1821
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC039 comprises: BMA031 (anti-TCR) scFv, human
IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3,
and human Ck(YAE)

<400> 793
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
ggacaggtcc aactagttca gtctggagca gaggttaaga agcctgggag ctcagtgaag 120
gtttcctgca aggcttccgg atataaattc actagctatg ttatgcactg ggtgaagcag 180
gcacctggcc aggggctcga gtggattgga tatattaatc cttacaatga tgttactaag 240
tacaatgaga agttcaaagg caaggccaca cttacggccg acgagtccac taatacagcc 300
tacatggagc tgagcagcct gagatctgag gacactgcgg tccattactg tgcaagaggg 360
agctactatg attacgacgg gtttgtttac tggggccaag gtaccctggt caccgtctca 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagatatc 480
cagatgaccc aatctccatc gaccctgagt gcatctgtcg gggacagagt caccatgacc 540
tgcagtgcca cctcaagtgt aagttacatg cactggtatc agcagaagcc cgggaaggct 600
cccaaaagat ggatctatga cacatccaaa ctggcttctg gagtccctgc gcgcttcatt 660
ggcagtgggt ctgggaccga gttcacgctc acaatcagca gcctgcagcc agatgatttc 720
gctacgtatt actgccagca gtggagtagt aacccgctca cgttcggtgg aggtaccaag 780
gtcgagatta aatcctcgag cgagcccaaa tcttctgaca aaactcacac atgcccaccg 840
tgcccagcac ctgaactcct gggtggaccg tcagtcttcc tcttcccccc aaaacccaag 900
gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac 960
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 1020
acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 1080
ctgcaccagg actggctgaa tggcaaggag tacaagtgca aggtctccaa caaagccctc 1140
ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg 1200
tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 1260
gtcaaaggct tctatccaag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1320
aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1380
aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1440
catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaatct 1500
agaactgtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 1560
ggaactgcct ctgttgtgtg cctgctgaat tacttctatc ccagagaggc caaagtacag 1620
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgccac agagcaggac 1680
agcaaggaca gcacctacag cctcagcagc gagctgacgc tgagcaaagc agactacgag 1740
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 1800
agcttcaaca ggggagagtg a 1821

<210> 794
<211> 1821
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC041 comprises: CRIS7 (anti-CD3) scFv, human
IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3,
and human Ck(YAE)

<400> 794
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<210> 795
<211> 1773
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC043 comprises: OKT3-M (Micromet variant
anti-CD3, see also US 7,635,472) scFv, human IgG1
SCC-P hinge, human IgG1 CH2, human IgG1 CH3, and
human Ck(YAE)

<400> 795
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<210> 796
<211> 2088
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC049 comprises: HD37 (anti-CD19) scFv, human IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human IgG1 CH3, and human IgG1 CH1

<400> 796
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<210> 797
<211> 2067
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC050 comprises: 2H7 (anti-CD20) scFv, human IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human IgG1 CH3, and human IgG1 CH1

<400> 797
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<210> 798
<211> 2055
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC051 comprises: P2C2 (anti-CD79) scFv, human IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human IgG1 CH3, and human IgG1 CH1

<400> 798

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<210> 799
<211> 1870
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC052 comprises: 5D5 (anti-cMet) scFv, human IgG1
SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human
IgG1 CH3, and human IgG1 CH1

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<210> 800
<211> 1827
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC053 comprises: G19-4 (anti CD3) scFv, human
IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null),
human IgG1 CH3, and human Ck(YAE)

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accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 1140
gccctcccag ccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1200
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1260
tgcctggtca aaggcttcta tccaagcgac atcgccgtgg agtgggagag caatgggcag 1320
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1380
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1440
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aaatctagaa ctgtggctgc accatctgtc ttcatcttcc cgccatctga tgagcagttg 1560
aaatctggaa ctgcctctgt tgtgtgcctg ctgaattact tctatcccag agaggccaaa 1620
gtacagtgga aggtggataa cgccctccaa tcgggtaact cccaggagag tgccacagag 1680
caggacagca aggacagcac ctacagcctc agcagcgagc tgacgctgag caaagcagac 1740
tacgagaaac acaaagtcta cgcctgcgaa gtcacccatc agggcctgag ctcgcccgtc 1800
acaaagagct tcaacagggg agagtga 1827

<210> 801
<211> 2707
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC064 comprises: G19-4 (anti-CD3) scFv, human
IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3,
human Ck(YAE), H75 linker, and Met021 (anti-c-Met)
scFv

<400> 801
atacgactca ctatagggag acccaagctt gccgccatgg aagcaccagc gcagcttctc 60
ttcctcctgc tactctggct cccagatacc accggtgagg tccagctgca acagtctgga 120
cctgaactgg tgaagcctgg agcttcaatg aagatttcct gcaaggcctc tggttactca 180
ttcactggct acatcgtgaa ctggctgaag cagagccatg gaaagaacct tgagtggatt 240
ggacttatta atccatacaa aggtcttact acctacaacc agaaattcaa gggcaaggcc 300
acattaactg tagacaagtc atccagcaca gcctacatgg agctcctcag tctgacatct 360
gaagactctg cagtctatta ctgtgcaaga tctgggtact atggtgactc ggactggtac 420
ttcgatgtct ggggcgcagg gaccacggtc accgtctcaa gcggtggcgg agggtctggg 480
ggtggcggat ccggaggtgg tggctctgca caagacatcc agatgacaca gactacatcc 540
tccctgtctg cctctctggg agacagagtc accatcagtt gcagggcaag tcaggacatt 600
cgcaattatt taaactggta tcagcagaaa ccagatggaa ctgttaaact cctgatctac 660
tacacatcaa gattacactc aggagtccca tcaaggttca gtggcagtgg gtctggaaca 720
gattattctc tcaccattgc caacctgcaa ccagaagata ttgccactta cttttgccaa 780
cagggtaata cgcttccgtg gacgttcggt ggaggcacca aactggtaac caaacgctcg 840
agcgagccca aatcttctga caaaactcac acatgcccac cgtgcccagc acctgaactc 900
ctgggtggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 960
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 1020
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1080
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1140
aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1200
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1260
cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 1320

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1380
cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1440
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1500
cactacacgc agaagagcct ctccctgtct ccgggtaaat ctagaactgt ggctgcacca 1560
tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg 1620
tgcctgctga attacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 1680
ctccaatcgg gtaactccca ggagagtgcc acagagcagg acagcaagga cagcacctac 1740
agcctcagca gcgagctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 1800
tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag 1860
cagaggcaca acaattcttc cctgaataca ggaactcaga tggcaggtca ttctccgaat 1920
tctgacatcc agatgaccca gtctccatcc tccctgtctg catctgtagg agacagagtc 1980
accatcactt gtcgggcaag tcagagcatt aggaactatt taaattggta tcagcaggaa 2040
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tcaaggttca gtggcagtgg atctgggaca gacttcattc tcaccatcag cagtctgcag 2160
cctgaagatt ttgcaactta ctactgtcaa cagagttacg ttaccccgct cactttcggc 2220
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ggtggatccg gtggcggcgg ctctgaagtt caattgttag agtctggtgg cggtcttgtt 2340
cagcctggtg gttctttacg tctttcttgc gctgcttccg gattcacttt ctctaagtac 2400
gatatgcttt gggttcgcca agctcctggt aaaggtttgg agtgggtttc ttatatctat 2460
ccttctggtg gccttactga gtatgctgac tccgttaaag gtcgcttcac tatctctaga 2520
gacaactcta agaatactct ctacttgcag atgaacagct taagggctga ggacacggcc 2580
gtgtattact gtgcgagacg ggctccccgg tcccttttctt ttgatatctg gggccaaggg 2640
acaatggtca ccgtctaagc ggccgctcta gagggcccta ttctatagtg tcacctaaat 2700
gctagag 2707

<210> 802
<211> 1812
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC076 comprises: OKT3 (anti-CD3) scFv, human IgG1
SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human
IgG1 CH3, and human Ck(YAE)

<400> 802
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caggtccagc tgcagcagtc tggggctgaa ctggcaagac ctggggcctc agtgaagatg 120
tcctgcaagg cttctggcta caccttttact aggtacacga tgcactgggt aaaacagagg 180
cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 240
aatcagaagt tcaaggacaa ggccacattg actacagaca aatcctccag cacagcctac 300
atgcaactga gcagcctgac atctgaggac tctgcagtct attactgtgc aagatattat 360
gatgatcatt actgccttga ctactggggc caaggcacca cggtcaccgt ctcaagcggt 420
ggcggagggt ctgggggtgg cggatccgga ggtggtggct ctgcacaaca aattgttctc 480
acccagtctc cagcaatcat gtctgcatct ccaggggaga aggtcaccat gacctgcagt 540
gccagctcaa gtgtaagtta catgaactgg taccagcaga agtcaggcac ctcccccaaa 600
agatggattt atgacacatc caaactggct tctggagtcc ctgctcactt caggggcagt 660
gggtctggga cctcttactc tctcacaatc agcggcatgg aggctgaaga tgctgccact 720
tattactgcc agcagtggag tagtaaccca ttcacgttcg gctcggggac aaagttggaa 780
ataaactcga gtgagcccaa atcttctgac aaaactcaca catgcccacc gtgcccagca 840
cctgaagccg cgggtgcacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 900
atgatctccc ggacccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 960
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 1020
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 1080
gactggctga atggcaaggc gtacgcgtgc gcggtctcca acaaagccct cccagccccc 1140
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1200
ccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1260
ttctatccaa gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1320
aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc 1380
gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1440
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaatc tagaactgtg 1500
gctgcaccat ctgtcttcat cttcccgcca tctgatgagc agttgaaatc tggaactgcc 1560
tctgttgtgt gcctgctgaa ttacttctat cccagagagg ccaaagtaca gtggaaggtg 1620
gataacgccc tccaatcggg taactcccag gagagtgcca cagagcagga cagcaaggac 1680
agcacctaca gcctcagcag cgagctgacg ctgagcaaag cagactacga gaaacacaaa 1740
gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac 1800
aggggagagt ga 1812

<210> 803
<211> 1821
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC077 comprises: HuM291 (anti-CD3) scFv, human IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human IgG1 CH3, and human Ck(YAE)

<400> 803
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
caggtccagc ttgtccagtc tggggctgaa gtcaagaaac ctggcgccag cgtgaaggtc 120
tcctgcaagg cttctggcta cacctttatt agttacacga tgcattgggt aaggcaggcc 180
cctggacagg gtctggaatg gatgggatat attaatccga gaagtgggta tactcattac 240
aatcagaagt taaaggacaa ggcaacactt accgcggaca aatccgcgag cacagcctac 300
atggaactga gcagcctgag atctgaggac accgcagtct attactgtgc aagatcggcc 360
tactatgatt atgacggctt tgcttactgg ggccaaggaa ccctggtcac cgtctcaagc 420
ggtggcggag ggtctggggg tggcggatcc ggaggtggtg gctctgcaca agatattcag 480
atgacccagt ctccatcttc cctctctgct agcgtcgggg atagggtcac cataacctgc 540
tctgccagct caagtgtaag ttacatgaac tggtaccagc agaagccagg caaagctccc 600
aagagactaa tttatgacac atccaaactg gcttctggag tcccttctag gttcagtggc 660
agtggatctg ggaccgattt caccctcaca atcagctctc tgcagccaga agatttcgcc 720
acttattact gccagcaatg gagtagtaac ccacccacgt tcggtggagg gaccaaggtg 780
gagatcaaac gaacctcgag tgagcccaaa tcttctgaca aaactcacac atgcccaccg 840
tgcccagcac ctgaagccgc gggtgcaccg tcagtcttcc tcttcccccc aaaacccaag 900
gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac 960
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 1020
acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 1080
ctgcaccagg actggctgaa tggcaaggcg tacgcgtgcg cggtctccaa caaagccctc 1140
ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg 1200
tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 1260
gtcaaaggct tctatccaag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1320
aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1380
aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1440
catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaatct 1500
agaactgtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 1560
ggaactgcct ctgttgtgtg cctgctgaat tacttctatc ccagagaggc caaagtacag 1620
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgccac agagcaggac 1680
agcaaggaca gcacctacag cctcagcagc gagctgacgc tgagcaaagc agactacgag 1740
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 1800
agcttcaaca ggggagagtg a 1821

<210> 804
<211> 1821
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC093 comprises from its amino to carboxy terminus: CRIS7 (anti-CD3) scFv, human IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human IgG1 CH3, and human Ck(YAE)

<400> 804
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
caggtccagc tggtgcagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 120
tcctgcaagg cttctggcta caccttttact agatctacga tgcactgggt aaggcaggcc 180
cctggaaagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 240
aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 300
ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 360
gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 480
cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 540
tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc cggcaaggcc 600
cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 660
ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 720
gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 780

ctacaaatta cacgctcgag tgagcccaaa tcttctgaca aaactcacac atgcccaccg 840
tgcccagcac ctgaagccgc gggtgcaccg tcagtcttcc tcttcccccc aaaacccaag 900
gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac 960
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 1020
acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 1080
ctgcaccagg actggctgaa tggcaaggcg tacgcgtgcg cggtctccaa caaagccctc 1140
ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg 1200
tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 1260
gtcaaaggct tctatccaag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1320
aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1380
aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1440
catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaatct 1500
agaactgtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 1560
ggaactgcct ctgttgtgtg cctgctgaat tacttctatc ccagagaggc caaagtacag 1620
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgccac agagcaggac 1680
agcaaggaca gcacctacag cctcagcagc gagctgacgc tgagcaaagc agactacgag 1740
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 1800
agcttcaaca ggggagagtg a 1821

<210> 805
<211> 1773
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC094 comprises: OKT3-M (Micromet variant
anti-CD3) scFv, human IgG1 SCC-P hinge, human IgG1
CH2(ADCC/CDC null), human IgG1 CH3, human Ck(YAE)

<400> 805
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gatatcaaac tgcagcagtc aggggctgaa ctggcaagac ctggggcctc agtgaagatg 120
tcctgcaaga cttctggcta caccttttact aggtacacga tgcactgggt aaaacagagg 180
cctggacagg gtctggaatg gattggatac attaatccta gccgtggtta tactaattac 240
aatcagaagt tcaaggacaa ggccacattg actacagaca aatcctccag cacagcctac 300
atgcaactga gcagcctgac atctgaggac tctgcagtct attactgtgc aagatattat 360
gatgatcatt actgccttga ctactggggc caaggcacca ctctcacagt ctcctcagtc 420
gaaggtggaa gtggaggttc tggtggaagt ggaggttcag gtggagtcga cgacattcag 480
ctgacccagt ctccagcaat catgtctgca tctccagggg agaaggtcac catgacctgc 540
agagccagtt caagtgtaag ttacatgaac tggtaccagc agaagtcagg cacctccccc 600
aaaagatgga tttatgacac atccaaagtg gcttctggag tcccttatcg cttcagtggc 660
agtgggtctg ggacctcata ctctctcaca atcagcagca tggaggctga agatgctgcc 720
acttattact gccaacagtg gagtagctcg agtgagccca aatcttctga caaaactcac 780
acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc 840
ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 900
gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 960
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1020
gtcctcaccg tcctgcacca ggactggctg aatggcaagg cgtacgcgtg cgcggtctcc 1080
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1140
gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1200
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gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1320
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tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1440
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acagagcagg acagcaagga cagcacctac agcctcagca gcgagctgac gctgagcaaa 1680
gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg 1740
cccgtcacaa agagcttcaa caggggagag tga 1773

<210> 806
<211> 1821
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC095 comprises: BMA031 (anti-TCR) scFv, human

IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null),
human IgG1 CH3, human Ck(YAE)

<400> 806
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
ggacaggtcc aactagttca gtctggagca gaggttaaga agcctgggag ctcagtgaag 120
gtttcctgca aggcttccgg atataaattc actagctatg ttatgcactg ggtgaagcag 180
gcacctggcc aggggctcga gtggattgga tatattaatc cttacaatga tgttactaag 240
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tacatggagc tgagcagcct gagatctgag gacactgcgg tccattactg tgcaagaggg 360
agctactatg attacgacgg gtttgtttac tggggccaag gtaccctggt caccgtctca 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagatatc 480
cagatgaccc aatctccatc gaccctgagt gcatctgtcg gggacagagt caccatgacc 540
tgcagtgcca cctcaagtgt aagttacatg cactggtatc agcagaagcc cgggaaggct 600
cccaaaagat ggatctatga cacatccaaa ctggcttctg gagtccctgc gcgcttcatt 660
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gctacgtatt actgccagca gtggagtagt aacccgctca cgttcggtgg aggtaccaag 780
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tgcccagcac ctgaagccgc gggtgcaccg tcagtcttcc tcttcccccc aaaacccaag 900
gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac 960
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 1020
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ctgcaccagg actggctgaa tggcaaggcg tacgcgtgcg cggtctccaa caaagccctc 1140
ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg 1200
tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 1260
gtcaaaggct tctatccaag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1320
aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1380
aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1440
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agaactgtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 1560
ggaactgcct ctgttgtgtg cctgctgaat tacttctatc ccagagaggc caaagtacag 1620
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgccac agagcaggac 1680
agcaaggaca gcacctacag cctcagcagc gagctgacgc tgagcaaagc agactacgag 1740
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 1800
agcttcaaca ggggagagtg a 1821

<210> 807
<211> 1836
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC096 comprises: HD37 (anti-CD19) scFv, human
IgG1 SCC-P hinge, human IgG1 CH2 (ADCC/CDC null),
human IgG1 CH3, human Ck(YAE)

<400> 807
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 180
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 240
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 300
cctgtggaga aggtggatgc tgcaacctat cactgccagc aaagtactga ggatccgtgg 360
acgttcggtg gaggcaccaa gctggaaatc aaaggtggcg gtggttcggg cggtggtggg 420
tcgggtggcg gcggagctag ccaggttcag ctgcagcagt ctggggctga gctggtgagg 480
cctgggtcct cagtgaagat ttcctgcaag gcttctggct atgcattcag tagctactgg 540
atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct 600
ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac 660
gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc 720
tatttctgtg caagacggga gactacgacg gtaggccgtt attactatgc tatggactac 780
tggggtcaag gaacctcagt caccgtctcc tcgagtgagc ccaaatcttc tgacaaaact 840
cacacatgcc caccgtgccc agcacctgaa gccgcgggtg caccgtcagt cttcctcttc 900
ccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 960
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gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 1080
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggcgtacgc gtgcgcggtc 1140
tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 1200
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1260

agcctgacct gcctggtcaa aggcttctat ccaagcgaca tcgccgtgga gtgggagagc 1320
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380
ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tctccgggta aatctagaac tgtggctgca ccatctgtct tcatcttccc gccatctgat 1560
gagcagttga aatctggaac tgcctctgtt gtgtgcctgc tgaattactt ctatcccaga 1620
gaggccaaag tacagtggaa ggtggataac gccctccaat cgggtaactc ccaggagagt 1680
gccacagagc aggacagcaa ggacagcacc tacagcctca gcagcgagct gacgctgagc 1740
aaagcagact acgagaaaca caaagtctac gcctgcgaag tcacccatca gggcctgagc 1800
tcgcccgtca caaagagctt caacagggga gagtga 1836

<210> 808
<211> 1812
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC097 comprises: 4C04 (anti-RON) scFv, human IgG1
SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human
IgG1 CH3, and human Ck(YAE) .

<400> 808
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gacattcaga tgacccagtc tcctgcctcc cagtctgcat ctctgggaga aagtgtcacc 120
atcacatgcc tggcaagtca gaccattggt acatggttag catggtatca gcagaaacca 180
gggaaatctc ctcagctcct gatttatgct gcaaccagct tggcagatgg ggtcccatca 240
aggttcagtg ctagtggatc tggcacaaaa ttttctttca agatcgacag cctacagtct 300
gaagattttg taagttatta ctgtcaacaa ctttacaata ctccgtggac gttcggtgga 360
ggcaccaagc tggaaatcaa aggtggcggt ggctctggcg gaggtggatc cggtggcggc 420
ggctctcaga tccagctgca gcagtctgga cctgagctgg tgaagcctgg gacttcagtg 480
aagatatcct gcaaggcttc tgactacaca ctcactgact tctatatgaa ctgggtgagg 540
cagaagcctg gacagggact tgagtggatt gggaggattt atcctggaac cgataaaact 600
agatacaatg agaaattcag ggacaaggcc atactgaccg tggacacgtc ctccagcaca 660
gcctacatgc agctcagcag cctgacatca gaggacactg ctgtctattt ctgtgcaaga 720
tccgcctact atggtaacta cgttgctatg gactactggg gtcaaggaac ctcagtcacc 780
gtctcctcga gtgagcccaa atcttctgac aaaactcaca catgcccacc gtgcccagca 840
cctgaagccg cgggtgcacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 900
atgatctccc ggacccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 960
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 1020
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 1080
gactggctga atggcaaggc gtacgcgtgc gcggtctcca acaaagccct cccagccccc 1140
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1200
cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1260
ttctatccaa gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1320
aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc 1380
gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1440
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaatc tagaactgtg 1500
gctgcaccat ctgtcttcat cttcccgcca tctgatgagc agttgaaatc tggaactgcc 1560
tctgttgtgt gcctgctgaa ttacttctat cccagagagg ccaaagtaca gtggaaggtg 1620
gataacgccc tccaatcggg taactcccag gagagtgcca cagagcagga cagcaaggac 1680
agcacctaca gcctcagcag cgagctgacg ctgagcaaag cagactacga gaaacacaaa 1740
gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac 1800
aggggagagt ga 1812

<210> 809
<211> 1608
<212> DNA
<213> Artificial Sequence

<220>
<223> Bispecific T-Cell Engaging molecule (BiTE) known
as bsc19x3

<400> 809
aagcttgccg ccatgggatg gagctgtatc atcctcttct tggtagcaac agctacaggt 60
gtccactccg actacaaaga tgatgacgat aaggatatcc agctgaccca gtctccagct 120
tctttggctg tgtctctagg gcagagggcc accatctcct gcaaggccag ccaaagtgtt 180
gattatgatg gtgatagtta tttgaactgg taccaacaga ttccaggaca gccacccaaa 240

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ctcctcatct atgatgcatc caatctagtt tctgggatcc cacccaggtt tagtggcagt 300
gggtctggga cagacttcac cctcaacatc catcctgtgg agaaggtgga tgctgcaacc 360
tatcactgtc agcaaagtac tgaggatccg tggacgttcg gtggagggac caagctcgag 420
atcaaaggtg gtggtggttc tggcggcggc ggctccggtg gtggtggttc tcaggtgcag 480
ctgcagcagt ctggggctga gctggtgagg cctgggtcct cagtgaagat ttcctgcaag 540
gcttctggct atgcattcag tagctactgg atgaactggg tgaagcagag gcctggacag 600
ggtcttgagt ggattggaca gatttggcct ggagatggtg atactaacta caatggaaag 660
ttcaagggta aagccactct gactgcagac gaatcctcca gcacagccta catgcaactc 720
agcagcctag catctgagga ctctgcggtc tatttctgtg caagacggga gactacgacg 780
gtaggccgtt attactatgc tatggactac tggggccaag ggaccacggt caccgtctcc 840
tccggaggtg gtggatccga tatcaaactg cagcagtcag gggctgaact ggcaagacct 900
ggggcctcag tgaagatgtc ctgcaagact tctggctaca cctttactag gtacacgatg 960
cactgggtaa aacagaggcc tggacagggt ctggaatgga ttggatacat taatcctagc 1020
cgtggttata ctaattacaa tcagaagttc aaggacaagg ccacattgac tacagacaaa 1080
tcctccagca cagcctacat gcaactgagc agcctgacat ctgaggactc tgcagtctat 1140
tactgtgcaa gatattatga tgatcattac tgccttgact actggggcca aggcaccact 1200
ctcacagtct cctcagtcga aggtggaagt ggaggttctg gtggaagtgg aggttcaggt 1260
ggagtcgacg acattcagct gacccagtct ccagcaatca tgtctgcatc tccaggggag 1320
aaggtcacca tgacctgcag agccagttca agtgtaagtt acatgaactg gtaccagcag 1380
aagtcaggca cctccccaa aagatggatt tatgacacat ccaaagtggc ttctggagtc 1440
ccttatcgct tcagtggcag tgggtctggg acctcatact ctctcacaat cagcagcatg 1500
gaggctgaag atgctgccac ttattactgc caacagtgga gtagtaaccc gctcacgttc 1560
ggtgctggga ccaagctgga gctgaaacat catcaccatc atcattag                1608
```

<210> 810
<211> 859
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC038 comprises: G19-4 (anti-CD3) scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3, human Ck(YAE), H75 linker and 3D1 (anti-CD86) scFv

<400> 810

```
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1               5                  10                  15
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
            20                  25                  30
Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
        35                  40                  45
Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
            100                 105                 110
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr
    130                 135                 140
Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
145                 150                 155                 160
Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
                165                 170                 175
Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
            180                 185                 190
Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205
Asp Tyr Ser Leu Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr
    210                 215                 220
Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly
225                 230                 235                 240
Thr Lys Leu Val Thr Lys Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys
                245                 250                 255
Thr His Thr Cys Pro Pro Cys Pro Ser Gly Ala Pro Glu Leu Leu Gly
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                260                 265                 270
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
    290                 295                 300
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305                 310                 315                 320
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
                325                 330                 335
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
        355                 360                 365
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
    370                 375                 380
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
385                 390                 395                 400
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
        435                 440                 445
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480
Pro Gly Lys Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                485                 490                 495
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
            500                 505                 510
Leu Asn Tyr Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
        515                 520                 525
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp
    530                 535                 540
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys
545                 550                 555                 560
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
                565                 570                 575
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Gln Arg
            580                 585                 590
His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser
        595                 600                 605
Pro Asn Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg
    610                 615                 620
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe
625                 630                 635                 640
Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu
                645                 650                 655
Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn
            660                 665                 670
Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser
        675                 680                 685
Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile
    690                 695                 700
Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly
705                 710                 715                 720
Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                725                 730                 735
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Ser
            740                 745                 750
Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly Glu Lys Val Thr Met
        755                 760                 765
Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn
    770                 775                 780
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu
785                 790                 795                 800
Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr
```

805 810 815
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln
820 825 830
Ala Glu Asp Leu Ala Val Tyr Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr
835 840 845
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
850 855

<210> 811
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC039 comprises from its amino to carboxyl terminus: BMA031 (anti-TCR) scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 811
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Lys Phe Thr Ser Tyr
20 25 30
Val Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Tyr Asn Asp Val Thr Lys Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val His Tyr Cys
85 90 95
Ala Arg Gly Ser Tyr Tyr Asp Tyr Asp Gly Phe Val Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125
Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser
130 135 140
Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
145 150 155 160
Ser Ala Thr Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro
165 170 175
Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser
180 185 190
Gly Val Pro Ala Arg Phe Ile Gly Ser Gly Ser Gly Thr Glu Phe Thr
195 200 205
Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
210 215 220
Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240
Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr
245 250 255
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
260 265 270
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
355 360 365
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro

```
    370                 375                 380
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385                 390                 395                 400
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                405                 410                 415
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            420                 425                 430
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
        435                 440                 445
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
    450                 455                 460
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg
465                 470                 475                 480
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
                485                 490                 495
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr
            500                 505                 510
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        515                 520                 525
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
    530                 535                 540
Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
545                 550                 555                 560
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                565                 570                 575
Val Thr Lys Ser Phe Asn Arg Gly Glu
            580                 585
```

<210> 812
<211> 586
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide TSC041 comprises from its amino to carboxy terminus: CRIS7 (anti-CD3) scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 812

```
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1                5                  10                  15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65                  70                  75                  80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
```

```
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His
                245                 250                 255
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
            260                 265                 270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275                 280                 285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    290                 295                 300
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
                325                 330                 335
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
            340                 345                 350
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        355                 360                 365
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        435                 440                 445
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    450                 455                 460
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser
465                 470                 475                 480
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
                485                 490                 495
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe
            500                 505                 510
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        515                 520                 525
Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser
    530                 535                 540
Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu
545                 550                 555                 560
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                565                 570                 575
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
            580                 585
```

<210> 813
<211> 570
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC043 comprises from its amino to carboxy terminus: OKT3-M (Micromet variant anti-CD3, see also US 7,635,472) scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3, and human Ck(YAE)

<400> 813

```
Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr
            20                  25                  30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
```

```
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly
        115                 120                 125
Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser
    130                 135                 140
Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys
145                 150                 155                 160
Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser
                165                 170                 175
Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190
Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser
        195                 200                 205
Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220
Gln Gln Trp Ser Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His
225                 230                 235                 240
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
                245                 250                 255
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            260                 265                 270
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
        275                 280                 285
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    290                 295                 300
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
305                 310                 315                 320
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                325                 330                 335
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
            340                 345                 350
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
        355                 360                 365
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    370                 375                 380
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385                 390                 395                 400
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
                405                 410                 415
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
            420                 425                 430
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        435                 440                 445
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser
    450                 455                 460
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
465                 470                 475                 480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe
                485                 490                 495
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
            500                 505                 510
Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser
        515                 520                 525
Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu
    530                 535                 540
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
545                 550                 555                 560
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
                565                 570
```

<210> 814

<211> 584
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC049 comprises from its amino to carboxy terminus: HD37 (anti-CD19) scFv, human IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human IgG1 CH3, and human IgG1 CH1

<400> 814

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1               5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
        115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Glu Pro Lys Ser
                245                 250                 255
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
            260                 265                 270
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
        275                 280                 285
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
    290                 295                 300
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
305                 310                 315                 320
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
                325                 330                 335
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            340                 345                 350
Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
        355                 360                 365
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
    370                 375                 380
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
385                 390                 395                 400
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
                405                 410                 415
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            420                 425                 430
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
        435                 440                 445
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
```

```
    450                 455                 460
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
465                 470                 475                 480
Ser Pro Gly Lys Ser Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
                485                 490                 495
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
            500                 505                 510
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
        515                 520                 525
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
    530                 535                 540
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
545                 550                 555                 560
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
                565                 570                 575
Asn Thr Lys Val Asp Lys Lys Val
            580


<210> 815
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC050 comprises from its amino to carboxy
      terminus: 2H7 (anti-CD20) scFv, human IgG1 SCC-P
      hinge, human IgG1 CH2(ADCC/CDC null), human IgG1
      CH3, and human IgG1 CH1

<400> 815
Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
 1                  5                  10                  15
Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
        35                  40                  45
Ala Pro Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    50                  55                  60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65                  70                  75                  80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe Asn Pro Pro Thr
                85                  90                  95
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Asp Gly Gly Gly Ser Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln Ala Tyr Leu Gln Gln
        115                 120                 125
Ser Gly Ala Glu Ser Val Arg Pro Gly Ala Ser Val Lys Met Ser Cys
    130                 135                 140
Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys
145                 150                 155                 160
Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly
                165                 170                 175
Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu
            180                 185                 190
Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
        195                 200                 205
Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Val Val Tyr Tyr
    210                 215                 220
Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp Gly Thr Gly Thr Thr Val
225                 230                 235                 240
Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys
                245                 250                 255
Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu
            260                 265                 270
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275                 280                 285
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
```

```
    290                 295                 300
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305                 310                 315                 320
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
                325                 330                 335
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala
            340                 345                 350
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
        355                 360                 365
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
    370                 375                 380
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385                 390                 395                 400
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
                405                 410                 415
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
            420                 425                 430
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
        435                 440                 445
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
    450                 455                 460
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Ala
465                 470                 475                 480
Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
                485                 490                 495
Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
            500                 505                 510
Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
        515                 520                 525
Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
    530                 535                 540
Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
545                 550                 555                 560
Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
                565                 570                 575
Val
```

<210> 816
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC051 comprises from its amino to carboxy terminus: P2C2 (anti-CD79) scFv, human IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human IgG1 CH3, and human IgG1 CH1

<400> 816

```
Asp Ile Val Met Ile Gln Asp Glu Leu Ser Asn Pro Val Ser Ser Gly
 1               5                  10                  15
Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asp Lys
            20                  25                  30
Glu Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser
        35                  40                  45
Pro Gln Leu Leu Ile Tyr Leu Met Ser Met Arg Glu Ser Gly Val Ser
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile
65                  70                  75                  80
Ser Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
                85                  90                  95
Val Glu Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
        115                 120                 125
Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr
```

```
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Phe Ser
145                 150                 155                 160
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Lys Trp Met Gly
                165                 170                 175
Trp Ile Asn Thr Glu Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Arg
            180                 185                 190
Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr Leu
        195                 200                 205
Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Thr
    210                 215                 220
Trp Ser Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser
225                 230                 235                 240
Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                245                 250                 255
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    290                 295                 300
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
            340                 345                 350
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Ala Ser Thr Lys Gly
465                 470                 475                 480
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
                485                 490                 495
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
            500                 505                 510
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
        515                 520                 525
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
    530                 535                 540
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
545                 550                 555                 560
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
                565                 570
```

<210> 817
<211> 580
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC052 comprises from its amino to carboxy terminus: 5D5 (anti-cMet) scFv, human IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human IgG1 CH3, and human IgG1 CH1

<400> 817

```
Asp Phe Met Met Ser Gln Ser Pro Ser Ser Leu Thr Val Ser Val Gly
 1               5                  10                  15
Glu Lys Val Thr Val Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Thr
            20                  25                  30
Ser Ser Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80
Ile Thr Ser Val Lys Ala Asp Asp Leu Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95
Tyr Tyr Ala Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu
            100                 105                 110
Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Ala
    130                 135                 140
Ser Val Lys Met Ser Cys Arg Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
145                 150                 155                 160
Trp Leu His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
                165                 170                 175
Gly Met Ile Asp Pro Ser Asn Ser Asp Thr Arg Phe Asn Pro Asn Phe
            180                 185                 190
Lys Asp Lys Ala Thr Leu Asn Val Asp Arg Ser Ser Asn Thr Ala Tyr
        195                 200                 205
Met Leu Leu Ser Ser Leu Thr Ser Ala Asp Ser Ala Val Tyr Tyr Cys
    210                 215                 220
Ala Thr Tyr Gly Ser Tyr Val Ser Pro Leu Asp Tyr Trp Gly Gln Gly
225                 230                 235                 240
Thr Ser Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr
                245                 250                 255
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser
            260                 265                 270
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
        275                 280                 285
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
    290                 295                 300
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
305                 310                 315                 320
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
                325                 330                 335
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr
            340                 345                 350
Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
        355                 360                 365
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
    370                 375                 380
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
385                 390                 395                 400
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
                405                 410                 415
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
            420                 425                 430
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
        435                 440                 445
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
    450                 455                 460
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475                 480
Ser Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
                485                 490                 495
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
            500                 505                 510
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
        515                 520                 525
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
```

530 535 540
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
545 550 555 560
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
565 570 575
Asp Lys Lys Val
580

<210> 818
<211> 588
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC053 comprises from its amino to carboxy terminus: G19-4 (anti CD3) scFv, human IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human IgG1 CH3, and human Ck(YAE)

<400> 818
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30
Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
35 40 45
Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
100 105 110
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr
130 135 140
Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
145 150 155 160
Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
165 170 175
Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
180 185 190
Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205
Asp Tyr Ser Leu Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr
210 215 220
Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly
225 230 235 240
Thr Lys Leu Val Thr Lys Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys
245 250 255
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro
260 265 270
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
275 280 285
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
290 295 300
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
305 310 315 320
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
325 330 335
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala
340 345 350
Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
355 360 365
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr

370 375 380
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
385 390 395 400
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
405 410 415
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
420 425 430
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
435 440 445
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
450 455 460
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475 480
Lys Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
485 490 495
Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
500 505 510
Tyr Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
515 520 525
Leu Gln Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys
530 535 540
Asp Ser Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp
545 550 555 560
Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
565 570 575
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
580 585

<210> 819
<211> 853
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC064 comprises from its amino to carboxy terminus: G19-4 (anti-CD3) scFv, human IgG1 SCC-P hinge, human IgG1 CH2, human IgG1 CH3, human Ck(YAE), H75 linker, and Met021 (anti-c-Met) scFv

<400> 819
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30
Ile Val Asn Trp Leu Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile
35 40 45
Gly Leu Ile Asn Pro Tyr Lys Gly Leu Thr Thr Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
100 105 110
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr
130 135 140
Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile
145 150 155 160
Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln
165 170 175
Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg
180 185 190
Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
195 200 205
Asp Tyr Ser Leu Thr Ile Ala Asn Leu Gln Pro Glu Asp Ile Ala Thr

```
    210                 215                 220
Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly
225                 230                 235                 240
Thr Lys Leu Val Thr Lys Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys
                245                 250                 255
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
            260                 265                 270
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
        275                 280                 285
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
    290                 295                 300
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
305                 310                 315                 320
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
                325                 330                 335
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
            340                 345                 350
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
        355                 360                 365
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
    370                 375                 380
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
385                 390                 395                 400
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                405                 410                 415
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
            420                 425                 430
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
        435                 440                 445
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
    450                 455                 460
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465                 470                 475                 480
Lys Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
                485                 490                 495
Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
            500                 505                 510
Tyr Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
        515                 520                 525
Leu Gln Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys
    530                 535                 540
Asp Ser Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp
545                 550                 555                 560
Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
                565                 570                 575
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Gln Arg His Asn
            580                 585                 590
Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn
        595                 600                 605
Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
    610                 615                 620
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Asn
625                 630                 635                 640
Tyr Leu Asn Trp Tyr Gln Gln Glu Pro Gly Lys Ala Pro Lys Leu Leu
                645                 650                 655
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
            660                 665                 670
Gly Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu Gln
        675                 680                 685
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Val Thr Pro
    690                 695                 700
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly
705                 710                 715                 720
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                725                 730                 735
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
            740                 745                 750
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
```

```
        755                 760                 765
Asp Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
    770                 775                 780
Ser Tyr Ile Tyr Pro Ser Gly Gly Leu Thr Glu Tyr Ala Asp Ser Val
785                 790                 795                 800
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
                805                 810                 815
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
            820                 825                 830
Ala Arg Arg Ala Pro Arg Ser Leu Ser Phe Asp Ile Trp Gly Gln Gly
        835                 840                 845
Thr Met Val Thr Val
    850
```

<210> 820
<211> 583
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC076 comprises from its amino to carboxy terminus: OKT3 (anti-CD3) scFv, human IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human IgG1 CH3, and human Ck(YAE)

<400> 820

```
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1                  5                  10                  15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20                  25                  30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125
Ser Gly Gly Gly Gly Ser Ala Gln Gln Ile Val Leu Thr Gln Ser Pro
    130                 135                 140
Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser
145                 150                 155                 160
Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly
                165                 170                 175
Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly
            180                 185                 190
Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
        195                 200                 205
Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
    210                 215                 220
Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu
225                 230                 235                 240
Ile Asn Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
                245                 250                 255
Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe
            260                 265                 270
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
        275                 280                 285
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
    290                 295                 300
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
305                 310                 315                 320
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
```

325 330 335
Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val
340 345 350
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
355 360 365
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
370 375 380
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
385 390 395 400
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
405 410 415
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
420 425 430
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
435 440 445
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
450 455 460
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Thr Val
465 470 475 480
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
485 490 495
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg
500 505 510
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
515 520 525
Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
530 535 540
Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
545 550 555 560
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
565 570 575
Lys Ser Phe Asn Arg Gly Glu
580

<210> 821
<211> 586
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC077 comprises: HuM291 (anti-CD3) scFv, human IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human IgG1 CH3, and human Ck(YAE)

<400> 821
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Ser Tyr
20 25 30
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Tyr Ile Asn Pro Arg Ser Gly Tyr Thr His Tyr Asn Gln Lys Leu
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Ala Tyr Tyr Asp Tyr Asp Gly Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125
Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser
130 135 140
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160
Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175

```
Gly Lys Ala Pro Lys Arg Leu Ile Tyr Asp Thr Ser Lys Leu Ala Ser
            180                 185                 190
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205
Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220
Gln Gln Trp Ser Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
225                 230                 235                 240
Glu Ile Lys Arg Thr Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His
                245                 250                 255
Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val
            260                 265                 270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275                 280                 285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    290                 295                 300
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
                325                 330                 335
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala
            340                 345                 350
Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        355                 360                 365
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        435                 440                 445
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    450                 455                 460
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser
465                 470                 475                 480
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
                485                 490                 495
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe
            500                 505                 510
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        515                 520                 525
Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser
    530                 535                 540
Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu
545                 550                 555                 560
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                565                 570                 575
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
            580                 585
```

<210> 822
<211> 586
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC093 comprises from its amino to carboxy terminus: CRIS7 (anti-CD3) scFv, human IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human IgG1 CH3, and human Ck(YAE)

<400> 822

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

```
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65                  70                  75                  80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His
                245                 250                 255
Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val
            260                 265                 270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275                 280                 285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    290                 295                 300
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
                325                 330                 335
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala
            340                 345                 350
Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        355                 360                 365
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        435                 440                 445
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    450                 455                 460
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser
465                 470                 475                 480
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
                485                 490                 495
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe
            500                 505                 510
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        515                 520                 525
Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser
    530                 535                 540
Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu
545                 550                 555                 560
```

```
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                565                 570                 575
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
            580                 585
```

<210> 823
<211> 570
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC094 comprises from its amino to carboxy terminus: OKT3-M (Micromet variant anti-CD3) scFv, human IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human IgG1 CH3, human Ck(YAE)

<400> 823

```
Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr
            20                  25                  30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly
        115                 120                 125
Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser
    130                 135                 140
Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys
145                 150                 155                 160
Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser
                165                 170                 175
Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190
Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser
        195                 200                 205
Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220
Gln Gln Trp Ser Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His
225                 230                 235                 240
Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val
                245                 250                 255
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            260                 265                 270
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
        275                 280                 285
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    290                 295                 300
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
305                 310                 315                 320
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala
                325                 330                 335
Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
            340                 345                 350
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
        355                 360                 365
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    370                 375                 380
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385                 390                 395                 400
```

```
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
                405                 410                 415
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
            420                 425                 430
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        435                 440                 445
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser
    450                 455                 460
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
465                 470                 475                 480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe
                485                 490                 495
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
            500                 505                 510
Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser
        515                 520                 525
Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu
    530                 535                 540
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
545                 550                 555                 560
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
                565                 570
```

<210> 824
<211> 586
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC095 comprises from its amino to carboxy terminus: BMA031 (anti-TCR) scFv, human IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human IgG1 CH3, human Ck(YAE)

<400> 824

```
Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
 1                5                  10                  15
Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Lys Phe Thr Ser
            20                  25                  30
Tyr Val Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp
        35                  40                  45
Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Val Thr Lys Tyr Asn Glu Lys
    50                  55                  60
Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Thr Asn Thr Ala
65                  70                  75                  80
Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val His Tyr
                85                  90                  95
Cys Ala Arg Gly Ser Tyr Tyr Asp Tyr Asp Gly Phe Val Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Thr Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ile Gly Ser Gly Ser Gly Thr Glu Phe
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His
                245                 250                 255
```

```
Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val
            260                 265                 270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275                 280                 285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    290                 295                 300
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
                325                 330                 335
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala
            340                 345                 350
Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        355                 360                 365
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        435                 440                 445
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    450                 455                 460
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser
465                 470                 475                 480
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
                485                 490                 495
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe
            500                 505                 510
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        515                 520                 525
Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser
    530                 535                 540
Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu
545                 550                 555                 560
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                565                 570                 575
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
            580                 585


<210> 825
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC096 comprises: HD37 (anti-CD19) scFv, human
      IgG1 SCC-P hinge, human IgG1 CH2 (ADCC/CDC null),
        human IgG1 CH3, human Ck(YAE)

<400> 825
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1                  5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
```

```
                100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
            115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Glu Pro Lys Ser
                245                 250                 255
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
            260                 265                 270
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
        275                 280                 285
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
    290                 295                 300
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
305                 310                 315                 320
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
                325                 330                 335
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            340                 345                 350
Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
        355                 360                 365
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
    370                 375                 380
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
385                 390                 395                 400
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
                405                 410                 415
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            420                 425                 430
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
        435                 440                 445
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
    450                 455                 460
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
465                 470                 475                 480
Ser Pro Gly Lys Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
                485                 490                 495
Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
            500                 505                 510
Leu Leu Asn Tyr Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
        515                 520                 525
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln
    530                 535                 540
Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser
545                 550                 555                 560
Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
                565                 570                 575
Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
            580                 585                 590
```

<210> 826
<211> 583
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC097 comprises from its amino to carboxy terminus: 4C04 (anti-RON) scFv, human IgG1 SCC-P hinge, human IgG1 CH2(ADCC/CDC null), human IgG1 CH3, and human Ck(YAE)

<400> 826

```
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Gln Ser Ala Ser Leu Gly
 1               5                  10                  15
Glu Ser Val Thr Ile Thr Cys Leu Ala Ser Gln Thr Ile Gly Thr Trp
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Thr Ser Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Ala
    50                  55                  60
Ser Gly Ser Gly Thr Lys Phe Ser Phe Lys Ile Asp Ser Leu Gln Ser
65                  70                  75                  80
Glu Asp Phe Val Ser Tyr Tyr Cys Gln Gln Leu Tyr Asn Thr Pro Trp
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
            100                 105                 110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile Gln Leu Gln Gln
        115                 120                 125
Ser Gly Pro Glu Leu Val Lys Pro Gly Thr Ser Val Lys Ile Ser Cys
    130                 135                 140
Lys Ala Ser Asp Tyr Thr Leu Thr Asp Phe Tyr Met Asn Trp Val Arg
145                 150                 155                 160
Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly
                165                 170                 175
Thr Asp Lys Thr Arg Tyr Asn Glu Lys Phe Arg Asp Lys Ala Ile Leu
            180                 185                 190
Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
        195                 200                 205
Thr Ser Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg Ser Ala Tyr Tyr
    210                 215                 220
Gly Asn Tyr Val Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
225                 230                 235                 240
Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
                245                 250                 255
Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe
            260                 265                 270
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
        275                 280                 285
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
    290                 295                 300
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
305                 310                 315                 320
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
                325                 330                 335
Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val
            340                 345                 350
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
        355                 360                 365
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
    370                 375                 380
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
385                 390                 395                 400
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
                405                 410                 415
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
            420                 425                 430
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
        435                 440                 445
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
    450                 455                 460
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Thr Val
465                 470                 475                 480
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
```

485 490 495
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg
500 505 510
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
515 520 525
Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
530 535 540
Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
545 550 555 560
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
565 570 575
Lys Ser Phe Asn Arg Gly Glu
580

<210> 827
<211> 512
<212> PRT
<213> Artificial Sequence

<220>
<223> Bispecific T-Cell Engaging molecule (BiTE) known as bsc19x3

<400> 827
Asp Tyr Lys Asp Asp Asp Asp Lys Asp Ile Gln Leu Thr Gln Ser Pro
1 5 10 15
Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
20 25 30
Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
35 40 45
Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
50 55 60
Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
65 70 75 80
Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
85 90 95
Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly
100 105 110
Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
130 135 140
Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
145 150 155 160
Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly
165 170 175
Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr
180 185 190
Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu
195 200 205
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp
210 215 220
Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg
225 230 235 240
Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
245 250 255
Ser Ser Gly Gly Gly Gly Ser Asp Ile Lys Leu Gln Gln Ser Gly Ala
260 265 270
Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Thr Ser
275 280 285
Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro
290 295 300
Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
305 310 315 320
Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp
325 330 335
Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu

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            340                 345                 350
Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys
        355                 360                 365
Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu
    370                 375                 380
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp
385                 390                 395                 400
Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
                405                 410                 415
Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
            420                 425                 430
Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
        435                 440                 445
Asp Thr Ser Lys Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser
    450                 455                 460
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
465                 470                 475                 480
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
                485                 490                 495
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys His His His His His His
            500                 505                 510


<210> 828
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<223> VH region of BMA031 (anti-TCR) scFv

<400> 828
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Lys Phe Thr Ser Tyr
            20                  25                  30
Val Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Tyr Asn Asp Val Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val His Tyr Cys
                85                  90                  95
Ala Arg Gly Ser Tyr Tyr Asp Tyr Asp Gly Phe Val Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 829
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<223> VL region of BMA031 (anti-TCR) scFv

<400> 829
Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser
 1               5                  10                  15
Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Thr Ser Ser Val Ser
            20                  25                  30
Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
        35                  40                  45
Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ile
    50                  55                  60
Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
```

65 70 75 80
Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
85 90 95
Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Ser Ser Ser
100 105 110

<210> 830
<211> 246
<212> PRT
<213> Homo sapiens

<220>
<223> BMA031 scFv

<400> 830
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Lys Phe Thr Ser Tyr
20 25 30
Val Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Tyr Asn Asp Val Thr Lys Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val His Tyr Cys
85 90 95
Ala Arg Gly Ser Tyr Tyr Asp Tyr Asp Gly Phe Val Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125
Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser
130 135 140
Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
145 150 155 160
Ser Ala Thr Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro
165 170 175
Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser
180 185 190
Gly Val Pro Ala Arg Phe Ile Gly Ser Gly Ser Gly Thr Glu Phe Thr
195 200 205
Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
210 215 220
Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240
Glu Ile Lys Ser Ser Ser
245

<210> 831
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<223> VH region of OKT3-M (anti-CD3) scFv

<400> 831
Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr

65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Leu Thr Val Ser Ser
115

<210> 832
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> OKT3-M Linker

<400> 832
Val Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
1 5 10 15
Val Asp

<210> 833
<211> 94
<212> PRT
<213> Homo sapiens

<220>
<223> VL region of OKT3-M (anti-CD3) scFv

<400> 833
Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15
Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30
Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45
Asp Thr Ser Lys Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Ser Ser
85 90

<210> 834
<211> 231
<212> PRT
<213> Homo sapiens

<220>
<223> OKT3-M scFv

<400> 834
Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

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Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110
Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly
        115                 120                 125
Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser
    130                 135                 140
Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys
145                 150                 155                 160
Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser
                165                 170                 175
Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
            180                 185                 190
Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser
        195                 200                 205
Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
    210                 215                 220
Gln Gln Trp Ser Ser Ser Ser
225                 230
```

<210> 835
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<223> VH region of HuM291 (anti-CD3) scFv

<400> 835

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Ser Tyr
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
Gly Tyr Ile Asn Pro Arg Ser Gly Tyr Thr His Tyr Asn Gln Lys Leu
    50                  55                  60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Ala Tyr Tyr Asp Tyr Asp Gly Phe Ala Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 836
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<223> VL region of HuM291 (anti-CD3) scFv

<400> 836

```
Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
 1               5                  10                  15
Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser
            20                  25                  30
Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu
        35                  40                  45
Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
                85                  90                  95
```

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

<210> 837
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<223> HuM291 scFv

<400> 837
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Ser Tyr
20 25 30
Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Tyr Ile Asn Pro Arg Ser Gly Tyr Thr His Tyr Asn Gln Lys Leu
50 55 60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Ala Tyr Tyr Asp Tyr Asp Gly Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125
Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser
130 135 140
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160
Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
165 170 175
Gly Lys Ala Pro Lys Arg Leu Ile Tyr Asp Thr Ser Lys Leu Ala Ser
180 185 190
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205
Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220
Gln Gln Trp Ser Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
225 230 235 240
Glu Ile Lys Arg Thr Ser Ser
245

<210> 838
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> mutated human Ck DAE

<400> 838
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asp Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu

100 105

<210> 839
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> mutated human Ck MAE

<400> 839
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Met Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 840
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> mutated human Ck SAE

<400> 840
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Ser Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 841
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> mutated human FAE

<400> 841
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Phe Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys

65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 842
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> mutated Ck L27E

<400> 842
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Glu Leu Asn Asn Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 843
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> mutated Ck L27K

<400> 843
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Lys Leu Asn Asn Phe Tyr
20 25 30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95
Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 844
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> mutated CH1 V68E

<400> 844
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser

```
        35                  40                  45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
Leu Ser Ser Glu Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
Lys Val
```

<210> 845
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> mutated CH1 V68K

<400> 845

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1               5                  10                  15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
Leu Ser Ser Lys Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
Lys Val
```

<210> 846
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> CH3-CH1 linker or CH3-Ck linker

<400> 846

```
Lys Ser Arg
 1
```

<210> 847
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CH3-CH1 linker

<400> 847

```
Gly Gly Gly Ser Ser
 1               5
```

<210> 848
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CH3-CH1 linker

<400> 848

```
Ser Tyr Ser Pro Asn Ser
```

1 5

<210> 849
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CH3-CH1 linker

<400> 849
Ser Ser Leu Asn Thr Pro Asn Ser
1 5

<210> 850
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CH3-Ck linker

<400> 850
Gly Gly Gly Ser Arg
1 5

<210> 851
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CH3-Ck linker

<400> 851
Ser Tyr Ser Pro Asn Ser Arg
1 5

<210> 852
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CH3-Ck linker

<400> 852
Ser Ser Leu Asn Thr Pro Asn Ser Arg
1 5

<210> 853
<211> 1806
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC145 (Cris7 scFv-hinge-CH2-CH3-GGGSS linker-CH1)

<400> 853
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
caggtccagc tggtgcagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 120
tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 180
cctggaaagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 240
aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 300
ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 360
gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 480
cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 540

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc cggcaaggcc 600
cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 660
ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 720
gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 780
ctacaaatta cacgctcgag tgagcccaaa tcttctgaca aaactcacac atgcccaccg 840
tgcccagcac ctgaagccgc gggtgcaccg tcagtcttcc tcttcccccc aaaacccaag 900
gacaccctca tgatctcccg gaccccctgag gtcacatgcg tggtggtgga cgtgagccac 960
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 1020
acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 1080
ctgcaccagg actggctgaa tggcaaggcg tacgcgtgcg cggtctccaa caaagccctc 1140
ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg 1200
tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 1260
gtcaaaggct tctatccaag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1320
aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1380
aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1440
catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtggcgga 1500
ggctcctcag cctccaccaa gggcccatcg gtcttccccc tggcaccctc ctccaagagc 1560
acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgagccggtg 1620
acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 1680
cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 1740
acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 1800
gtttga 1806

<210> 854
<211> 1809
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC146 (Cris7 scFv-hinge-CH2-CH3-SYSPNS
linker-CH1)

<400> 854
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
caggtccagc tggtgcagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 120
tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 180
cctggaaagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 240
aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 300
ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 360
gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 480
cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 540
tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc cggcaaggcc 600
cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 660
ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 720
gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 780
ctacaaatta cacgctcgag tgagcccaaa tcttctgaca aaactcacac atgcccaccg 840
tgcccagcac ctgaagccgc gggtgcaccg tcagtcttcc tcttcccccc aaaacccaag 900
gacaccctca tgatctcccg gaccccctgag gtcacatgcg tggtggtgga cgtgagccac 960
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 1020
acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 1080
ctgcaccagg actggctgaa tggcaaggcg tacgcgtgcg cggtctccaa caaagccctc 1140
ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg 1200
tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 1260
gtcaaaggct tctatccaag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1320
aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1380
aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1440
catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtagttac 1500
agcccgaact ctgcctccac caagggccca tcggtcttcc ccctggcacc ctcctccaag 1560
agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgagccg 1620
gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 1680
ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 1740
ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 1800
aaagtttga 1809

<210> 855
<211> 1815
<212> DNA

<213> Artificial Sequence

<220>
<223> TSC147 (Cris7 scFv-hinge-CH2-CH3-SSLNTPNS linker-CH1)

<400> 855
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
caggtccagc tggtgcagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 120
tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 180
cctggaaagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 240
aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 300
ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 360
gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 480
cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 540
tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc cggcaaggcc 600
cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 660
ggcagtgggt ctgggaccga ctatacctc acaatcagca gcctgcagcc cgaagatttc 720
gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 780
ctacaaatta cacgctcgag tgagcccaaa tcttctgaca aaactcacac atgcccaccg 840
tgcccagcac ctgaagccgc gggtgcaccg tcagtcttcc tcttcccccc aaaacccaag 900
gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac 960
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 1020
acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 1080
ctgcaccagg actggctgaa tggcaaggcg tacgcgtgcg cggtctccaa caaagccctc 1140
ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg 1200
tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 1260
gtcaaaggct tctatccaag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1320
aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1380
aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1440
catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggttcttcc 1500
ctgaatacac cgaactctgc ctccaccaag ggcccatcgg tcttcccccct ggcaccctcc 1560
tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 1620
gagccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 1680
gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 1740
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 1800
gacaagaaag tttga 1815

<210> 856
<211> 1842
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC148 (HD37 scFv-hinge-CH2-CH3-GGGSR linker-Ck)

<400> 856
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 180
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 240
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 300
cctgtggaga aggtggatgc tgcaacctat cactgccagc aaagtactga ggatccgtgg 360
acgttcggtg gaggcaccaa gctggaaatc aaaggtggcg gtggttcggg cggtggtggg 420
tcgggtggcg gcggagctag ccaggttcag ctgcagcagt ctggggctga gctggtgagg 480
cctgggtcct cagtgaagat ttcctgcaag gcttctggct atgcattcag tagctactgg 540
atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct 600
ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac 660
gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc 720
tatttctgtg caagacggga gactacgacg gtaggccgtt attactatgc tatggactac 780
tggggtcaag gaacctcagt caccgtctcc tcgagtgagc ccaaatcttc tgacaaaact 840
cacacatgcc caccgtgccc agcacctgaa gccgcgggtg caccgtcagt cttcctcttc 900
cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 960
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 1080
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggcgtacgc gtgcgcggtc 1140
tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 1200

cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1260
agcctgacct gcctggtcaa aggcttctat ccaagcgaca tcgccgtgga gtgggagagc 1320
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380
ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tctccgggtg gcggaggctc caggactgtg gctgcaccat ctgtcttcat cttcccgcca 1560
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa ttacttctat 1620
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 1680
gagagtgcca cagagcagga cagcaaggac agcacctaca gcctcagcag cgagctgacg 1740
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 1800
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt ga 1842

<210> 857
<211> 1848
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC149 (HD37 scFv-hinge-CH2-CH3-SYSPNSR linker-Ck)

<400> 857
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 180
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 240
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 300
cctgtggaga aggtggatgc tgcaacctat cactgccagc aaagtactga ggatccgtgg 360
acgttcggtg gaggcaccaa gctggaaatc aaaggtggcg gtggttcggg cggtggtggg 420
tcgggtggcg gcggagctag ccaggttcag ctgcagcagt ctggggctga gctggtgagg 480
cctgggtcct cagtgaagat ttcctgcaag gcttctggct atgcattcag tagctactgg 540
atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct 600
ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac 660
gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc 720
tatttctgtg caagacggga gactacgacg gtaggccgtt attactatgc tatggactac 780
tggggtcaag gaacctcagt caccgtctcc tcgagtgagc ccaaatcttc tgacaaaact 840
cacacatgcc caccgtgccc agcacctgaa gccgcgggtg caccgtcagt cttcctcttc 900
cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 960
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 1080
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggcgtacgc gtgcgcggtc 1140
tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 1200
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1260
agcctgacct gcctggtcaa aggcttctat ccaagcgaca tcgccgtgga gtgggagagc 1320
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380
ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tctccgggta gttacagccc gaactctagg actgtggctg caccatctgt cttcatcttc 1560
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaattac 1620
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 1680
tcccaggaga gtgccacaga gcaggacagc aaggacagca cctacagcct cagcagcgag 1740
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 1800
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtga 1848

<210> 858
<211> 1854
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC150 (HD37 scFv-hinge-CH2-CH3-SSLNTPNSR
linker-Ck)

<400> 858
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 180
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 240
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 300

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cctgtggaga aggtggatgc tgcaacctat cactgccagc aaagtactga ggatccgtgg      360
acgttcggtg gaggcaccaa gctggaaatc aaaggtggcg gtggttcggg cggtggtggg      420
tcgggtggcg gcggagctag ccaggttcag ctgcagcagt ctggggctga gctggtgagg      480
cctgggtcct cagtgaagat ttcctgcaag gcttctggct atgcattcag tagctactgg      540
atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct      600
ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac      660
gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc      720
tatttctgtg caagacggga gactacgacg gtaggccgtt attactatgc tatggactac      780
tggggtcaag gaacctcagt caccgtctcc tcgagtgagc ccaaatcttc tgacaaaact      840
cacacatgcc caccgtgccc agcacctgaa gccgcgggtg caccgtcagt cttcctcttc      900
cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg      960
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag     1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc     1080
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggcgtacgc gtgcgcggtc     1140
tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc     1200
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc     1260
agcctgacct gcctggtcaa aggcttctat ccaagcgaca tcgccgtgga gtgggagagc     1320
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc     1380
ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc     1440
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg     1500
tctccgggtt cttccctgaa tacaccgaac tctaggactg tggctgcacc atctgtcttc     1560
atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg     1620
aattacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg     1680
ggtaactccc aggagagtgc cacagagcag gacagcaagg acagcaccta cagcctcagc     1740
agcgagctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc     1800
acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtga            1854

<210> 859
<211> 581
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC145 (Cris7 scFv-hinge-CH2-CH3-GGGSS linker-CH1)

<400> 859
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65                  70                  75                  80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His
                245                 250                 255
```

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Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val
            260                 265                 270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275                 280                 285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    290                 295                 300
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
                325                 330                 335
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala
            340                 345                 350
Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        355                 360                 365
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        435                 440                 445
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    450                 455                 460
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly
465                 470                 475                 480
Gly Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
                485                 490                 495
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
            500                 505                 510
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
        515                 520                 525
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
    530                 535                 540
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
545                 550                 555                 560
Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
                565                 570                 575
Val Asp Lys Lys Val
            580
```

<210> 860
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC146 (Cris7 scFv-hinge-CH2-CH3-SYSPNS linker-CH1)

<400> 860

```
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1                  5                  10                  15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65                  70                  75                  80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
```

```
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His
                245                 250                 255
Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val
            260                 265                 270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275                 280                 285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    290                 295                 300
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
                325                 330                 335
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala
            340                 345                 350
Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        355                 360                 365
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        435                 440                 445
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    450                 455                 460
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Ser Tyr
465                 470                 475                 480
Ser Pro Asn Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
                485                 490                 495
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
            500                 505                 510
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
        515                 520                 525
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
    530                 535                 540
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
545                 550                 555                 560
Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
                565                 570                 575
Lys Val Asp Lys Lys Val
            580
```

<210> 861
<211> 584
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC147 (Cris7 scFv-hinge-CH2-CH3-SSLNTPNS linker-CH1)

<400> 861

```
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65                  70                  75                  80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His
                245                 250                 255
Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val
            260                 265                 270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275                 280                 285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    290                 295                 300
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
                325                 330                 335
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala
            340                 345                 350
Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        355                 360                 365
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        435                 440                 445
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    450                 455                 460
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Ser Ser
465                 470                 475                 480
Leu Asn Thr Pro Asn Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
                485                 490                 495
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
            500                 505                 510
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
        515                 520                 525
```

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
530 535 540
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
545 550 555 560
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
565 570 575
Asn Thr Lys Val Asp Lys Lys Val
580

<210> 862
<211> 593
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC148 (HD37 scFv-hinge-CH2-CH3-GGGSR linker-Ck)

<400> 862
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
115 120 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
130 135 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145 150 155 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
165 170 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
180 185 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
195 200 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
210 215 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225 230 235 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Glu Pro Lys Ser
245 250 255
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
260 265 270
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
275 280 285
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
290 295 300
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
305 310 315 320
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
325 330 335
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
340 345 350
Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
355 360 365
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
370 375 380
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
385 390 395 400

```
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
                405                 410                 415
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            420                 425                 430
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
        435                 440                 445
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
    450                 455                 460
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
465                 470                 475                 480
Ser Pro Gly Gly Gly Gly Ser Arg Thr Val Ala Ala Pro Ser Val Phe
                485                 490                 495
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
            500                 505                 510
Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
        515                 520                 525
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Ala Thr
    530                 535                 540
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Glu Leu Thr
545                 550                 555                 560
Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
                565                 570                 575
Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
            580                 585                 590
Glu
```

<210> 863
<211> 595
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC149 (HD37 scFv-hinge-CH2-CH3-SYSPNSR linker-Ck)

<400> 863

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1                  5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
        115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Glu Pro Lys Ser
                245                 250                 255
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Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
            260                 265                 270
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
        275                 280                 285
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
    290                 295                 300
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
305                 310                 315                 320
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
                325                 330                 335
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            340                 345                 350
Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
        355                 360                 365
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
    370                 375                 380
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
385                 390                 395                 400
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
                405                 410                 415
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            420                 425                 430
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
        435                 440                 445
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
    450                 455                 460
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
465                 470                 475                 480
Ser Pro Gly Ser Tyr Ser Pro Asn Ser Arg Thr Val Ala Ala Pro Ser
                485                 490                 495
Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
            500                 505                 510
Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu Ala Lys Val
        515                 520                 525
Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
    530                 535                 540
Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Glu
545                 550                 555                 560
Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
                565                 570                 575
Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
            580                 585                 590
Arg Gly Glu
        595

<210> 864
<211> 597
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC150 (HD37 scFv-hinge-CH2-CH3-SSLNTPNSR
      linker-Ck)

<400> 864
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1                  5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
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                100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
            115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Glu Pro Lys Ser
                245                 250                 255
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
            260                 265                 270
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
        275                 280                 285
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
    290                 295                 300
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
305                 310                 315                 320
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
                325                 330                 335
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            340                 345                 350
Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
        355                 360                 365
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
    370                 375                 380
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
385                 390                 395                 400
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
                405                 410                 415
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            420                 425                 430
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
        435                 440                 445
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
    450                 455                 460
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
465                 470                 475                 480
Ser Pro Gly Ser Ser Leu Asn Thr Pro Asn Ser Arg Thr Val Ala Ala
                485                 490                 495
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
            500                 505                 510
Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu Ala
        515                 520                 525
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
    530                 535                 540
Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
545                 550                 555                 560
Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
                565                 570                 575
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
            580                 585                 590
Phe Asn Arg Gly Glu
        595
```

<210> 865
<211> 1800
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC125 (Cris7 scFv-CH2-CH3-CH1)

<400> 865
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
caggtccagc tggtgcagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 120
tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 180
cctggaaagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 240
aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 300
ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 360
gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 480
cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 540
tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc cggcaaggcc 600
cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 660
ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 720
gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 780
ctacaaatta cacgctcgag tgagcccaaa tcttctgaca aaactcacac atgcccaccg 840
tgcccagcac ctgaagccgc gggtgcaccg tcagtcttcc tcttcccccc aaaacccaag 900
gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac 960
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 1020
acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 1080
ctgcaccagg actggctgaa tggcaaggcg tacgcgtgcg cggtctccaa caaagccctc 1140
ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg 1200
tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 1260
gtcaaaggct tctatccaag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1320
aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1380
aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1440
catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaatct 1500
agagcctcca ccaagggccc atcggtcttc cccctggcac cctcctccaa gagcacctct 1560
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgagcc ggtgacggtg 1620
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 1680
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 1740
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagtttga 1800

<210> 866
<211> 1785
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC157 (Cris7 scFv-IgA2UH-CH2-CH3-CH1)

<400> 866
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
caggtccagc tggtgcagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 120
tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 180
cctggaaagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 240
aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 300
ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 360
gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 480
cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 540
tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc cggcaaggcc 600
cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 660
ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 720
gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 780
ctacaaatta cacgctcgag ccccccacct cccccatgcc caccgtgccc agcacctgaa 840
gccgcgggtg caccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 900
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 960
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1020
gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1080
ctgaatggca aggcgtacgc gtgcgcggtc tccaacaaag ccctcccagc ccccatcgag 1140
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 1200
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1260
ccaagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1320
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1380

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1440
aaccactaca cgcagaagag cctctccctg tctccgggta aatctagagc ctccaccaag 1500
ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 1560
ctgggctgcc tggtcaagga ctacttcccc gagccggtga cggtgtcgtg gaactcaggc 1620
gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 1680
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 1740
gtgaatcaca agcccagcaa caccaaggtg gacaagaaag tttga 1785

<210> 867
<211> 1815
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC158 (Cris7 scFv-IgG1miniUH-CH2-CH3-CH1)

<400> 867
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
caggtccagc tggtgcagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 120
tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 180
cctggaaagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 240
aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 300
ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 360
gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 480
cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 540
tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc cggcaaggcc 600
cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 660
ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 720
gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 780
ctacaaatta cacgctcgag cgagcccaaa tcttctgaca aaactcacac aagcccaccg 840
agcccatgcc caccgtgccc agcacctgaa gccgcgggtg caccgtcagt cttcctcttc 900
cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg 960
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 1080
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggcgtacgc gtgcgcggtc 1140
tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 1200
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1260
agcctgacct gcctggtcaa aggcttctat ccaagcgaca tcgccgtgga gtgggagagc 1320
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380
ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tctccgggta aatctagagc ctccaccaag ggcccatcgg tcttcccccc ggcaccctcc 1560
tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 1620
gagccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 1680
gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 1740
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 1800
gacaagaaag tttga 1815

<210> 868
<211> 1815
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC159 (Cris7 scFv-IgG3UH-CH2-CH3-CH1)

<400> 868
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
caggtccagc tggtgcagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 120
tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 180
cctggaaagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 240
aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 300
ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 360
gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 480
cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 540
tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc cggcaaggcc 600

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cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt     660
ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc     720
gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag     780
ctacaaatta cacgctcgag cgagcccaaa tctagcgaca cacctccccc aagcccacgg     840
tccccatgcc caccgtgccc agcacctgaa gccgcgggtg caccgtcagt cttcctcttc     900
cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg     960
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag    1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc    1080
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggcgtacgc gtgcgcggtc    1140
tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc    1200
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc    1260
agcctgacct gcctggtcaa aggcttctat ccaagcgaca tcgccgtgga gtgggagagc    1320
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc    1380
ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc    1440
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg    1500
tctccgggta aatctagagc ctccaccaag ggcccatcgg tcttcccct ggcaccctcc    1560
tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtcaagga ctacttcccc    1620
gagccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg    1680
gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc    1740
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg    1800
gacaagaaag tttga                                                     1815

<210> 869
<211> 2103
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC160 (Cris7 scFv-IgMCH2UH-CH2-CH3-CH1)

<400> 869
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt      60
caggtccagc tggtgcagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg     120
tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc     180
cctggaaagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac     240
aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc     300
ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa     360
gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct     420
agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc     480
cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc     540
tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc cggcaaggcc     600
cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt     660
ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc     720
gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag     780
ctacaaatta cacgctcgag cattgccgag ctgcctccca aagtgagcgt cttcgtccca     840
ccccgcgacg gcttcttcgg caacccccgc aagtccaagc tcatctgcca ggccacgggt     900
ttcagtcccc ggcagattca ggtgtcctgg ctgcgcgagg ggaagcaggt ggggtctggc     960
gtcaccacgg accaggtgca ggctgaggcc aaagagtctg ggcccacgac ctacaaggtg    1020
accagcacac tgaccatcaa agagagcgac tggctcagcc agagcatgtt cacctgccgc    1080
gtggatcaca ggggcctgac cttccagcag aatgcgtcct ccatgagtgt cccctgccca    1140
ccgtgcccag cacctgaagc cgcgggtgca ccgtcagtct tcctcttccc cccaaaaccc    1200
aaggacaccc tcatgatctc ccggaccccc gaggtcacat gcgtggtggt ggacgtgagc    1260
cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc    1320
aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc    1380
gtcctgcacc aggactggct gaatggcaag gcgtacgcgt gcgcggtctc caacaaagcc    1440
ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag    1500
gtgtacaccc tgccccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc    1560
ctggtcaaag gcttctatcc aagcgacatc gccgtggagt gggagagcaa tgggcagccg    1620
gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac    1680
agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg    1740
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa    1800
tctagagcct ccaccaaggg cccatcggtc ttcccccctgg caccctcctc caagagcacc    1860
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga gccggtgacg    1920
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag    1980
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc    2040
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt    2100
tga                                                                 2103
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<210> 870
<211> 1821
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC161 (HD37 scFv-IgA2UH-CH2-CH3-Ck)

<400> 870
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 180
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 240
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 300
cctgtggaga aggtggatgc tgcaacctat cactgccagc aaagtactga ggatccgtgg 360
acgttcggtg gaggcaccaa gctggaaatc aaaggtggcg gtggttcggg cggtggtggg 420
tcgggtggcg gcggagctag ccaggttcag ctgcagcagt ctggggctga gctggtgagg 480
cctgggtcct cagtgaagat ttcctgcaag gcttctggct atgcattcag tagctactgg 540
atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct 600
ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac 660
gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc 720
tatttctgtg caagacggga gactacgacg gtaggccgtt attactatgc tatggactac 780
tggggtcaag gaacctcagt caccgtctcc tcgagccccc cacctccccc atgcccaccg 840
tgcccagcac ctgaagccgc gggtgcaccg tcagtcttcc tcttcccccc aaaacccaag 900
gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac 960
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 1020
acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 1080
ctgcaccagg actggctgaa tggcaaggcg tacgcgtgcg cggtctccaa caaagccctc 1140
ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg 1200
tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 1260
gtcaaaggct tctatccaag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1320
aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1380
aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1440
catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaatct 1500
agaactgtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 1560
ggaactgcct ctgttgtgtg cctgctgaat tacttctatc ccagagaggc caaagtacag 1620
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgccac agagcaggac 1680
agcaaggaca gcacctacag cctcagcagc gagctgacgc tgagcaaagc agactacgag 1740
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 1800
agcttcaaca ggggagagtg a 1821

<210> 871
<211> 1851
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC162 (HD37 scFv-IgG1miniUH-CH2-CH3-Ck)

<400> 871
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 180
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 240
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 300
cctgtggaga aggtggatgc tgcaacctat cactgccagc aaagtactga ggatccgtgg 360
acgttcggtg gaggcaccaa gctggaaatc aaaggtggcg gtggttcggg cggtggtggg 420
tcgggtggcg gcggagctag ccaggttcag ctgcagcagt ctggggctga gctggtgagg 480
cctgggtcct cagtgaagat ttcctgcaag gcttctggct atgcattcag tagctactgg 540
atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct 600
ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac 660
gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc 720
tatttctgtg caagacggga gactacgacg gtaggccgtt attactatgc tatggactac 780
tggggtcaag gaacctcagt caccgtctcc tcgagcgagc ccaaatcttc tgacaaaact 840
cacacaagcc caccgagccc atgcccaccg tgcccagcac ctgaagccgc gggtgcaccg 900
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 960
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 1020
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 1080

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggcg 1140
tacgcgtgcg cggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1200
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1260
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatccaag cgacatcgcc 1320
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1380
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1440
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1500
aagagcctct ccctgtctcc gggtaaatct agaactgtgg ctgcaccatc tgtcttcatc 1560
ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 1620
tacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 1680
aactcccagg agagtgccac agagcaggac agcaaggaca gcacctacag cctcagcagc 1740
gagctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 1800
catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg a 1851

<210> 872
<211> 1851
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC163 (HD37 scFv-IgG3UH-CH2-CH3-Ck)

<400> 872
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 180
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 240
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 300
cctgtggaga aggtggatgc tgcaacctat cactgccagc aaagtactga ggatccgtgg 360
acgttcggtg gaggcaccaa gctggaaatc aaaggtggcg gtggttcggg cggtggtggg 420
tcgggtggcg gcggagctag ccaggttcag ctgcagcagt ctggggctga gctggtgagg 480
cctgggtcct cagtgaagat ttcctgcaag gcttctggct atgcattcag tagctactgg 540
atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct 600
ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac 660
gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc 720
tatttctgtg caagacggga gactacgacg gtaggccgtt attactatgc tatggactac 780
tggggtcaag gaacctcagt caccgtctcc tcgagcgagc ccaaatctag cgacacacct 840
cccccaagcc cacggtcccc atgcccaccg tgcccagcac ctgaagccgc gggtgcaccg 900
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 960
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 1020
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 1080
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggcg 1140
tacgcgtgcg cggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1200
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1260
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatccaag cgacatcgcc 1320
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1380
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1440
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1500
aagagcctct ccctgtctcc gggtaaatct agaactgtgg ctgcaccatc tgtcttcatc 1560
ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 1620
tacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 1680
aactcccagg agagtgccac agagcaggac agcaaggaca gcacctacag cctcagcagc 1740
gagctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 1800
catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg a 1851

<210> 873
<211> 2139
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC164 (HD37 scFv-IgMCH2UH-CH2-CH3-Ck)

<400> 873
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gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 120
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 180
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 240

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gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat     300
cctgtggaga aggtggatgc tgcaacctat cactgccagc aaagtactga ggatccgtgg     360
acgttcggtg gaggcaccaa gctggaaatc aaaggtggcg gtggttcggg cggtggtggg     420
tcgggtggcg gcggagctag ccaggttcag ctgcagcagt ctggggctga gctggtgagg     480
cctgggtcct cagtgaagat ttcctgcaag gcttctggct atgcattcag tagctactgg     540
atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct     600
ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac     660
gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc     720
tatttctgtg caagacggga gactacgacg gtaggccgtt attactatgc tatggactac     780
tggggtcaag gaacctcagt caccgtctcc tcgagcattg ccgagctgcc tcccaaagtg     840
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tgccaggcca cgggtttcag tccccggcag attcaggtgt cctggctgcg cgaggggaag     960
caggtggggt ctggcgtcac cacggaccag gtgcaggctg aggccaaaga gtctgggccc    1020
acgacctaca aggtgaccag cacactgacc atcaaagaga gcgactggct cagccagagc    1080
atgttcacct gccgcgtgga tcacaggggc ctgaccttcc agcagaatgc gtcctccatg    1140
agtgtcccct gcccaccgtg cccagcacct gaagccgcgg gtgcaccgtc agtcttcctc    1200
ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg    1260
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg    1320
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg    1380
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggcgta cgcgtgcgcg    1440
gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag    1500
ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag    1560
gtcagcctga cctgcctggt caaaggcttc tatccaagcg acatcgccgt ggagtgggag    1620
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tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc    1740
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc    1800
ctgtctccgg gtaaatctag aactgtggct gcaccatctg tcttcatctt cccgccatct    1860
gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaatta cttctatccc    1920
agagaggcca aagtacagtg gaaggtggat aacgccctcc aatcgggtaa ctcccaggag    1980
agtgccacag agcaggacag caaggacagc acctacagcc tcagcagcga gctgacgctg    2040
agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg    2100
agctcgcccg tcacaaagag cttcaacagg ggagagtga                            2139
```

<210> 874
<211> 579
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC125 (Cris7 scFv-CH2-CH3-CH1)

<400> 874

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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
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            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65                  70                  75                  80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
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Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His
                245                 250                 255
Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val
            260                 265                 270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275                 280                 285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    290                 295                 300
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
                325                 330                 335
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala
            340                 345                 350
Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        355                 360                 365
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        435                 440                 445
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    450                 455                 460
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser
465                 470                 475                 480
Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
                485                 490                 495
Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
            500                 505                 510
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
        515                 520                 525
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
    530                 535                 540
Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
545                 550                 555                 560
Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
                565                 570                 575
Lys Lys Val
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<210> 875
<211> 574
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC157 (Cris7 scFv-IgA2UH-CH2-CH3-CH1)

<400> 875

```
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65                  70                  75                  80
```

```
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Ser Ser Pro Pro Pro Pro Pro Cys Pro Pro Cys
                245                 250                 255
Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335
His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn
            340                 345                 350
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
    370                 375                 380
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Ala Ser Thr Lys
465                 470                 475                 480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
                485                 490                 495
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
            500                 505                 510
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
        515                 520                 525
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
    530                 535                 540
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
545                 550                 555                 560
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
                565                 570
```

<210> 876
<211> 584
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC158 (Cris7 scFv-IgG1miniUH-CH2-CH3-CH1)

<400> 876

```
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65                  70                  75                  80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His
                245                 250                 255
Thr Ser Pro Pro Ser Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
            260                 265                 270
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
        275                 280                 285
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
    290                 295                 300
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
305                 310                 315                 320
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
                325                 330                 335
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            340                 345                 350
Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
        355                 360                 365
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
    370                 375                 380
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
385                 390                 395                 400
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
                405                 410                 415
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            420                 425                 430
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
        435                 440                 445
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
    450                 455                 460
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
465                 470                 475                 480
Ser Pro Gly Lys Ser Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
                485                 490                 495
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
            500                 505                 510
```

```
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
        515                 520                 525
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
    530                 535                 540
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
545                 550                 555                 560
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
                565                 570                 575
Asn Thr Lys Val Asp Lys Lys Val
            580
```

<210> 877
<211> 584
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC159 (Cris7 scFv-IgG3UH-CH2-CH3-CH1)

<400> 877

```
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65                  70                  75                  80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Ser Ser Glu Pro Lys Ser Ser Asp Thr Pro Pro
                245                 250                 255
Pro Ser Pro Arg Ser Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
            260                 265                 270
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
        275                 280                 285
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
    290                 295                 300
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
305                 310                 315                 320
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
                325                 330                 335
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            340                 345                 350
Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
        355                 360                 365
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
    370                 375                 380
```

```
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
385                 390                 395                 400
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
                405                 410                 415
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            420                 425                 430
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
        435                 440                 445
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
    450                 455                 460
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
465                 470                 475                 480
Ser Pro Gly Lys Ser Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
                485                 490                 495
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
            500                 505                 510
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
        515                 520                 525
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
    530                 535                 540
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
545                 550                 555                 560
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
                565                 570                 575
Asn Thr Lys Val Asp Lys Lys Val
            580

<210> 878
<211> 680
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC160 (Cris7 scFv-IgMCH2UH-CH2-CH3-CH1)

<400> 878
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1                  5                  10                  15
Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65                  70                  75                  80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95
Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
    130                 135                 140
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145                 150                 155                 160
Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
                165                 170                 175
Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala
            180                 185                 190
Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
        195                 200                 205
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220
Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys
225                 230                 235                 240
Leu Gln Ile Thr Arg Ser Ser Ile Ala Glu Leu Pro Pro Lys Val Ser
                245                 250                 255
```

```
Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser
            260                 265                 270
Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val
        275                 280                 285
Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp
    290                 295                 300
Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val
305                 310                 315                 320
Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Ser Gln Ser Met
                325                 330                 335
Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala
            340                 345                 350
Ser Ser Met Ser Val Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
        355                 360                 365
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
    370                 375                 380
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
385                 390                 395                 400
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
                405                 410                 415
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
            420                 425                 430
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
        435                 440                 445
Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
    450                 455                 460
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
465                 470                 475                 480
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
                485                 490                 495
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
            500                 505                 510
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
        515                 520                 525
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
    530                 535                 540
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
545                 550                 555                 560
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
                565                 570                 575
Ser Pro Gly Lys Ser Arg Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
            580                 585                 590
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
        595                 600                 605
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
    610                 615                 620
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
625                 630                 635                 640
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
                645                 650                 655
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
            660                 665                 670
Asn Thr Lys Val Asp Lys Lys Val
        675                 680

<210> 879
<211> 586
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC161 (HD37 scFv-IgA2UH-CH2-CH3-Ck)

<400> 879
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1                  5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
```

```
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
        115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Pro Pro Pro Pro
                245                 250                 255
Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val
            260                 265                 270
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
        275                 280                 285
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
    290                 295                 300
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305                 310                 315                 320
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
                325                 330                 335
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala
            340                 345                 350
Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
        355                 360                 365
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    370                 375                 380
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385                 390                 395                 400
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                405                 410                 415
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
            420                 425                 430
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        435                 440                 445
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    450                 455                 460
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser
465                 470                 475                 480
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
                485                 490                 495
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe
            500                 505                 510
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        515                 520                 525
Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser
    530                 535                 540
Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu
545                 550                 555                 560
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                565                 570                 575
```

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
580 585

<210> 880
<211> 596
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC162 (HD37 scFv-IgG1miniUH-CH2-CH3-Ck)

<400> 880
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
115 120 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
130 135 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145 150 155 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
165 170 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
180 185 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
195 200 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
210 215 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225 230 235 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Glu Pro Lys Ser
245 250 255
Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Cys Pro Pro Cys Pro
260 265 270
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
275 280 285
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
290 295 300
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
305 310 315 320
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
325 330 335
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
340 345 350
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
355 360 365
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
370 375 380
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
385 390 395 400
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
405 410 415
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
420 425 430
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
435 440 445

```
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    450                 455                 460
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
465                 470                 475                 480
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Thr Val Ala Ala Pro
                485                 490                 495
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
            500                 505                 510
Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu Ala Lys
        515                 520                 525
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
    530                 535                 540
Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
545                 550                 555                 560
Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
                565                 570                 575
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
            580                 585                 590
Asn Arg Gly Glu
        595

<210> 881
<211> 596
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC163 (HD37 scFv-IgG3UH-CH2-CH3-Ck)

<400> 881
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1                  5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
        115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Glu Pro Lys Ser
                245                 250                 255
Ser Asp Thr Pro Pro Pro Ser Pro Arg Ser Pro Cys Pro Pro Cys Pro
            260                 265                 270
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
        275                 280                 285
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    290                 295                 300
```

```
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
305                 310                 315                 320
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
                325                 330                 335
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
            340                 345                 350
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
        355                 360                 365
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    370                 375                 380
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
385                 390                 395                 400
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                405                 410                 415
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            420                 425                 430
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        435                 440                 445
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    450                 455                 460
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
465                 470                 475                 480
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Thr Val Ala Ala Pro
                485                 490                 495
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
            500                 505                 510
Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu Ala Lys
        515                 520                 525
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
    530                 535                 540
Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
545                 550                 555                 560
Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
                565                 570                 575
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
            580                 585                 590
Asn Arg Gly Glu
        595
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<211> 692
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC164 (HD37 scFv-IgMCH2UH-CH2-CH3-Ck)

<400> 882

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Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30
Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
        115                 120                 125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser
    130                 135                 140
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp
145                 150                 155                 160
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Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
                165                 170                 175
Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys
            180                 185                 190
Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met
        195                 200                 205
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
    210                 215                 220
Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr
225                 230                 235                 240
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ser Ile Ala Glu Leu
                245                 250                 255
Pro Pro Lys Val Ser Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly
            260                 265                 270
Asn Pro Arg Lys Ser Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro
        275                 280                 285
Arg Gln Ile Gln Val Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser
    290                 295                 300
Gly Val Thr Thr Asp Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro
305                 310                 315                 320
Thr Thr Tyr Lys Val Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp
                325                 330                 335
Leu Ser Gln Ser Met Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr
            340                 345                 350
Phe Gln Gln Asn Ala Ser Ser Met Ser Val Pro Cys Pro Pro Cys Pro
        355                 360                 365
Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
    370                 375                 380
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
385                 390                 395                 400
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
                405                 410                 415
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
            420                 425                 430
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
        435                 440                 445
Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys
    450                 455                 460
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
465                 470                 475                 480
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
                485                 490                 495
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
            500                 505                 510
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
        515                 520                 525
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
    530                 535                 540
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
545                 550                 555                 560
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
                565                 570                 575
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Thr Val Ala Ala Pro
            580                 585                 590
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        595                 600                 605
Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu Ala Lys
    610                 615                 620
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
625                 630                 635                 640
Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                645                 650                 655
Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            660                 665                 670
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        675                 680                 685
Asn Arg Gly Glu
    690
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