SEQUENCE LISTING

<110> Emergent Biosolutions Product Development Seattle, LLC.
Natarajan, Sateesh K
Tan, Philip H
McMahan, Catherine J

<120> CD3 Binding Polypetides

<130> 2479.113PC03/EJH/BNC

<140> To be assigned
<141> Herewith

<150> US 61/799,849
<151> 2013-03-15

<150> US 61/718,635
<151> 2012-10-25

<150> US 61/636,557
<151> 2012-04-20

<160> 255

<170> PatentIn version 3.5

<210> 1
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cgagga 66

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<211> 22
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<220>
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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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Val Ile Met Ser Arg Gly
20

<210> 3
<211> 1434
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<223> DRA209 (H2 L1 with IgG4 AA ADCC-CDC null Fc)

<400> 3

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tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 120

cctggaaagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 180

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 240

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 300

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 360

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 420

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 480

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc 540

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 600

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 660

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 720

ctacaaatta cacgacgaac tgagcccaaa tcttctgaca aaactcacac atgcccaccg 780

tgcccagcac ctgaagccgc agctccgtca gtcttcctct tccccccaaa acccaaggac 840

accctcatga tctcccggac ccctgaggtc acgtgcgtgg tggtggacgt gagccaggaa 900

gaccccgagg tccagttcaa ctggtacgtg gatggcgtgg aggtgcataa tgccaagaca 960

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tcctccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagagcc acaggtgtac 1140

accctgcccc catcccagga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1200

aaaggcttct accccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1260

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcagg 1320

ctaaccgtgg acaagagccg gtggcaggag gggaatgtct tctcatgctc cgtgatgcat 1380

gaggctctgc acaaccacta cacacagaag agcctctccc tgtctccggg taaa 1434

<210> 4
<211> 478
<212> PRT
<213> Artificial

<220>
<223> DRA209 (H3 L1 with IgG4 AA ADCC-CDC null Fc)

<400> 4

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 Arg Thr Glu Pro Lys Ser Ser Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala 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 Gln Glu Asp Pro Glu Val
290 295 300

Gln 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 Phe Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys
340 345 350

Ala Val Ser Asn Lys Gly Leu Pro Ser Ser 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 Gln Glu Glu Met 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 Arg Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Glu 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
465 470 475

<210> 5
<211> 1434
<212> DNA
<213> Artificial

<220>
<223> DRA219 (H3 L1 IgG4 AA ADCC-CDC null Fc)

<400> 5
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tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 120

cctggaaagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 180

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 240

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 300

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 360

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 420

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 480

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc 540

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 600

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 660

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 720

ctacaaatta catcctcgag cgagcccaaa tcttctgaca aaactcacac atgcccaccg 780

tgcccagcac ctgaagccgc agctccgtca gtcttcctct tccccccaaa acccaaggac 840

accctcatga tctcccggac ccctgaggtc acgtgcgtgg tggtggacgt gagccaggaa 900

gaccccgagg tccagttcaa ctggtacgtg gatggcgtgg aggtgcataa tgccaagaca 960

aagccgcggg aggagcagtt caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 1020

caccaggact ggctgaacgg caaggcatac gcctgcgctg tctccaacaa aggcctcccg 1080

tcctccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagagcc acaggtgtac 1140

accctgcccc catcccagga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1200

aaaggcttct accccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1260

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcagg 1320

ctaaccgtgg acaagagccg gtggcaggag gggaatgtct tctcatgctc cgtgatgcat 1380

gaggctctgc acaaccacta cacacagaag agcctctccc tgtctccggg taaa 1434

<210> 6
<211> 478
<212> PRT
<213> Artificial

<220>
<223> DRA219 (H3 L1 IgG4 AA ADCC-CDC null Fc)

<400> 6

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

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            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 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 Ala 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 Gln Glu Asp Pro Glu Val
    290                 295                 300

Gln 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 Phe Asn Ser Thr Tyr Arg Val Val Ser Val
                325                 330                 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys
            340                 345                 350

Ala Val Ser Asn Lys Gly Leu Pro Ser Ser 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
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370 375 380

Ser Gln Glu Glu Met 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 Arg Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Glu 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
465 470 475

<210> 7
<211> 1434
<212> DNA
<213> Artificial

<220>
<223> DRA222 (H4 L1 with IgG4 AA ADCC-CDC null Fc)

<400> 7
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tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 120

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 180

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 240

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 300

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 360

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 420

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 480

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc 540

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 600

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 660

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 720

ctacaaatta catcctcgag cgagcccaaa tcttctgaca aaactcacac atgcccaccg 780

tgcccagcac ctgaagccgc agctccgtca gtcttcctct tccccccaaa acccaaggac 840

accctcatga tctcccggac ccctgaggtc acgtgcgtgg tggtggacgt gagccaggaa 900

gaccccgagg tccagttcaa ctggtacgtg gatggcgtgg aggtgcataa tgccaagaca 960

aagccgcggg aggagcagtt caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 1020

caccaggact ggctgaacgg caaggcatac gcctgcgctg tctccaacaa aggcctcccg 1080

tcctccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagagcc acaggtgtac 1140

accctgcccc catcccagga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1200

aaaggcttct accccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1260

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcagg 1320

ctaaccgtgg acaagagccg gtggcaggag gggaatgtct tctcatgctc cgtgatgcat 1380

gaggctctgc acaaccacta cacacagaag agcctctccc tgtctccggg taaa 1434

<210> 8
<211> 478
<212> PRT
<213> Artificial

<220>
<223> DRA222 (H4 L1 with IgG4 AA ADCC-CDC null Fc)

<400> 8

Gln Val Gln Leu Val Glu 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 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 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 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 Ala 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 Gln Glu Asp Pro Glu Val
290 295 300

Gln 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 Phe Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys
340 345 350

Ala Val Ser Asn Lys Gly Leu Pro Ser Ser 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 Gln Glu Glu Met 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 Arg Leu Thr Val Asp Lys Ser Arg Trp

435 440 445

Gln Glu 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
465 470 475

<210> 9
<211> 1434
<212> DNA
<213> Artificial

<220>
<223> DRA221 (H4 L3 with IgG4 AA ADCC-CDC null Fc)

<400> 9
caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 60

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 120

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 180

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 240

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 300

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 360

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 420

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 480

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc 540

cccaaactcc tcatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 600

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 660

gccacttatt actgccagca gtggagtcgt aacccaccca ctttcggcgg agggaccaag 720

gtggagatca aatcctcgag cgagcccaaa tcttctgaca aaactcacac atgcccaccg 780

tgcccagcac ctgaagccgc agctccgtca gtcttcctct tccccccaaa acccaaggac 840

accctcatga tctcccggac ccctgaggtc acgtgcgtgg tggtggacgt gagccaggaa 900

gaccccgagg tccagttcaa ctggtacgtg gatggcgtgg aggtgcataa tgccaagaca 960

aagccgcggg aggagcagtt caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 1020

caccaggact ggctgaacgg caaggcatac gcctgcgctg tctccaacaa aggcctcccg 1080

tcctccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagagcc acaggtgtac 1140

accctgcccc catcccagga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1200

aaaggcttct accccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1260

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcagg 1320

ctaaccgtgg acaagagccg gtggcaggag gggaatgtct tctcatgctc cgtgatgcat 1380

gaggctctgc acaaccacta cacacagaag agcctctccc tgtctccggg taaa 1434

<210> 10
<211> 478
<212> PRT
<213> Artificial

<220>
<223> DRA221 (H4 L3 with IgG4 AA ADCC-CDC null Fc)

<400> 10

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Gln Val Gln Leu Val Glu 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 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 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 Leu Leu 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
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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 Ala 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 Gln Glu Asp Pro Glu Val
290 295 300

Gln 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 Phe Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys
340 345 350

Ala Val Ser Asn Lys Gly Leu Pro Ser Ser 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 Gln Glu Glu Met 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 Arg Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Glu 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
465 470 475

<210> 11
<211> 1434
<212> DNA
<213> Artificial

<220>
<223> DRA223 (H3 L3 with IgG4 AA ADCC-CDC null Fc)

<400> 11
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tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 120

cctggaaagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 180

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 240

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 300

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 360

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 420

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 480

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc 540

cccaaactcc tcatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 600

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 660

gccacttatt actgccagca gtggagtcgt aacccaccca ctttcggcgg agggaccaag 720

gtggagatca aatcctcgag cgagcccaaa tcttctgaca aaactcacac atgcccaccg 780

tgcccagcac ctgaagccgc agctccgtca gtcttcctct tcccccaaa acccaaggac 840

accctcatga tctcccggac ccctgaggtc acgtgcgtgg tggtggacgt gagccaggaa 900

gaccccgagg tccagttcaa ctggtacgtg gatggcgtgg aggtgcataa tgccaagaca 960

aagccgcggg aggagcagtt caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 1020

caccaggact ggctgaacgg caaggcatac gcctgcgctg tctccaacaa aggcctcccg 1080

tcctccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagagcc acaggtgtac 1140

accctgcccc catcccagga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1200

aaaggcttct accccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1260

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcagg 1320

ctaaccgtgg acaagagccg gtggcaggag gggaatgtct tctcatgctc cgtgatgcat 1380

gaggctctgc acaaccacta cacacagaag agcctctccc tgtctccggg taaa 1434

<210> 12
<211> 478
<212> PRT
<213> Artificial

<220>
<223> DRA223 (H3 L3 with IgG4 AA ADCC-CDC null Fc)

<400> 12

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 Leu Leu 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

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 Ala 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 Gln Glu Asp Pro Glu Val
```

290 295 300

Gln 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 Phe Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys
340 345 350

Ala Val Ser Asn Lys Gly Leu Pro Ser Ser 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 Gln Glu Glu Met 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 Arg Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Glu 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
465 470 475

<210> 13
<211> 1443
<212> DNA
<213> Artificial

<220>
<223> DRA224 (H5 L4 with IgG4 AA ADCC-CDC null Fc)

<400> 13
caggtccagc ttgtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata caccttcact agatctacga tgcactgggt gcgccaggcc 120

cccggacaaa ggcttgagtg gatgggatac attaatccta gcagtgctta tactaattac 180

aatcagaaat tcaaggacag agtcaccatt accagggaca catccgcgag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagaccccaa 300

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc 360

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga 420

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc 480

accctctcct gcagtgccag ctcaagtgta agttacatga actggtacca acagaaacct 540

ggccaggctc ccaggctcct catctatgac tcatccaaac tggcttctgg catcccagcc 600

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 660

gaagattttg cagtttatta ctgtcagcag tggagtcgta acccacccac tttcggcgga 720

gggaccaagg tggagatcaa atcctcgagc gagcccaaat cttctgacaa aactcacaca 780

tgcccaccgt gcccagcacc tgaagccgca gctccgtcag tcttcctctt cccccccaaaa 840

cccaaggaca ccctcatgat ctcccggacc cctgaggtca cgtgcgtggt ggtggacgtg 900

agccaggaag accccgaggt ccagttcaac tggtacgtgg atggcgtgga ggtgcataat 960

gccaagacaa agccgcggga ggagcagttc aacagcacgt accgtgtggt cagcgtcctc 1020

accgtcctgc accaggactg gctgaacggc aaggcatacg cctgcgctgt ctccaacaaa 1080

ggcctcccgt cctccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagagcca 1140

caggtgtaca ccctgccccc atcccaggag gagatgacca agaaccaggt cagcctgacc 1200

tgcctggtca aaggcttcta ccccagcgac atcgccgtgg agtgggagag caatgggcag 1260

ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1320

tacagcaggc taaccgtgga caagagccgg tggcaggagg ggaatgtctt ctcatgctcc 1380

gtgatgcatg aggctctgca caaccactac acacagaaga gcctctccct gtctccgggt 1440

aaa 1443

<210> 14
<211> 481
<212> PRT
<213> Artificial

<220>
<223> DRA224 (H5 L4 with IgG4 AA ADCC-CDC null Fc)

<400> 14

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 Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
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 Val Thr Ile Thr Arg Asp Thr 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 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 Gly Gly Gly Gly Ser Glu Ile Val
    130                 135                 140

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145                 150                 155                 160

Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ser Ser
            180                 185                 190

Lys Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala
    210                 215                 220

Val Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gln Glu Asp
    290                 295                 300

Pro Glu Val Gln 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 Phe 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 Gly Leu Pro Ser Ser 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 Gln Glu Glu Met 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 Arg Leu Thr Val Asp Lys
        435                 440                 445

Ser Arg Trp Gln Glu 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
```

<210> 15
<211> 1443
<212> DNA
<213> Artificial

<220>
<223> DRA225 (H6 L4 with IgG4 AA ADCC-CDC null Fc)

<400> 15

```
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctgggggtc cctgagactc       60

tcctgtgcag cctctggatt caccttcagt agatctacga tgcactgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcatac attaatccta gcagtgctta tactaattac      180

aatcagaaat tcaaggaccg attcaccatc tccagagaca acgccaagaa ctcactgtat      240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaccccaa      300

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc      360

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga      420

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc      480

accctctcct gcagtgccag ctcaagtgta agttacatga actggtacca acagaaacct      540

ggccaggctc ccaggctcct catctatgac tcatccaaac tggcttctgg catcccagcc      600

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct      660
```

gaagattttg cagtttatta ctgtcagcag tggagtcgta acccacccac tttcggcgga 720

gggaccaagg tggagatcaa atcctcgagc gagcccaaat cttctgacaa aactcacaca 780

tgcccaccgt gcccagcacc tgaagccgca gctccgtcag tcttcctctt ccccccaaaa 840

cccaaggaca ccctcatgat ctcccggacc cctgaggtca cgtgcgtggt ggtggacgtg 900

agccaggaag accccgaggt ccagttcaac tggtacgtgg atggcgtgga ggtgcataat 960

gccaagacaa agccgcggga ggagcagttc aacagcacgt accgtgtggt cagcgtcctc 1020

accgtcctgc accaggactg gctgaacggc aaggcatacg cctgcgctgt ctccaacaaa 1080

ggcctcccgt cctccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagagcca 1140

caggtgtaca ccctgccccc atcccaggag gagatgacca agaaccaggt cagcctgacc 1200

tgcctggtca aaggcttcta ccccagcgac atcgccgtgg agtgggagag caatgggcag 1260

ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1320

tacagcaggc taaccgtgga caagagccgg tggcaggagg ggaatgtctt ctcatgctcc 1380

gtgatgcatg aggctctgca caaccactac acacagaaga gcctctccct gtctccgggt 1440

aaa 1443

<210> 16
<211> 481
<212> PRT
<213> Artificial

<220>
<223> DRA225 (H6 L4 with IgG4 AA ADCC-CDC null Fc)

<400> 16

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Ser
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser 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 Arg Asp Asn Ala Lys Asn Ser 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 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 Gly Gly Gly Gly Ser Glu Ile Val
130 135 140

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145 150 155 160

Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ser Ser
180 185 190

Lys Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala
210 215 220

Val Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser Asp
245 250 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala 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 Gln Glu Asp
290 295 300

Pro Glu Val Gln 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 Phe 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 Gly Leu Pro Ser Ser 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 Gln Glu Glu Met 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 Arg Leu Thr Val Asp Lys
435 440 445

Ser Arg Trp Gln Glu 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

<210> 17
<211> 1434
<212> DNA
<213> Artificial

<220>
<223> DRA233 (H3 L1 with IgG4 AA N297A mutations - different Fc tail than the top constructs)

<400> 17
caggtccagc tggtgcagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 60

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 120

cctggaaagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 180

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 240

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 300

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 360

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 420

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 480

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc 540

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 600

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 660

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 720

ctacaaatta catcctcgag cgagcccaaa tcttctgaca aaactcacac atgcccaccg 780

tgcccagcac ctgaagccgc agctccgtca gtcttcctct tcccccccaaa acccaaggac 840

accctcatga tctcccggac ccctgaggtc acgtgcgtgg tggtggacgt gagccaggaa 900

gaccccgagg tccagttcaa ctggtacgtg gatggcgtgg aggtgcataa tgccaagaca 960

aagccgcggg aggagcagtt cgccagcacg taccgtgtgg tcagcgtcct caccgtcctg 1020

caccaggact ggctgaacgg caaggagtac aagtgcaagg tctccaacaa aggcctcccg 1080

tcctccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagagcc acaggtgtac 1140

accctgcccc catcccagga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1200

aaaggcttct accccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1260

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcagg 1320

ctaaccgtgg acaagagccg gtggcaggag gggaatgtct tctcatgctc cgtgatgcat 1380

gaggctctgc acaaccacta cacacagaag agcctctccc tgtctccggg taaa 1434

<210> 18
<211> 478
<212> PRT
<213> Artificial

<220>
<223> DRA233 (H3 L1 with IgG4 AA N297A mutations - different Fc tail than the top constructs)

<400> 18

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 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 Ala 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 Gln Glu Asp Pro Glu Val
    290                 295                 300

Gln 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 Phe Ala 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 Gly Leu Pro Ser Ser 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 Gln Glu Glu Met 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 Arg Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Glu 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
465 470 475

<210> 19
<211> 1434
<212> DNA
<213> Artificial

<220>
<223> DRA234 (H4 L1 with IgG4 AA N297A mutations - same Fc tails as DRA233)

<400> 19
caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 60

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 120

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 180

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 240

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 300

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 360

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 420

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 480

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc 540

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 600

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 660

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 720

ctacaaatta catcctcgag cgagcccaaa tcttctgaca aaactcacac atgcccaccg 780

tgcccagcac ctgaagccgc agctccgtca gtcttcctct tcccccaaa acccaaggac 840

accctcatga tctcccggac ccctgaggtc acgtgcgtgg tggtggacgt gagccaggaa 900

gaccccgagg tccagttcaa ctggtacgtg gatggcgtgg aggtgcataa tgccaagaca 960

aagccgcggg aggagcagtt cgccagcacg taccgtgtgg tcagcgtcct caccgtcctg 1020

caccaggact ggctgaacgg caaggagtac aagtgcaagg tctccaacaa aggcctcccg 1080

tcctccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagagcc acaggtgtac 1140

accctgcccc catcccagga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1200

aaaggcttct accccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1260

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcagg 1320

ctaaccgtgg acaagagccg gtggcaggag gggaatgtct tctcatgctc cgtgatgcat 1380

gaggctctgc acaaccacta cacacagaag agcctctccc tgtctccggg taaa 1434

<210> 20
<211> 478
<212> PRT
<213> Artificial

<220>
<223> DRA234 (H4 L1 with IgG4 AA N297A mutations - same Fc tails as DRA233)

<400> 20

Gln Val Gln Leu Val Glu 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 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 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 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 Ala 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 Gln Glu Asp Pro Glu Val
290 295 300

Gln 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 Phe Ala 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 Gly Leu Pro Ser Ser 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 Gln Glu Glu Met 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 Arg Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Glu 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
465 470 475

<210> 21

<211> 363
<212> DNA
<213> Artificial

<220>
<223> H1 chain

<400> 21
caggtccagc tggtgcagtc tggggctgaa gtgaagaagc ctggggcctc agtgaaggtg 60

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaaacaggcc 120

cctggacagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 180

aatcagaaat tcaaggacaa ggccacattg actgcagaca aatcctccag tacagcctac 240

atgcaactga gtagcctgag gtctgaggac accgcagtct attactgtgc acggccccaa 300

gtccactatg attacaacgg gtttccttac tggggccaag gactctggt cactgtctct 360

agc 363

<210> 22
<211> 121
<212> PRT
<213> Artificial

<220>
<223> H1 chain

<400> 22

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
115 120

<210> 23
<211> 363
<212> DNA

<213> Artificial

<220>
<223> H2 chain

<400> 23
caggtccagc tggtgcagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 60

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 120

cctggaaagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 180

aatcagaaat tcaaggacaa ggccacattg actgcagaca aatccaagaa cacagcctac 240

atggagctga gtagcctgag gtctgaggac accgcagtct attactgtgc acggccccaa 300

gtccactatg attacaacgg gtttccttac tggggccaag gactctggt cactgtctct 360

agc 363

<210> 24
<211> 121
<212> PRT
<213> Artificial

<220>
<223> H2 chain

<400> 24

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> 25
<211> 363
<212> DNA
<213> Artificial

<220>
<223> H3 chain

<400> 25
caggtccagc tggtgcagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 60

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 120

cctggaaagg gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 180

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 240

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 300

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 360

agc 363

<210> 26
<211> 121
<212> PRT
<213> Artificial

<220>
<223> H3 chain

<400> 26

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> 27
<211> 363
<212> DNA
<213> Artificial

<220>
<223> H4 chain

<400> 27
caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 60

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 120

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 180

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 240

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 300

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 360

agc 363

<210> 28
<211> 121
<212> PRT
<213> Artificial

<220>
<223> H4 chain

<400> 28

Gln Val Gln Leu Val Glu 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 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 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> 29
<211> 363
<212> DNA
<213> Artificial

<220>
<223> H5 chain

<400> 29

caggtccagc ttgtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata caccttcact agatctacga tgcactgggt gcgccaggcc 120

cccggacaaa ggcttgagtg gatgggatac attaatccta gcagtgctta tactaattac 180

aatcagaaat tcaaggacag agtcaccatt accagggaca catccgcgag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagaccccaa 300

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc 360

tca 363

<210> 30
<211> 121
<212> PRT
<213> Artificial

<220>
<223> H5 chain

<400> 30

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 Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
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 Val Thr Ile Thr Arg Asp Thr 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 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> 31
<211> 363
<212> DNA
<213> Artificial

<220>
<223> H6 chain

<400> 31
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agatctacga tgcactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcatac attaatccta gcagtgctta tactaattac 180

aatcagaaat tcaaggaccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaccccaa 300

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc 360

tca 363

<210> 32
<211> 121
<212> PRT
<213> Artificial

<220>
<223> H6 chain

<400> 32

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Ser
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser 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 Arg Asp Asn Ala Lys Asn Ser 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 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> 33
<211> 324
<212> DNA
<213> Artificial

<220>
<223> L1 chain

<400> 33
gcacaagaca tccagatgac ccagtctcca agcagcctgt ctgcaagcgt gggggacagg 60

gtcaccatga cctgcagtgc cagctcaagt gtaagttaca tgaactggta ccagcagaag 120

ccgggcaagg cccccaaaag atggatttat gactcatcca aactggcttc tggagtccct 180

gctcgcttca gtggcagtgg gtctgggacc gactataccc tcacaatcag cagcctgcag 240

cccgaagatt tcgccactta ttactgccag cagtggagtc gtaacccacc cacgttcgga 300

gggggggacca agctacaaat taca 324

<210> 34
<211> 108
<212> PRT
<213> Artificial

<220>
<223> L1 chain

<400> 34

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 Met 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 Trp
35 40 45

Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Tyr 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 Arg Asn Pro
85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr
100 105

<210> 35
<211> 324
<212> DNA
<213> Artificial

<220>
<223> L2 chain

<400> 35
gcacaagaca tccagatgac ccagtctcca agcagcctgt ctgcaagcgt gggggacagg 60

gtcaccatca cctgcagtgc cagctcaagt gtaagttaca tgaactggta ccagcagacc 120

cccggcaagg cccccaaaag atggatttat gactcatcca aactggcttc tggagtccct 180

agccgcttca gtggcagtgg gtctgggacc gacttcaccc tcacaatcag cagcctgcag 240

cccgaagata tcgccactta ttactgccag cagtggagtc gtaacccacc cacgttcgga 300

caggggacca agctacaaat taca 324

<210> 36
<211> 108
<212> PRT
<213> Artificial

<220>
<223> L2 chain

<400> 36

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 Thr Pro Gly Lys Ala Pro Lys Arg Trp
35 40 45

Ile Tyr Asp Ser 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 Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr
100 105

<210> 37
<211> 324
<212> DNA
<213> Artificial

<220>
<223> L3 chain

<400> 37
gcacaagaca tccagatgac ccagtctcca agcagcctgt ctgcaagcgt gggggacagg 60

gtcaccatga cctgcagtgc cagctcaagt gtaagttaca tgaactggta ccagcagaag 120

ccgggcaagg cccccaaact cctcatttat gactcatcca aactggcttc tggagtccct 180

gctcgcttca gtggcagtgg gtctgggacc gactataccc tcacaatcag cagcctgcag 240

cccgaagatt tcgccactta ttactgccag cagtggagtc gtaacccacc cactttcggc 300

ggagggacca aggtggagat caaa 324

<210> 38
<211> 108
<212> PRT
<213> Artificial

<220>
<223> L3 chain

<400> 38

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 Met 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 Leu Leu
35 40 45

Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Tyr 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 Arg Asn Pro
85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 39
<211> 318
<212> DNA
<213> Artificial

<220>
<223> L4 chain

<400> 39
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gtgccagctc aagtgtaagt tacatgaact ggtaccaaca gaaacctggc 120

caggctccca ggctcctcat ctatgactca tccaaactgg cttctggcat cccagccagg 180

ttcagtggca gtgggtctgg gacagacttc actctcacca tcagcagcct agagcctgaa 240

gattttgcag tttattactg tcagcagtgg agtcgtaacc cacccacttt cggcggaggg 300

accaaggtgg agatcaaa 318

<210> 40
<211> 106
<212> PRT
<213> Artificial

<220>
<223> L4 chain

<400> 40

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

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met

20 25 30

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

Asp Ser Ser Lys Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

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

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 41
<211> 244
<212> PRT
<213> Artificial

<220>
<223> DRA209 binding domains

<400> 41

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
```

<210> 42
<211> 247
<212> PRT
<213> Artificial

<220>
<223> DRA209 plus junction sequence

<400> 42

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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 Arg Thr
245

<210> 43
<211> 98
<212> PRT
<213> Artificial

<220>
<223> IGHV1-69*1

<400> 43

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 Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr 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

<210> 44
<211> 98
<212> PRT
<213> Artificial

<220>
<223> IGHV3-30*01

<400> 44

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr 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

<210> 45
<211> 115
<212> PRT
<213> Artificial

<220>
<223> CRIS7 VH

<400> 45

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
115

<210> 46
<211> 107
<212> PRT
<213> Artificial

<220>
<223> CRIS7 VL

<400> 46

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> 47
<211> 121
<212> PRT
<213> Artificial

<220>
<223> DRA161 VH

<400> 47

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>  48
<211>  107
<212>  PRT
<213>  Artificial

<220>
<223>  DRA161 VL

<400>  48

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>  49
```

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

<220>
<223> CRIS7 VH CDR1

<400> 49

Arg Ser Thr Met His
1 5

<210> 50
<211> 17
<212> PRT
<213> Artificial

<220>
<223> CRIS7 VH CDR2

<400> 50

Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asp

<210> 51
<211> 11
<212> PRT
<213> Artificial

<220>
<223> CRIS7 VHCDR3

<400> 51

Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr
1 5 10

<210> 52
<211> 10
<212> PRT
<213> Artificial

<220>
<223> CRIS7 VL CDR1

<400> 52

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn
1 5 10

<210> 53
<211> 7
<212> PRT
<213> Artificial

<220>
<223> CRIS7 VL CDR2

<400> 53

Asp Ser Ser Lys Leu Ala Ser
1 5

<210> 54
<211> 9
<212> PRT
<213> Artificial

<220>
<223> CRIS7 VL CDR3

<400> 54

Gln Gln Trp Ser Arg Asn Pro Pro Thr
1 5

<210> 55
<211> 216
<212> PRT
<213> Artificial

<220>
<223> DRA161 modified Fc domain

<400> 55

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> 56
<211> 2289
<212> DNA
<213> Artificial

<220>
<223> Humanized TSC249 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFv)

<400> 56
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc 660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca 720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg 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

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct 1500

tccctgaata caggaactca gatggcaggt cattctccga attctcaggt ccagctggtg 1560

gagtctgggg gcggagtggt gcagcctggg cggtcactga ggctgtcctg caaggcttct 1620

ggctacacct ttactagatc tacgatgcac tgggtaaggc aggcccctgg acaaggtctg 1680

gaatggattg gatacattaa tcctagcagt gcttatacta attacaatca gaaattcaag 1740

gacaggttca caatcagcgc agacaaatcc aagagcacag ccttcctgca gatggacagc 1800

ctgaggcccg aggacaccgg cgtctatttc tgtgcacggc cccaagtcca ctatgattac 1860

aacgggtttc cttactgggg ccaagggact cccgtcactg tctctagcgg tggcggaggg 1920

tctgggggtg gcggatccgg aggtggtggc tctgcacaag acatccagat gacccagtct 1980

ccaagcagcc tgtctgcaag cgtgggggac agggtcacca tgacctgcag tgccagctca 2040

agtgtaagtt acatgaactg gtaccagcag aagccgggca aggccccaa aagatggatt 2100

tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 2160

accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc 2220

cagcagtgga gtcgtaaccc acccacgttc ggaggggga ccaagctaca aattacatcc 2280

tccagctaa 2289

<210> 57
<211> 742
<212> PRT
<213> Artificial

<220>
<223> Humanized TSC249 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFV)

<400> 57

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

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

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

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

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

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

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
100 105 110

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

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
130 135 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145 150 155 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
165 170 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
180 185 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
195 200 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
210 215 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225 230 235 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
245 250 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala 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 Ala Tyr Ala Cys Ala Val Ser
340 345 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys

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        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 Gln Arg His Asn Asn Ser
465                 470                 475                 480

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

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
            500                 505                 510

Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr
        515                 520                 525

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
    530                 535                 540

Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
545                 550                 555                 560

Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe Leu
                565                 570                 575

Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala
            580                 585                 590

Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln
        595                 600                 605

Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser
```

625 630 635 640

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
645 650 655

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
660 665 670

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
675 680 685

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
690 695 700

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
705 710 715 720

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
725 730 735

Gln Ile Thr Ser Ser Ser
740

<210> 58
<211> 2268
<212> DNA
<213> Artificial

<220>
<223> Humanized TSC250 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFv, with H81 linker)

<400> 58
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc 660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca 720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg 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

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtgaagttca aattcccttg 1500

accgaaagtt acagcccgaa ttctcaggtc cagctggtgg agtctggggg cggagtggtg 1560

cagcctgggc ggtcactgag gctgtcctgc aaggcttctg gctacacctt tactagatct 1620

acgatgcact gggtaaggca ggcccctgga caaggtctgg aatggattgg atacattaat 1680

cctagcagtg cttatactaa ttacaatcag aaattcaagg acaggttcac aatcagcgca 1740

gacaaatcca agagcacagc cttcctgcag atggacagcc tgaggcccga ggacaccggc 1800

gtctatttct gtgcacggcc ccaagtccac tatgattaca acgggtttcc ttactggggc 1860

caagggactc ccgtcactgt ctctagcggt ggcggagggt ctgggggtgg cggatccgga 1920

ggtggtggct ctgcacaaga catccagatg acccagtctc caagcagcct gtctgcaagc 1980

gtgggggaca gggtcaccat gacctgcagt gccagctcaa gtgtaagtta catgaactgg 2040

taccagcaga agccgggcaa ggcccccaaa agatggattt atgactcatc caaactggct 2100

tctggagtcc ctgctcgctt cagtggcagt gggtctggga ccgactatac cctcacaatc 2160

agcagcctgc agcccgaaga tttcgccact tattactgcc agcagtggag tcgtaaccca 2220

cccacgttcg gaggggggac caagctacaa attacatcct ccagctaa 2268

<210> 59
<211> 1477
<212> PRT
<213> Artificial

<220>
<223> Humanized TSC250 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFv, with H81 linker)

<400> 59

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
            100                 105                 110

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

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
    130                 135                 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145                 150                 155                 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
                165                 170                 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
            180                 185                 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
        195                 200                 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
    210                 215                 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225                 230                 235                 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
                245                 250                 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala 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
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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 Ala Tyr Ala Cys Ala 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 Gln Arg His Asn Asn Ser
465                 470                 475                 480

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

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
            500                 505                 510

Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr
        515                 520                 525

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
    530                 535                 540

Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
545                 550                 555                 560

Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe Leu
                565                 570                 575
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Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala
            580                 585                 590

Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln
        595                 600                 605

Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser
625                 630                 635                 640

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                645                 650                 655

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            660                 665                 670

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        675                 680                 685

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
    690                 695                 700

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
705                 710                 715                 720

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
                725                 730                 735

Gln Ile Thr Ser Ser Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ala
            740                 745                 750

Met Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
        755                 760                 765

Lys Ser Ile Ser Lys Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys
    770                 775                 780

Val Pro Lys Leu Arg Ile His Ser Gly Ser Thr Leu Gln Ser Gly Val
785                 790                 795                 800

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
                805                 810                 815

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
            820                 825                 830

His Ile Glu Tyr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
        835                 840                 845
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Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    850                 855                 860

Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
865                 870                 875                 880

Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp
                885                 890                 895

Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
            900                 905                 910

Met Gly Tyr Phe Asn Pro Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys
        915                 920                 925

Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala
    930                 935                 940

Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr
945                 950                 955                 960

Cys Ala Arg Ser Asp Gly Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln
                965                 970                 975

Gly Thr Thr Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys
            980                 985                 990

Thr His Thr Cys Pro Pro Cys Pro  Ala Pro Glu Ala Ala  Gly Ala Pro
        995                 1000                1005

Ser Val  Phe Leu Phe Pro Pro  Lys Pro Lys Asp Thr  Leu Met Ile
    1010                1015                1020

Ser Arg  Thr Pro Glu Val Thr  Cys Val Val Val Asp  Val Ser His
    1025                1030                1035

Glu Asp  Pro Glu Val Lys Phe  Asn Trp Tyr Val Asp  Gly Val Glu
    1040                1045                1050

Val His  Asn Ala Lys Thr Lys  Pro Arg Glu Glu Gln  Tyr Asn Ser
    1055                1060                1065

Thr Tyr  Arg Val Val Ser Val  Leu Thr Val Leu His  Gln Asp Trp
    1070                1075                1080

Leu Asn  Gly Lys Ala Tyr Ala  Cys Ala Val Ser Asn  Lys Ala Leu
    1085                1090                1095

Pro Ala  Pro Ile Glu Lys Thr  Ile Ser Lys Ala Lys  Gly Gln Pro
    1100                1105                1110
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Arg Glu  Pro Gln Val Tyr Thr  Leu Pro Pro Ser Arg  Asp Glu Leu
    1115                 1120                 1125

Thr Lys  Asn Gln Val Ser Leu  Thr Cys Leu Val Lys  Gly Phe Tyr
    1130                 1135                 1140

Pro Ser  Asp Ile Ala Val Glu  Trp Glu Ser Asn Gly  Gln Pro Glu
    1145                 1150                 1155

Asn Asn  Tyr Lys Thr Thr Pro  Pro Val Leu Asp Ser  Asp Gly Ser
    1160                 1165                 1170

Phe Phe  Leu Tyr Ser Lys Leu  Thr Val Asp Lys Ser  Arg Trp Gln
    1175                 1180                 1185

Gln Gly  Asn Val Phe Ser Cys  Ser Val Met His Glu  Ala Leu His
    1190                 1195                 1200

Asn His  Tyr Thr Gln Lys Ser  Leu Ser Leu Ser Pro  Gly Glu Val
    1205                 1210                 1215

Gln Ile  Pro Leu Thr Glu Ser  Tyr Ser Pro Asn Ser  Gln Val Gln
    1220                 1225                 1230

Leu Val  Glu Ser Gly Gly Gly  Val Val Gln Pro Gly  Arg Ser Leu
    1235                 1240                 1245

Arg Leu  Ser Cys Lys Ala Ser  Gly Tyr Thr Phe Thr  Arg Ser Thr
    1250                 1255                 1260

Met His  Trp Val Arg Gln Ala  Pro Gly Gln Gly Leu  Glu Trp Ile
    1265                 1270                 1275

Gly Tyr  Ile Asn Pro Ser Ser  Ala Tyr Thr Asn Tyr  Asn Gln Lys
    1280                 1285                 1290

Phe Lys  Asp Arg Phe Thr Ile  Ser Ala Asp Lys Ser  Lys Ser Thr
    1295                 1300                 1305

Ala Phe  Leu Gln Met Asp Ser  Leu Arg Pro Glu Asp  Thr Gly Val
    1310                 1315                 1320

Tyr Phe  Cys Ala Arg Pro Gln  Val His Tyr Asp Tyr  Asn Gly Phe
    1325                 1330                 1335

Pro Tyr  Trp Gly Gln Gly Thr  Pro Val Thr Val Ser  Ser Gly Gly
    1340                 1345                 1350

Gly Gly  Ser Gly Gly Gly Gly  Ser Gly Gly Gly Gly  Ser Ala Gln
    1355                 1360                 1365
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1370 1375 1380

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
1385 1390 1395

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg
1400 1405 1410

Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg
1415 1420 1425

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
1430 1435 1440

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp
1445 1450 1455

Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile
1460 1465 1470

Thr Ser Ser Ser
1475

<210> 60
<211> 2274
<212> DNA
<213> Artificial

<220>
<223> Humanized TSC251 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFv, with H83 linker)

<400> 60
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc 660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca 720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg 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

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gttcttccct gaatacagga 1500

actcagatgg caggtcattc tccgaattct caggtccagc tggtggagtc tgggggcgga 1560

gtggtgcagc ctgggcggtc actgaggctg tcctgcaagg cttctggcta cacctttact 1620

agatctacga tgcactgggt aaggcaggcc cctggacaag gtctggaatg gattggatac 1680

attaatccta gcagtgctta tactaattac aatcagaaat tcaaggacag gttcacaatc 1740

agcgcagaca aatccaagag cacagccttc ctgcagatgg acagcctgag gcccgaggac 1800

accggcgtct atttctgtgc acggccccaa gtccactatg attacaacgg gtttccttac 1860

tggggccaag ggactcccgt cactgtctct agcggtggcg gagggtctgg gggtggcgga 1920

tccggaggtg gtggctctgc acaagacatc cagatgaccc agtctccaag cagcctgtct 1980

gcaagcgtgg gggacagggt caccatgacc tgcagtgcca gctcaagtgt aagttacatg 2040

aactggtacc agcagaagcc gggcaaggcc cccaaaagat ggatttatga ctcatccaaa 2100

ctggcttctg gagtccctgc tcgcttcagt ggcagtgggt ctgggaccga ctataccctc 2160

acaatcagca gcctgcagcc cgaagatttc gccacttatt actgccagca gtggagtcgt 2220

aacccaccca cgttcggagg ggggaccaag ctacaaatta catcctccag ctaa 2274

<210> 61
<211> 737
<212> PRT
<213> Artificial

<220>
<223> Humanized TSC251 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFv, with H83 linker)

<400> 61

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr

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            20                  25                  30

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
            100                 105                 110

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

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
    130                 135                 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145                 150                 155                 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
                165                 170                 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
            180                 185                 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
        195                 200                 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
    210                 215                 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225                 230                 235                 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
                245                 250                 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala 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
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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 Ala Tyr Ala Cys Ala 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 Ser Ser Leu Asn Thr Gly
465 470 475 480

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

Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys
500 505 510

Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg
515 520 525

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
530 535 540

Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile
545 550 555 560

Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu

565 570 575

Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His
580 585 590

Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr
595 600 605

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
610 615 620

Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
625 630 635 640

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
645 650 655

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
660 665 670

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg
675 680 685

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser
690 695 700

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg
705 710 715 720

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser
725 730 735

Ser

<210> 62
<211> 2286
<212> DNA
<213> Artificial

<220>
<223> Huamnized TSC252 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFv, with H91 linker)

<400> 62
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 420
ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 480
gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540
cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 600
actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc 660
acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca 720
agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 780
tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020
gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080
tggctgaatg gcaaggcgta cgcgtgcgcg 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
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaactcatt agcaaaccaa 1500
gaagttcaaa ttcccttgac cgaaagttac agcccgaatt ctcaggtcca gctggtggag 1560
tctgggggcg gagtggtgca gcctgggcgg tcactgaggc tgtcctgcaa ggcttctggc 1620
tacaccttta ctagatctac gatgcactgg gtaaggcagg cccctggaca aggtctggaa 1680
tggattggat acattaatcc tagcagtgct tatactaatt acaatcagaa attcaaggac 1740
aggttcacaa tcagcgcaga caaatccaag agcacagcct tcctgcagat ggacagcctg 1800
aggcccgagg acaccggcgt ctatttctgt gcacggcccc aagtccacta tgattacaac 1860
gggtttcctt actggggcca agggactccc gtcactgtct ctagcggtgg cggagggtct 1920
gggggtggcg gatccggagg tggtggctct gcacaagaca tccagatgac ccagtctcca 1980
agcagcctgt ctgcaagcgt gggggacagg gtcaccatga cctgcagtgc cagctcaagt 2040
gtaagttaca tgaactggta ccagcagaag ccgggcaagg cccccaaaag atggatttat 2100
gactcatcca aactggcttc tggagtccct gctcgcttca gtggcagtgg gtctgggacc 2160
gactataccc tcacaatcag cagcctgcag cccgaagatt tcgccactta ttactgccag 2220
cagtggagtc gtaacccacc cacgttcgga ggggggacca agctacaaat tacatcctcc 2280
agctaa 2286

<210> 63
<211> 741
<212> PRT
<213> Artificial

<220>
<223> Humanized TSC252 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFv, with H91 linker)

<400> 63

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
100 105 110

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

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
130 135 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145 150 155 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
165 170 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
180 185 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
195 200 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
210 215 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val

225 230 235 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
245 250 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala 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 Ala Tyr Ala Cys Ala 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 Asn Ser Leu Ala Asn Gln
465 470 475 480

Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser Gln Val
485 490 495

Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu

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            500                 505                 510

Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met
        515                 520                 525

His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr
    530                 535                 540

Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp
545                 550                 555                 560

Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln
                565                 570                 575

Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg
            580                 585                 590

Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly
        595                 600                 605

Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    610                 615                 620

Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro
625                 630                 635                 640

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser
                645                 650                 655

Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
            660                 665                 670

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly
        675                 680                 685

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu
    690                 695                 700

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
705                 710                 715                 720

Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln
                725                 730                 735

Ile Thr Ser Ser Ser
            740
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<210> 64
<211> 2250
<212> DNA
<213> Artificial

<220>
<223> Humanized TSC295 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFv, with H9 linker)

<400> 64
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc 660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca 720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg 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

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtgggagccc accttcaccg 1500

aattctcagg tccagctggt ggagtctggg ggcggagtgg tgcagcctgg gcggtcactg 1560

aggctgtcct gcaaggcttc tggctacacc tttactagat ctacgatgca ctgggtaagg 1620

caggcccctg gacaaggtct ggaatggatt ggatacatta atcctagcag tgcttatact 1680

aattacaatc agaaattcaa ggacaggttc acaatcagcg cagacaaatc caagagcaca 1740

gccttcctgc agatggacag cctgaggccc gaggacaccg gcgtctattt ctgtgcacgg 1800

ccccaagtcc actatgatta caacgggttt ccttactggg gccaagggac tcccgtcact 1860

gtctctagcg gtggcggagg gtctgggggt ggcggatccg gaggtggtgg ctctgcacaa 1920

gacatccaga tgacccagtc tccaagcagc ctgtctgcaa gcgtggggga cagggtcacc 1980

atgacctgca gtgccagctc aagtgtaagt tacatgaact ggtaccagca gaagccgggc 2040

aaggccccca aaagatggat ttatgactca tccaaactgg cttctggagt ccctgctcgc 2100

ttcagtggca gtgggtctgg gaccgactat accctcacaa tcagcagcct gcagcccgaa 2160

gatttcgcca cttattactg ccagcagtgg agtcgtaacc cacccacgtt cggaggggg 2220

accaagctac aaattacatc ctccagctaa 2250

<210> 65
<211> 729
<212> PRT
<213> Artificial

<220>
<223> Humanized TSC295 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFv, with H9 linker)

<400> 65

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
100 105 110

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

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
130 135 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145 150 155 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
165 170 175

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Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
            180                 185                 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
        195                 200                 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
    210                 215                 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225                 230                 235                 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
                245                 250                 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala 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 Ala Tyr Ala Cys Ala 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
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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 Gly Ser Pro Pro Ser Pro
465                 470                 475                 480

Asn Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro
                485                 490                 495

Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
            500                 505                 510

Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
        515                 520                 525

Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln
    530                 535                 540

Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr
545                 550                 555                 560

Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr
                565                 570                 575

Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr
            580                 585                 590

Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        595                 600                 605

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met
    610                 615                 620

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
625                 630                 635                 640

Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
                645                 650                 655

Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys
            660                 665                 670

Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
        675                 680                 685

Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    690                 695                 700

Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly
705                 710                 715                 720
```

Thr Lys Leu Gln Ile Thr Ser Ser Ser
725

<210> 66
<211> 2283
<212> DNA
<213> Artificial

<220>
<223> Humanized TSC296 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFv, with H94 linker)

<400> 66
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc 660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca 720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg 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

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gttctggtgg aggcggttca 1500

ggcggaggtg gctccggcgg tggcggatcg ccgaattctc aggtccagct ggtggagtct 1560

gggggcggag tggtgcagcc tgggcggtca ctgaggctgt cctgcaaggc ttctggctac 1620

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cccgaggaca ccggcgtcta tttctgtgca cggccccaag tccactatga ttacaacggg 1860

tttccttact ggggccaagg gactcccgtc actgtctcta gcggtggcgg agggtctggg 1920

ggtggcggat ccggaggtgg tggctctgca caagacatcc agatgaccca gtctccaagc 1980

agcctgtctg caagcgtggg ggacagggtc accatgacct gcagtgccag ctcaagtgta 2040

agttacatga actggtacca gcagaagccg ggcaaggccc ccaaaagatg gatttatgac 2100

tcatccaaac tggcttctgg agtccctgct cgcttcagtg gcagtgggtc tgggaccgac 2160

tataccctca caatcagcag cctgcagccc gaagatttcg ccacttatta ctgccagcag 2220

tggagtcgta acccacccac gttcggaggg gggaccaagc tacaaattac atcctccagc 2280

taa 2283

<210> 67
<211> 740
<212> PRT
<213> Artificial

<220>
<223> Humanized TSC296 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFv, with H94 linker)

<400> 67

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
100 105 110

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

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Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
    130                 135                 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145                 150                 155                 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
                165                 170                 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
            180                 185                 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
        195                 200                 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
    210                 215                 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225                 230                 235                 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
                245                 250                 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala 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 Ala Tyr Ala Cys Ala 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
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```
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 Ser Gly Gly Gly Gly Ser
465                 470                 475                 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Pro Asn Ser Gln Val Gln
                485                 490                 495

Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg
            500                 505                 510

Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His
        515                 520                 525

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
    530                 535                 540

Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg
545                 550                 555                 560

Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met
                565                 570                 575

Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro
            580                 585                 590

Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr
        595                 600                 605

Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    610                 615                 620

Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser
625                 630                 635                 640

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala
                645                 650                 655

Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys
            660                 665                 670
```

```
Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val
        675                 680                 685

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr
    690                 695                 700

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
705                 710                 715                 720

Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile
                725                 730                 735

Thr Ser Ser Ser
            740
```

<210> 68
<211> 2274
<212> DNA
<213> Artificial

<220>
<223> Humanized TSC301 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFv, with H105 linker)

<400> 68

```
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt       60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc      120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca      180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct      240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct      300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa      360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt      420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca      480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg      540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat      600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc      660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca      720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc      780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct      840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg      900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag      960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg     1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac     1080

tggctgaatg gcaaggcgta cgcgtgcgcg 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

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gttctggtgg aggcggttca 1500

ggcggaggtg gctccggcgg tggcggatcg caggtccagc tggtggagtc tgggggcgga 1560

gtggtgcagc ctgggcggtc actgaggctg tcctgcaagg cttctggcta cacctttact 1620

agatctacga tgcactgggt aaggcaggcc cctggacaag gtctggaatg gattggatac 1680

attaatccta gcagtgctta tactaattac aatcagaaat tcaaggacag gttcacaatc 1740

agcgcagaca aatccaagag cacagccttc ctgcagatgg acagcctgag gcccgaggac 1800

accggcgtct atttctgtgc acggccccaa gtccactatg attacaacgg gtttccttac 1860

tggggccaag ggactcccgt cactgtctct agcggtggcg gagggtctgg gggtggcgga 1920

tccggaggtg gtggctctgc acaagacatc cagatgaccc agtctccaag cagcctgtct 1980

gcaagcgtgg gggacagggt caccatgacc tgcagtgcca gctcaagtgt aagttacatg 2040

aactggtacc agcagaagcc gggcaaggcc cccaaaagat ggatttatga ctcatccaaa 2100

ctggcttctg gagtccctgc tcgcttcagt ggcagtgggt ctgggaccga ctataccctc 2160

acaatcagca gcctgcagcc cgaagatttc gccacttatt actgccagca gtggagtcgt 2220

aacccaccca cgttcggagg ggggaccaag ctacaaatta catcctccag ctaa 2274

<210> 69
<211> 737
<212> PRT
<213> Artificial

<220>
<223> Humanized TSC301 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFv, with H105 linker)

<400> 69

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

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

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

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
100 105 110

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

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
130 135 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145 150 155 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
165 170 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
180 185 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
195 200 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
210 215 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225 230 235 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
245 250 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala 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 Ala Tyr Ala Cys Ala 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 Ser Gly Gly Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu
485 490 495

Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys
500 505 510

Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg
515 520 525

Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
530 535 540

Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile
545 550 555 560

Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu
565 570 575

Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His
580 585 590

Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr
595 600 605

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

610 615 620

Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
625 630 635 640

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
645 650 655

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
660 665 670

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg
675 680 685

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser
690 695 700

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg
705 710 715 720

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser
725 730 735

Ser

<210> 70
<211> 2280
<212> DNA
<213> Artificial

<220>
<223> Humanized TSC302 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFv, with H106 linker)

<400> 70
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc 660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca 720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg 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

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct 1500

tccctgaata caggaactca gatggcaggt cattctcagg tccagctggt ggagtctggg 1560

ggcggagtgg tgcagcctgg gcggtcactg aggctgtcct gcaaggcttc tggctacacc 1620

tttactagat ctacgatgca ctgggtaagg caggcccctg gacaaggtct ggaatggatt 1680

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacaggttc 1740

acaatcagcg cagacaaatc caagagcaca gccttcctgc agatggacag cctgaggccc 1800

gaggacaccg gcgtctattt ctgtgcacgg ccccaagtcc actatgatta caacgggttt 1860

ccttactggg gccaagggac tcccgtcact gtctctagcg gtggcggagg gtctgggggt 1920

ggcggatccg gaggtggtgg ctctgcacaa gacatccaga tgacccagtc tccaagcagc 1980

ctgtctgcaa gcgtggggga cagggtcacc atgacctgca gtgccagctc aagtgtaagt 2040

tacatgaact ggtaccagca gaagccgggc aaggccccca aaagatggat ttatgactca 2100

tccaaactgg cttctggagt ccctgctcgc ttcagtggca gtgggtctgg gaccgactat 2160

accctcacaa tcagcagcct gcagcccgaa gatttcgcca cttattactg ccagcagtgg 2220

agtcgtaacc cacccacgtt cggaggggggg accaagctac aaattacatc ctccagctaa 2280

<210> 71
<211> 739
<212> PRT
<213> Artificial

<220>
<223> Humanizede TSC302 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-DRA222 scFv, with H106 linker)

<400> 71

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
            100                 105                 110

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

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
    130                 135                 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145                 150                 155                 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
                165                 170                 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
            180                 185                 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
        195                 200                 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
    210                 215                 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225                 230                 235                 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
                245                 250                 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala 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
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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 Ala Tyr Ala Cys Ala 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 Gln Arg His Asn Asn Ser
465                 470                 475                 480

Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Gln Val Gln Leu
                485                 490                 495

Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu
            500                 505                 510

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        515                 520                 525

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
    530                 535                 540

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe
545                 550                 555                 560
```

```
Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp
                565                 570                 575

Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln
            580                 585                 590

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro
        595                 600                 605

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    610                 615                 620

Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
625                 630                 635                 640

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser
                645                 650                 655

Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
            660                 665                 670

Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro
        675                 680                 685

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
    690                 695                 700

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp
705                 710                 715                 720

Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr
                725                 730                 735

Ser Ser Ser
```

<210> 72
<211> 106
<212> PRT
<213> Artificial

<220>
<223> HuM291 VL

<400> 72

```
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 Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr
```

35 40 45

Asp Thr 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 Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Pro Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 73
<211> 120
<212> PRT
<213> Artificial

<220>
<223> HuM291 VH

<400> 73

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> 74
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Linker

<400> 74

Gly Gly Gly Gly Ser
1 5

<210> 75
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Linker

<400> 75

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 76
<211> 15
<212> PRT
<213> Artificial

<220>
<223> Linker

<400> 76

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 77
<211> 20
<212> PRT
<213> Artificial

<220>
<223> Linker

<400> 77

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> 78
<211> 25
<212> PRT
<213> Artificial

<220>
<223> Linker

<400> 78

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser

20 25

<210> 79
<211> 20
<212> PRT
<213> Artificial

<220>
<223> a secretory signal sequence

<400> 79

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> 80
<211> 98
<212> PRT
<213> Artificial

<220>
<223> a wild-type human igG1 CH1 domain

<400> 80

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> 81
<211> 107
<212> PRT
<213> Artificial

<220>
<223> a wild-type human CK domain

<400> 81

```
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>  82
<211>  106
<212>  PRT
<213>  Artificial

<220>
<223>  a wild-type human CA domain

<400>  82

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>  83
```

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

<220>
<223> a CK domain

<400> 83

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> 84
<211> 105
<212> PRT
<213> Artificial

<220>
<223> a CA domain

<400> 84

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> 85
<211> 110
<212> PRT
<213> Artificial

<220>
<223> a wild-type human IgG1 CH2 domain

<400> 85

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> 86
<211> 110
<212> PRT
<213> Artificial

<220>
<223> a wild-type human IgG1 CH2 domain

<400> 86

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> 87
<211> 13
<212> PRT
<213> Artificial

<220>
<223> RON-e01 VL CDR1

<400> 87

Arg Ala Ser Gln Asp Ile Gly Ser Ser Leu Ser Trp Leu
1 5 10

<210> 88
<211> 11
<212> PRT
<213> Artificial

<220>
<223> RON-e01 VL CDR2

<400> 88

Arg Leu Ile Tyr Ser Thr Ser Ser Leu Asp Ser
1 5 10

<210> 89
<211> 9
<212> PRT
<213> Artificial

<220>
<223> RON-e01 VL CDR3

<400> 89

Leu Gln Tyr Ala Ser Ser Pro Trp Thr
1 5

<210> 90
<211> 13
<212> PRT
<213> Artificial

<220>
<223> RON-f01 VL CDR1

<400> 90

Leu Ala Ser Gln Thr Ile Gly Thr Trp Leu Ala Trp Tyr

1 5 10

<210> 91
<211> 11
<212> PRT
<213> Artificial

<220>
<223> RON-f01 VL CDR2

<400> 91

Leu Leu Ile Tyr Ala Ala Thr Ser Leu Ala Asp
1 5 10

<210> 92
<211> 9
<212> PRT
<213> Artificial

<220>
<223> RON-f01 VL CDR3

<400> 92

Gln Gln Leu Tyr Asn Thr Pro Trp Thr
1 5

<210> 93
<211> 10
<212> PRT
<213> Artificial

<220>
<223> RON-e01 VH CDR1

<400> 93

Gly Tyr Thr Phe Thr Ser Tyr Trp Ile His
1 5 10

<210> 94
<211> 20
<212> PRT
<213> Artificial

<220>
<223> RON-e01 VH CDR2

<400> 94

Trp Ile Gly Tyr Ile Tyr Pro Thr Thr Gly Tyr Thr Glu Ser Asn Gln
1 5 10 15

Lys Phe Lys Asp
20

<210> 95
<211> 10
<212> PRT
<213> Artificial

<220>
<223> RON-e01 VH CDR3

<400> 95

Phe Leu Leu Arg Pro Trp Tyr Phe Asp Val
1 5 10

<210> 96
<211> 10
<212> PRT
<213> Artificial

<220>
<223> RON-f01 VH CDR1

<400> 96

Asp Tyr Thr Leu Thr Asp Phe Tyr Met Asn
1 5 10

<210> 97
<211> 20
<212> PRT
<213> Artificial

<220>
<223> RON-f01 VH CDR2

<400> 97

Trp Ile Gly Arg Ile Tyr Pro Gly Thr Asp Lys Thr Arg Tyr Asn Glu
1 5 10 15

Lys Phe Arg Asp
20

<210> 98
<211> 14
<212> PRT
<213> Artificial

<220>
<223> RON-f01 VH CDR3

<400> 98

Ala Arg Ser Ala Tyr Tyr Gly Asn Tyr Val Ala Met Asp Tyr
1 5 10

<210> 99
<211> 107
<212> PRT
<213> Artificial

<220>
<223> RON-e01 murine VL

<400> 99

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>  100
<211>  107
<212>  PRT
<213>  Artificial

<220>
<223>  RON-f01 murine VL

<400>  100

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>  101
<211>  117
<212>  PRT
<213>  Artificial
```

<220>
<223> RON-e01 murine VH

<400> 101

```
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
```

<210> 102
<211> 121
<212> PRT
<213> Artificial

<220>
<223> RON-f01 murine VH

<400> 102

```
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 Leu
115 120

<210> 103
<211> 121
<212> PRT
<213> Artificial

<220>
<223> RON-f01 murine VH variant

<400> 103

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> 104
<211> 107
<212> PRT
<213> Artificial

<220>
<223> RON-e01h6 humanized VL

<400> 104

Ala Ile Gln Leu 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 Asp Ile Gly Ser Ser

20 25 30

Leu Ser Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ser Thr Ser Ser Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 105
<211> 107
<212> PRT
<213> Artificial

<220>
<223> RON-e01h7 humanized VL

<400> 105

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 Asp Ile Gly Ser Ser
20 25 30

Leu Ser Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ser Thr Ser Ser Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 106
<211> 107
<212> PRT
<213> Artificial

<220>
<223> RON-f01h2 humanized VL

<400> 106

```
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 Leu Ala Ser Gln Thr Ile Gly Thr Trp
            20                  25                  30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Tyr Asn Thr Pro Trp
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 107
<211> 117
<212> PRT
<213> Artificial

<220>
<223> RON-e01h8 humanized VH

<400> 107

```
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 Ser Tyr
            20                  25                  30

Trp Ile His Trp Val Arg Gln Ala 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 Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

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

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

Val Thr Val Ser Ser
        115

<210> 108
<211> 117
<212> PRT
<213> Artificial

<220>
<223> RON-e01h9 humanized VH

<400> 108

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 Ser Tyr
            20   25   30

Trp Ile His Trp Val Arg Gln Ala Thr 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 Arg Val Thr Met Thr Arg Asn Thr Ser Ile 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

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

Val Thr Val Ser Ser
        115

<210> 109
<211> 117
<212> PRT
<213> Artificial

<220>
<223> RON-e01h10 humanized VH

<400> 109

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 Ser Tyr
            20   25   30

Trp Ile His Trp Val Arg Gln Ala 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 Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65   70   75   80

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

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

Val Thr Val Ser Ser
        115

<210> 110
<211> 121
<212> PRT
<213> Artificial

<220>
<223> RON-f01h4 humanized VH

<400> 110

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

Thr Val Lys Ile Ser Cys Lys Val Ser Asp Tyr Thr Leu Thr Asp Phe
            20   25   30

Tyr Met Asn Trp Val Gln Gln Ala Pro Gly Lys 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 Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asp 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 Gly Asn Tyr Val Ala Met Asp Tyr Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 111
<211> 121
<212> PRT
<213> Artificial

<220>
<223> RON-f01h5 humanized VH

<400> 111

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 Asp Tyr Thr Leu Thr Asp Phe
20 25 30

Tyr Met Asn Trp Val Arg Gln Ala 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 Arg Val Thr Ile Thr Ala Asp Lys Ser Thr 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 Gly Asn Tyr Val Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 112
<211> 15
<212> PRT
<213> Artificial

<220>
<223> sss(s)-hlgG1 hinge

<400> 112

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Ser
1 5 10 15

<210> 113
<211> 15
<212> PRT
<213> Artificial

<220>
<223> csc(s)-hlgG1 hinge

<400> 113

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

<210> 114
<211> 15
<212> PRT

<213> Artificial

<220>
<223> ssc(s)-hlgG1 hinge

<400> 114

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

<210> 115
<211> 15
<212> PRT
<213> Artificial

<220>
<223> scc(s)-hlg1 hinge

<400> 115

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

<210> 116
<211> 15
<212> PRT
<213> Artificial

<220>
<223> css(s)-hlgG1 hinge

<400> 116

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

<210> 117
<211> 15
<212> PRT
<213> Artificial

<220>
<223> scs(s)-hlgG1 hinge

<400> 117

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

<210> 118
<211> 15
<212> PRT
<213> Artificial

<220>
<223> ccc(s)-hlgG1 hinge

<400> 118

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

<210> 119

<211> 15
<212> PRT
<213> Artificial

<220>
<223> ccc(p)-hlgG1 hinge

<400> 119

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

<210> 120
<211> 15
<212> PRT
<213> Artificial

<220>
<223> sss(p)-hlgG1 hinge

<400> 120

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
1 5 10 15

<210> 121
<211> 15
<212> PRT
<213> Artificial

<220>
<223> csc(p)-hlgG1 hinge

<400> 121

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

<210> 122
<211> 15
<212> PRT
<213> Artificial

<220>
<223> ssc(p)-hlgG1 hinge

<400> 122

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

<210> 123
<211> 15
<212> PRT
<213> Artificial

<220>
<223> scc(p)-hlgG1 hinge

<400> 123

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

<210> 124
<211> 15
<212> PRT
<213> Artificial

<220>
<223> css(p)-hlgG1 hinge

<400> 124

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

<210> 125
<211> 15
<212> PRT
<213> Artificial

<220>
<223> scs(p)-hlgG1 hinge

<400> 125

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

<210> 126
<211> 6
<212> PRT
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<220>
<223> Scppcp

<400> 126

Ser Cys Pro Pro Cys Pro
1 5

<210> 127
<211> 20
<212> PRT
<213> Artificial

<220>
<223> STD1

<400> 127

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> 128
<211> 38
<212> PRT
<213> Artificial

<220>
<223> STD2

<400> 128

Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10 15

Ser Gly Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Asn Ser
35

<210> 129
<211> 2
<212> PRT
<213> Artificial

<220>
<223> H1

<400> 129

Asn Ser
1

<210> 130
<211> 8
<212> PRT
<213> Artificial

<220>
<223> H2

<400> 130

Gly Gly Gly Gly Ser Gly Asn Ser
1 5

<210> 131
<211> 10
<212> PRT
<213> Artificial

<220>
<223> H3

<400> 131

Asn Tyr Gly Gly Gly Gly Ser Gly Asn Ser
1 5 10

<210> 132
<211> 13
<212> PRT
<213> Artificial

<220>
<223> H4

<400> 132

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser

1 5 10

<210> 133
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H5

<400> 133

Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser
1 5 10 15

<210> 134
<211> 18
<212> PRT
<213> Artificial

<220>
<223> H6

<400> 134

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Asn Ser

<210> 135
<211> 8
<212> PRT
<213> Artificial

<220>
<223> H7

<400> 135

Gly Cys Pro Pro Cys Pro Asn Ser
1 5

<210> 136
<211> 8
<212> PRT
<213> Artificial

<220>
<223> H9

<400> 136

Gly Ser Pro Pro Ser Pro Asn Ser
1 5

<210> 137
<211> 15
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<220>
<223> (G4S)3

<400> 137

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 138
<211> 16
<212> PRT
<213> Artificial

<220>
<223> H105

<400> 138

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 139
<211> 20
<212> PRT
<213> Artificial

<220>
<223> (G4S)4

<400> 139

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> 140
<211> 21
<212> PRT
<213> Artificial

<220>
<223> H75 (NKG2A quadruple mutant)

<400> 140

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> 141
<211> 16
<212> PRT
<213> Artificial

<220>
<223> H83 (NKG2A derived)

<400> 141

Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser
1 5 10 15

<210> 142
<211> 18
<212> PRT
<213> Artificial

<220>
<223> H106 (NKG2A derived)

<400> 142

Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
1 5 10 15

His Ser

<210> 143
<211> 14
<212> PRT
<213> Artificial

<220>
<223> H81 (NKG2D derived)

<400> 143

Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser
1 5 10

<210> 144
<211> 20
<212> PRT
<213> Artificial

<220>
<223> H91 (NKG2D derived)

<400> 144

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> 145
<211> 19
<212> PRT
<213> Artificial

<220>
<223> H94

<400> 145

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

Pro Asn Ser

<210> 146
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H16

<400> 146

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

<210> 147
<211> 20
<212> PRT
<213> Artificial

<220>
<223> H17

<400> 147

Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Ser Cys Pro Pro
1 5 10 15

Cys Pro Asn Ser
20

<210> 148
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H18

<400> 148

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

<210> 149
<211> 20
<212> PRT
<213> Artificial

<220>
<223> H19

<400> 149

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> 150
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H20

<400> 150

Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Asn Ser
1 5 10 15

<210> 151
<211> 20
<212> PRT
<213> Artificial

<220>
<223> H21

<400> 151

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> 152
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H22

<400> 152

Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Asn Ser
1 5 10 15

<210> 153
<211> 21
<212> PRT
<213> Artificial

<220>
<223> H23

<400> 153

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> 154
<211> 15
<212> PRT

<213> Artificial

<220>
<223> H24

<400> 154

Arg Glu Gln Leu Ala Glu Val Thr Leu Ser Leu Lys Ala Asn Ser
1 5 10 15

<210> 155
<211> 20
<212> PRT
<213> Artificial

<220>
<223> H25

<400> 155

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> 156
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H26

<400> 156

Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
1 5 10 15

<210> 157
<211> 20
<212> PRT
<213> Artificial

<220>
<223> H27

<400> 157

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> 158
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H28

<400> 158

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

<210> 159
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H30

<400> 159

Leu Pro Pro Glu Thr Gln Glu Ser Gln Glu Val Thr Leu Asn Ser
1 5 10 15

<210> 160
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H32

<400> 160

Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro Asn Ser
1 5 10 15

<210> 161
<211> 20
<212> PRT
<213> Artificial

<220>
<223> H33

<400> 161

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> 162
<211> 13
<212> PRT
<213> Artificial

<220>
<223> H36

<400> 162

Gly Cys Pro Pro Cys Pro Gly Gly Gly Gly Ser Asn Ser
1 5 10

<210> 163

<211> 9
<212> PRT
<213> Artificial

<220>
<223> H40

<400> 163

Gly Cys Pro Pro Cys Pro Ala Asn Ser
1 5

<210> 164
<211> 9
<212> PRT
<213> Artificial

<220>
<223> H41

<400> 164

Gly Cys Pro Pro Cys Pro Ala Asn Ser
1 5

<210> 165
<211> 8
<212> PRT
<213> Artificial

<220>
<223> H42

<400> 165

Gly Cys Pro Pro Cys Pro Asn Ser
1 5

<210> 166
<211> 13
<212> PRT
<213> Artificial

<220>
<223> H44

<400> 166

Gly Gly Gly Ala Ser Cys Pro Pro Cys Pro Gly Asn Ser
1 5 10

<210> 167
<211> 13
<212> PRT
<213> Artificial

<220>
<223> H45

<400> 167

Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Gly Asn Ser
1 5 10

<210> 168
<211> 12
<212> PRT
<213> Artificial

<220>
<223> H46

<400> 168

Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Asn Ser
1 5 10

<210> 169
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H47

<400> 169

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

<210> 170
<211> 11
<212> PRT
<213> Artificial

<220>
<223> H48

<400> 170

Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
1 5 10

<210> 171
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H50

<400> 171

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

<210> 172
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H51

<400> 172

Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser

1 5 10 15

<210> 173
<211> 11
<212> PRT
<213> Artificial

<220>
<223> H52

<400> 173

Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ser
1 5 10

<210> 174
<211> 16
<212> PRT
<213> Artificial

<220>
<223> H53

<400> 174

Ser Gln Pro Glu Ile Val Pro Ile Ser Cys Pro Pro Cys Pro Asn Ser
1 5 10 15

<210> 175
<211> 19
<212> PRT
<213> Artificial

<220>
<223> H54

<400> 175

Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Ser Cys Pro Pro Cys
1 5 10 15

Pro Asn Ser

<210> 176
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H55

<400> 176

Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
1 5 10 15

<210> 177
<211> 12
<212> PRT
<213> Artificial

<220>
<223> H56

<400> 177

Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
1 5 10

<210> 178
<211> 10
<212> PRT
<213> Artificial

<220>
<223> H57

<400> 178

Val Ser Glu Arg Pro Phe Pro Pro Asn Ser
1 5 10

<210> 179
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H58

<400> 179

Lys Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys Pro Asn Ser
1 5 10 15

<210> 180
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H59

<400> 180

Lys Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys Pro Asn Ser
1 5 10 15

<210> 181
<211> 15
<212> PRT
<213> Artificial

<220>
<223> H60

<400> 181

Gln Tyr Asn Cys Pro Gly Gln Tyr Thr Phe Ser Met Pro Asn Ser
1 5 10 15

<210> 182
<211> 21
<212> PRT

<213> Artificial

<220>
<223> H61

<400> 182

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> 183
<211> 21
<212> PRT
<213> Artificial

<220>
<223> H62

<400> 183

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> 184
<211> 20
<212> PRT
<213> Artificial

<220>
<223> H63

<400> 184

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> 185
<211> 2307
<212> DNA
<213> TSC275 (hu4C04 x DRA222 null2 Scorpion)

<400> 185
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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc tggcaagtca gaccattggt acatggttag catggtatca gcagaaacca 180

gggaaagccc ctaagctcct gatttatgct gcaaccagct tggcagatgg ggtcccatca 240

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 300

gaagattttg caacttacta ctgtcaacaa ctttacaata ctccgtggac gttcggcgga 360

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caagtccact atgattacaa cgggtttcct tactggggcc aagggactcc cgtcactgtc 1920
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<210> 186
<211> 748
<212> PRT
<213> Artificial

<220>
<223> TSC275 (hu4C04 x DRA222 null2 Scorpion)

<400> 186

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 Leu Ala Ser Gln Thr Ile Gly Thr Trp
20 25 30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Tyr Asn Thr Pro Trp
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 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Thr
130 135 140

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

Met Asn Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly
165 170 175

Arg Ile Tyr Pro Gly Thr Asp Lys Thr Arg Tyr Asn Glu Lys Phe Arg
180 185 190

Asp Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asp Thr Ala Tyr Met
195 200 205

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
210 215 220

Arg Ser Ala Tyr Tyr Gly Asn Tyr Val Ala Met Asp Tyr Trp Gly Gln
225 230 235 240

```
Gly Thr Thr Val Thr Val Ser 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

Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
                485                 490                 495

His Ser Pro Asn Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
            500                 505                 510
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Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr
        515                 520                 525

Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln
    530                 535                 540

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn
545                 550                 555                 560

Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser
                565                 570                 575

Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr
            580                 585                 590

Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly
        595                 600                 605

Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
    610                 615                 620

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp
625                 630                 635                 640

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
                645                 650                 655

Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn
            660                 665                 670

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
        675                 680                 685

Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
    690                 695                 700

Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
705                 710                 715                 720

Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe
                725                 730                 735

Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
            740                 745
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<210> 187
<211> 107
<212> PRT
<213> Artificial

<220>

<223> hu4C04 VL

<400> 187

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 Leu Ala Ser Gln Thr Ile Gly Thr Trp
20 25 30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Tyr Asn Thr Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 188
<211> 121
<212> PRT
<213> Artificial

<220>
<223> hu4C04 VH

<400> 188

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

Thr Val Lys Ile Ser Cys Lys Val Ser Asp Tyr Thr Leu Thr Asp Phe
20 25 30

Tyr Met Asn Trp Val Gln Gln Ala Pro Gly Lys 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 Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asp 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 Gly Asn Tyr Val Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 189
<211> 2307
<212> DNA
<213> TSC277 (hu4C04 (A43K Q240E) x DRA222 null2 Scorpion)

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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc tggcaagtca gaccattggt acatggttag catggtatca gcagaaacca 180

gggaaaaagc ctaagctcct gatttatgct gcaaccagct tggcagatgg ggtcccatca 240

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gaagattttg caacttacta ctgtcaacaa ctttacaata ctccgtggac gttcggcgga 360

gggaccaagg tggagatcaa agggggtgga ggctctggtg gcggtggctc tggcggaggt 420

ggatccggcg ggggtggctc tgaggtccag ctggtacagt ctggggctga ggtgaagaag 480

cctggggcta cagtgaaaat ctcctgcaag gtttctgact acacactcac tgacttctat 540

atgaactggg tgcaacaggc ccctggaaaa gggcttgagt ggattgggag gatttatcct 600

ggaaccgata aaactagata caatgagaaa ttcagggaca gagtcaccat aaccgcggac 660

acgtctacag acacagccta catggagctg agcagcctga gatctgagga cacggccgtg 720

tattactgtg caagatccgc ctactatggt aactacgttg ctatggacta ctgggggggag 780

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ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt cccccccaaaa 900

cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 960

agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 1020

gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 1080

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gccctcccag cccccatcga 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

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gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1500

cagaggcaca acaattcttc cctgaataca ggaactcaga tggcaggtca ttctccgaat 1560

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caagtccact atgattacaa cgggtttcct tactggggcc aagggactcc cgtcactgtc 1920

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atccagatga cccagtctcc aagcagcctg tctgcaagcg tgggggacag ggtcaccatg 2040

acctgcagtg ccagctcaag tgtaagttac atgaactggt accagcagaa gccgggcaag 2100

gcccccaaaa gatggattta tgactcatcc aaactggctt ctggagtccc tgctcgcttc 2160

agtggcagtg ggtctgggac cgactatacc ctcacaatca gcagcctgca gcccgaagat 2220

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aagctacaaa ttacatcctc cagctaa 2307

<210> 190
<211> 748
<212> PRT
<213> Artificial

<220>
<223> TSC277 (hu4C04 (A43K Q240E) x DRA222 null2 Scorpion)

<400> 190

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 Leu Ala Ser Gln Thr Ile Gly Thr Trp
20 25 30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Tyr Asn Thr Pro Trp
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 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Thr
130 135 140

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

Met Asn Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly
                165                 170                 175

Arg Ile Tyr Pro Gly Thr Asp Lys Thr Arg Tyr Asn Glu Lys Phe Arg
            180                 185                 190

Asp Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asp Thr Ala Tyr Met
        195                 200                 205

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
    210                 215                 220

Arg Ser Ala Tyr Tyr Gly Asn Tyr Val Ala Met Asp Tyr Trp Gly Glu
225                 230                 235                 240

Gly Thr Thr Val Thr Val Ser 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
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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

Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
                485                 490                 495

His Ser Pro Asn Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
            500                 505                 510

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr
        515                 520                 525

Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln
    530                 535                 540

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn
545                 550                 555                 560

Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser
                565                 570                 575

Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr
            580                 585                 590

Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly
        595                 600                 605

Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
    610                 615                 620

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp
625                 630                 635                 640

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
                645                 650                 655

Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn
            660                 665                 670

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
        675                 680                 685
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Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
690 695 700

Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
705 710 715 720

Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe
725 730 735

Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
740 745

<210> 191
<211> 2307
<212> DNA
<213> TSC278 (hu4C04 (A43T) x DRA222 null2 Scorpion)

<400> 191
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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc tggcaagtca gaccattggt acatggttag catggtatca gcagaaacca 180

gggaaaaccc ctaagctcct gatttatgct gcaaccagct tggcagatgg ggtcccatca 240

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 300

gaagattttg caacttacta ctgtcaacaa ctttacaata ctccgtggac gttcggcgga 360

gggaccaagg tggagatcaa agggggtgga ggctctggtg gcggtggctc tggcggaggt 420

ggatccggcg ggggtggctc tgaggtccag ctggtacagt ctggggctga ggtgaagaag 480

cctggggcta cagtgaaaat ctcctgcaag gtttctgact acacactcac tgacttctat 540

atgaactggg tgcaacaggc ccctggaaaa gggcttgagt ggattgggag gatttatcct 600

ggaaccgata aaactagata caatgagaaa ttcagggaca gagtcaccat aaccgcggac 660

acgtctacag acacagccta catggagctg agcagcctga gatctgagga cacggccgtg 720

tattactgtg caagatccgc ctactatggt aactacgttg ctatggacta ctgggggcaa 780

gggaccacgg tcaccgtctc ctcgagtgag cccaaatctt ctgacaaaac tcacacatgc 840

ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag 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 aaggcgtacg cgtgcgcggt ctccaacaaa 1140

gccctcccag cccccatcga 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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cagaggcaca acaattcttc cctgaataca ggaactcaga tggcaggtca ttctccgaat 1560

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ttcctgcaga tggacagcct gaggcccgag gacaccggcg tctatttctg tgcacggccc 1860

caagtccact atgattacaa cgggtttcct tactggggcc aagggactcc cgtcactgtc 1920

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gcccccaaaa gatggattta tgactcatcc aaactggctt ctggagtccc tgctcgcttc 2160

agtggcagtg ggtctgggac cgactatacc ctcacaatca gcagcctgca gcccgaagat 2220

ttcgccactt attactgcca gcagtggagt cgtaacccac ccacgttcgg agggggggacc 2280

aagctacaaa ttacatcctc cagctaa 2307

<210> 192
<211> 748
<212> PRT
<213> Artificial

<220>
<223> TSC278 (hu4C04 (A43T) x DRA222 null2 Scorpion)

<400> 192

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 Leu Ala Ser Gln Thr Ile Gly Thr Trp
20 25 30

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Tyr Asn Thr Pro Trp
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 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Thr
    130                 135                 140

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

Met Asn Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly
                165                 170                 175

Arg Ile Tyr Pro Gly Thr Asp Lys Thr Arg Tyr Asn Glu Lys Phe Arg
            180                 185                 190

Asp Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asp Thr Ala Tyr Met
        195                 200                 205

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
    210                 215                 220

Arg Ser Ala Tyr Tyr Gly Asn Tyr Val Ala Met Asp Tyr Trp Gly Gln
225                 230                 235                 240

Gly Thr Thr Val Thr Val Ser 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
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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

Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
                485                 490                 495

His Ser Pro Asn Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
            500                 505                 510

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr
        515                 520                 525

Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln
    530                 535                 540

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn
545                 550                 555                 560

Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser
                565                 570                 575

Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr
            580                 585                 590

Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly
        595                 600                 605

Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
    610                 615                 620

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp
625                 630                 635                 640
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```
Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
                645                 650                 655

Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn
            660                 665                 670

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
        675                 680                 685

Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
    690                 695                 700

Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
705                 710                 715                 720

Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe
                725                 730                 735

Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
            740                 745


<210>  193
<211>  2307
<212>  DNA
<213>  TSC279 (hu4C04 (Q165R) x DRA222 null2 Scorpion )

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gggaaagccc ctaagctcct gatttatgct gcaaccagct tggcagatgg ggtcccatca      240

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gaagattttg caacttacta ctgtcaacaa ctttacaata ctccgtggac gttcggcgga      360

gggaccaagg tggagatcaa agggggtgga ggctctggtg gcggtggctc tggcggaggt      420

ggatccggcg ggggtggctc tgaggtccag ctggtacagt ctggggctga ggtgaagaag      480

cctggggcta cagtgaaaat ctcctgcaag gtttctgact acacactcac tgacttctat      540

atgaactggg tgagacaggc ccctggaaaa gggcttgagt ggattgggag gatttatcct      600

ggaaccgata aaactagata caatgagaaa ttcagggaca gagtcaccat aaccgcggac      660

acgtctacag acacagccta catggagctg agcagcctga gatctgagga cacggccgtg      720

tattactgtg caagatccgc ctactatggt aactacgttg ctatggacta ctgggggcaa      780

gggaccacgg tcaccgtctc ctcgagtgag cccaaatctt ctgacaaaac tcacacatgc      840

ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt ccccccaaaa      900

cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg      960

agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat     1020
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gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 1080

accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 1140

gccctcccag cccccatcga 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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gcccctggac aaggtctgga atggattgga tacattaatc ctagcagtgc ttatactaat 1740

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ttcctgcaga tggacagcct gaggcccgag gacaccggcg tctatttctg tgcacggccc 1860

caagtccact atgattacaa cgggtttcct tactggggcc aagggactcc cgtcactgtc 1920

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atccagatga cccagtctcc aagcagcctg tctgcaagcg tgggggacag ggtcaccatg 2040

acctgcagtg ccagctcaag tgtaagttac atgaactggt accagcagaa gccgggcaag 2100

gcccccaaaa gatggattta tgactcatcc aaactggctt ctggagtccc tgctcgcttc 2160

agtggcagtg ggtctgggac cgactatacc ctcacaatca gcagcctgca gcccgaagat 2220

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aagctacaaa ttacatcctc cagctaa 2307

<210> 194
<211> 748
<212> PRT
<213> Artificial

<220>
<223> TSC279 (hu4C04 (Q165R) x DRA222 null2 Scorpion)

<400> 194

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1 5 10 15

Asp Arg 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 Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Thr Ser Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Tyr Asn Thr Pro Trp
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 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Thr
130 135 140

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

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly
165 170 175

Arg Ile Tyr Pro Gly Thr Asp Lys Thr Arg Tyr Asn Glu Lys Phe Arg
180 185 190

Asp Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asp Thr Ala Tyr Met
195 200 205

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
210 215 220

Arg Ser Ala Tyr Tyr Gly Asn Tyr Val Ala Met Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser 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

Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
485 490 495

His Ser Pro Asn Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val
500 505 510

Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr
515 520 525

Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln
530 535 540

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn
545 550 555 560

Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser
565 570 575

Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr
580 585 590

Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly

595 600 605

Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly
610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp
625 630 635 640

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
645 650 655

Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn
660 665 670

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp
675 680 685

Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
690 695 700

Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
705 710 715 720

Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe
725 730 735

Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
740 745

<210> 195
<211> 2316
<212> DNA
<213> TSC233 (HD37 x DRA221 scorpion, H75 linker)

<400> 195
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

tctccgggtc agaggcacaa caattcttcc ctgaatacag gaactcagat ggcaggtcat 1560

tctccgaatt ctcaggtcca gctggtggag tctgggggcg gagtggtgca gcctgggcgg 1620

tcactgaggc tgtcctgcaa ggcttctggc tacaccttta ctagatctac gatgcactgg 1680

gtaaggcagg cccctggaca aggtctggaa tggattggat acattaatcc tagcagtgct 1740

tatactaatt acaatcagaa attcaaggac aggttcacaa tcagcgcaga caaatccaag 1800

agcacagcct tcctgcagat ggacagcctg aggcccgagg acaccggcgt ctatttctgt 1860

gcacggcccc aagtccacta tgattacaac gggtttcctt actggggcca agggactccc 1920

gtcactgtct ctagcggtgg cggagggtct gggggtggcg gatccggagg tggtggctct 1980

gcacaagaca tccagatgac ccagtctcca agcagcctgt ctgcaagcgt gggggacagg 2040

gtcaccatga cctgcagtgc cagctcaagt gtaagttaca tgaactggta ccagcagaag 2100

ccgggcaagg cccccaaact cctcatttat gactcatcca aactggcttc tggagtccct 2160

gctcgcttca gtggcagtgg gtctgggacc gactataccc tcacaatcag cagcctgcag 2220

cccgaagatt tcgccactta ttactgccag cagtggagtc gtaacccacc cactttcggc 2280

ggagggacca aggtggagat caaatcctcc agctaa 2316

<210> 196
<211> 751
<212> PRT
<213> Artificial

<220>
<223> TSC233 (HD37 x DRA221 scorpion, H75 linker)

<400> 196

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 Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln
                485                 490                 495

Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu Val Glu Ser Gly
            500                 505                 510

Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala
        515                 520                 525

Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala
    530                 535                 540

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
545                 550                 555                 560
```

```
Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala
                565                 570                 575

Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro
            580                 585                 590

Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp
        595                 600                 605

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser
    610                 615                 620

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
625                 630                 635                 640

Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
                645                 650                 655

Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
            660                 665                 670

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        675                 680                 685

Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
    690                 695                 700

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
705                 710                 715                 720

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro
                725                 730                 735

Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Ser Ser Ser
            740                 745                 750
```

<210> 197
<211> 2316
<212> DNA
<213> TSC234 (HD37 x DRA222 scorpion, H75 linker)

<400> 197

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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

tctccgggtc agaggcacaa caattcttcc ctgaatacag gaactcagat ggcaggtcat 1560

tctccgaatt ctcaggtcca gctggtggag tctgggggcg gagtggtgca gcctgggcgg 1620

tcactgaggc tgtcctgcaa ggcttctggc tacaccttta ctagatctac gatgcactgg 1680

gtaaggcagg cccctggaca aggtctggaa tggattggat acattaatcc tagcagtgct 1740

tatactaatt acaatcagaa attcaaggac aggttcacaa tcagcgcaga caaatccaag 1800

agcacagcct tcctgcagat ggacagcctg aggcccgagg acaccggcgt ctatttctgt 1860

gcacggcccc aagtccacta tgattacaac gggtttcctt actggggcca agggactccc 1920

gtcactgtct ctagcggtgg cggagggtct gggggtggcg gatccggagg tggtggctct 1980

gcacaagaca tccagatgac ccagtctcca agcagcctgt ctgcaagcgt gggggacagg 2040

gtcaccatga cctgcagtgc cagctcaagt gtaagttaca tgaactggta ccagcagaag 2100

ccgggcaagg cccccaaaag atggatttat gactcatcca aactggcttc tggagtccct 2160

gctcgcttca gtggcagtgg gtctgggacc gactataccc tcacaatcag cagcctgcag 2220

cccgaagatt tcgccactta ttactgccag cagtggagtc gtaacccacc cacgttcgga 2280

ggggggacca agctacaaat tacatcctcc agctaa 2316

<210> 198

<211> 751
<212> PRT
<213> Artificial

<220>
<223> TSC234 (HD37 x DRA222 scorpion, H75 linker)

<400> 198

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 Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln
                485                 490                 495

Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu Val Glu Ser Gly
            500                 505                 510
```

```
Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala
        515                 520                 525

Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala
    530                 535                 540

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
545                 550                 555                 560

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala
                565                 570                 575

Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro
            580                 585                 590

Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp
        595                 600                 605

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser
    610                 615                 620

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
625                 630                 635                 640

Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
                645                 650                 655

Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
            660                 665                 670

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
        675                 680                 685

Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
    690                 695                 700

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
705                 710                 715                 720

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro
                725                 730                 735

Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
            740                 745                 750
```

<210> 199
<211> 2325
<212> DNA
<213> TSC235 (HD37 x DRA224 scorpion, H75 linker)

<400> 199
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

tctccgggtc agaggcacaa caattcttcc ctgaatacag gaactcagat ggcaggtcat 1560

tctccgaatt ctcaggtcca gcttgtgcag tctggggctg aggtgaagaa gcctggggcc 1620

tcagtgaagg tttcctgcaa ggcttctgga tacaccttca ctagatctac gatgcactgg 1680

gtgcgccagg cccccggaca aaggcttgag tggatgggat acattaatcc tagcagtgct 1740

tatactaatt acaatcagaa attcaaggac agagtcacca ttaccaggga cacatccgcg 1800

agcacagcct acatggagct gagcagcctg agatctgaag acacggctgt gtattactgt 1860

gcgagacccc aagtccacta tgattacaac gggtttcctt actggggcca aggaaccctg 1920

gtcaccgtct cctcaggtgg aggcggttca ggcggaggtg gatccggcgg tggcggatcg 1980

ggtggcggcg gatctgaaat tgtgttgaca cagtctccag ccaccctgtc tttgtctcca 2040

ggggaaagag ccaccctctc ctgcagtgcc agctcaagtg taagttacat gaactggtac 2100

caacagaaac ctggccaggc tcccaggctc ctcatctatg actcatccaa actggcttct 2160

ggcatcccag ccaggttcag tggcagtggg tctgggacag acttcactct caccatcagc 2220

agcctagagc ctgaagattt tgcagtttat tactgtcagc agtggagtcg taacccaccc 2280

actttcggcg gagggaccaa ggtggagatc aaatcctcca gctaa 2325

<210> 200
<211> 754
<212> PRT
<213> Artificial

<220>
<223> TSC235 (HD37 x DRA224 scorpion, H75 linker)

<400> 200

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
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Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
465                 470                 475                 480

Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln
                485                 490                 495

Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu Val Gln Ser Gly
            500                 505                 510

Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala
        515                 520                 525

Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala
    530                 535                 540

Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Ile Asn Pro Ser Ser Ala
545                 550                 555                 560

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Arg
                565                 570                 575

Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
            580                 585                 590

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp
        595                 600                 605

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
    610                 615                 620

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
625                 630                 635                 640

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

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser
            660                 665                 670

Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
        675                 680                 685

Arg Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Ile Pro Ala
    690                 695                 700

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
705                 710                 715                 720

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser
                725                 730                 735
```

Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Ser
740 745 750

Ser Ser

<210> 201
<211> 2295
<212> DNA
<213> TSC240 (HD37 x DRA222 scorpion, H81 linker)

<400> 201
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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 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 aagttcaaat tcccttgacc gaaagttaca gcccgaattc tcaggtccag 1560

ctggtggagt ctgggggcgg agtggtgcag cctgggcggt cactgaggct gtcctgcaag 1620

gcttctggct acacctttac tagatctacg atgcactggg taaggcaggc ccctggacaa 1680

ggtctggaat ggattggata cattaatcct agcagtgctt atactaatta caatcagaaa 1740

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gacagcctga ggcccgagga caccggcgtc tatttctgtg cacggcccca agtccactat 1860

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cagtctccaa gcagcctgtc tgcaagcgtg ggggacaggg tcaccatgac ctgcagtgcc 2040

agctcaagtg taagttacat gaactggtac cagcagaagc cgggcaaggc ccccaaaaga 2100

tggatttatg actcatccaa actggcttct ggagtccctg ctcgcttcag tggcagtggg 2160

tctgggaccg actatacccct cacaatcagc agcctgcagc ccgaagattt cgccacttat 2220

tactgccagc agtggagtcg taacccaccc acgttcggag gggggaccaa gctacaaatt 2280

acatcctcca gctaa 2295

<210> 202
<211> 744
<212> PRT
<213> Artificial

<220>
<223> TSC240 (HD37 x DRA222 scorpion, H81 linker)

<400> 202

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 Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn
485 490 495

Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly
500 505 510

Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg
515 520 525

Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
530 535 540

Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys
545 550 555 560

Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala
565 570 575

Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe
580 585 590

Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp
595 600 605

Gly Gln Gly Thr Pro 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 Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met
645 650 655

Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
660 665 670

Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu

675 680 685

Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
690 695 700

Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
705 710 715 720

Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr
725 730 735

Lys Leu Gln Ile Thr Ser Ser Ser
740

<210> 203
<211> 2301
<212> DNA
<213> TSC241 (HD37 x DRA222 scorpion, H83 linker)

<400> 203
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

tctccgggtt cttccctgaa tacaggaact cagatggcag gtcattctcc gaattctcag 1560

gtccagctgg tggagtctgg gggcggagtg gtgcagcctg ggcggtcact gaggctgtcc 1620

tgcaaggctt ctggctacac ctttactaga tctacgatgc actgggtaag gcaggcccct 1680

ggacaaggtc tggaatggat tggatacatt aatcctagca gtgcttatac taattacaat 1740

cagaaattca aggacaggtt cacaatcagc gcagacaaat ccaagagcac agccttcctg 1800

cagatggaca gcctgaggcc cgaggacacc ggcgtctatt tctgtgcacg gccccaagtc 1860

cactatgatt acaacgggtt tccttactgg ggccaaggga ctcccgtcac tgtctctagc 1920

ggtggcggag ggtctggggg tggcggatcc ggaggtggtg gctctgcaca agacatccag 1980

atgacccagt ctccaagcag cctgtctgca agcgtggggg acagggtcac catgacctgc 2040

agtgccagct caagtgtaag ttacatgaac tggtaccagc agaagccggg caaggccccc 2100

aaaagatgga tttatgactc atccaaactg gcttctggag tccctgctcg cttcagtggc 2160

agtgggtctg ggaccgacta taccctcaca atcagcagcc tgcagcccga agatttcgcc 2220

acttattact gccagcagtg gagtcgtaac ccacccacgt tcggaggggg gaccaagcta 2280

caaattacat cctccagcta a 2301

<210> 204
<211> 746
<212> PRT
<213> Artificial

<220>
<223> TSC241 (HD37 x DRA222 scorpion, H83 linker)

<400> 204

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

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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
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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 Gly Thr Gln Met Ala Gly His Ser
                485                 490                 495

Pro Asn Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
            500                 505                 510

Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        515                 520                 525

Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    530                 535                 540

Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn
545                 550                 555                 560

Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser
                565                 570                 575

Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val
            580                 585                 590

Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro
        595                 600                 605

Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly
    610                 615                 620

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln
625                 630                 635                 640
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Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
                645                 650                 655

Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
            660                 665                 670

Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser
        675                 680                 685

Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
    690                 695                 700

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
705                 710                 715                 720

Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly
                725                 730                 735

Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
            740                 745
```

<210> 205
<211> 2313
<212> DNA
<213> TSC242 (HD37 x DRA222 scorpion, H91 linker)

<400> 205

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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 tcgagtgagc ccaaatcttc tgacaaaact      840

cacacatgcc caccgtgccc agcacctgaa gccgcgggtg caccgtcagt cttcctcttc      900

cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg      960
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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 actcattagc aaaccaagaa gttcaaattc ccttgaccga aagttacagc 1560

ccgaattctc aggtccagct ggtggagtct gggggcggag tggtgcagcc tgggcggtca 1620

ctgaggctgt cctgcaaggc ttctggctac acctttacta gatctacgat gcactgggta 1680

aggcaggccc ctggacaagg tctggaatgg attggataca ttaatcctag cagtgcttat 1740

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ggcaaggccc ccaaaagatg gatttatgac tcatccaaac tggcttctgg agtccctgct 2160

cgcttcagtg gcagtgggtc tgggaccgac tataccctca caatcagcag cctgcagccc 2220

gaagatttcg ccacttatta ctgccagcag tggagtcgta acccacccac gttcggaggg 2280

gggaccaagc tacaaattac atcctccagc taa 2313

<210> 206
<211> 750
<212> PRT
<213> Artificial

<220>
<223> TSC242 (HD37 x DRA222 scorpion, H91 linker)

<400> 206

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 Asn Ser Leu Ala Asn Gln Glu Val Gln Ile Pro Leu Thr
                485                 490                 495

Glu Ser Tyr Ser Pro Asn Ser Gln Val Gln Leu Val Glu Ser Gly Gly
            500                 505                 510

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
        515                 520                 525

Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro
    530                 535                 540

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr
545                 550                 555                 560

Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp
                565                 570                 575

Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
            580                 585                 590
```

```
Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
        595                 600                 605

Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser
    610                 615                 620

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
625                 630                 635                 640

Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
                645                 650                 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
            660                 665                 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
        675                 680                 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly
    690                 695                 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705                 710                 715                 720

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
                725                 730                 735

Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
            740                 745                 750
```

<210> 207
<211> 1815
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC049

<400> 207

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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
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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 aatctagagc 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> 208
<211> 584
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC049

<400> 208

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 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> 209

<211> 1836
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC096

<400> 209
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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 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 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> 210
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC096

<400> 210

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 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> 211
<211> 1809
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC192

<400> 211

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gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc      120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca      180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct      240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct      300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa      360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt      420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca      480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg      540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat      600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc      660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca      720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc      780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct      840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg      900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag      960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg     1020
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gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg 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

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatctag aactgtggct 1500

gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct 1560

gttgtgtgcc tgctgaatta cttctatccc agagaggcca aagtacagtg gaaggtggat 1620

aacgccctcc aatcgggtaa ctcccaggag agtgccacag agcaggacag caaggacagc 1680

acctacagcc tcagcagcga gctgacgctg agcaaagcag actacgagaa acacaaagtc 1740

tacgcctgcg aagtcaccca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 1800

ggagagtga 1809

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

<220>
<223> TSC192

<400> 212

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val

115 120 125

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
130 135 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145 150 155 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
165 170 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
180 185 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
195 200 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
210 215 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225 230 235 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
245 250 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala 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 Ala Tyr Ala Cys Ala 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 Thr Val Ala
465 470 475 480

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
485 490 495

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu
500 505 510

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
515 520 525

Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
530 535 540

Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
545 550 555 560

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
565 570 575

Ser Phe Asn Arg Gly Glu
580

<210> 213
<211> 1809
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC193

<400> 213
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gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 420

ggtggctctg aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggctaca 480

gtgaagatct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540

caacaggccc ctggaaaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 600

actagatacg cagagaagtt ccagggcaga gtcaccataa ccgcggacac gtctacagac 660

acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgca 720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg 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

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatctag aactgtggct 1500

gcaccatctg tcttcatctt cccgccatct gatgagcagt tgaaatctgg aactgcctct 1560

gttgtgtgcc tgctgaatta cttctatccc agagaggcca aagtacagtg gaaggtggat 1620

aacgccctcc aatcgggtaa ctcccaggag agtgccacag agcaggacag caaggacagc 1680

acctacagcc tcagcagcga gctgacgctg agcaaagcag actacgagaa acacaaagtc 1740

tacgcctgcg aagtcaccca tcagggcctg agctcgcccg tcacaaagag cttcaacagg 1800

ggagagtga 1809

<210> 214
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC193

<400> 214

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
            100                 105                 110

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

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Thr Val Lys Ile Ser
    130                 135                 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145                 150                 155                 160

Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
                165                 170                 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Glu Lys Phe Gln Gly Arg Val Thr
            180                 185                 190

Ile Thr Ala Asp Thr Ser Thr Asp Thr Ala Tyr Met Glu Leu Ser Ser
        195                 200                 205

Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
    210                 215                 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225                 230                 235                 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
                245                 250                 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala 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 Ala Tyr Ala Cys Ala 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 Thr Val Ala
465                 470                 475                 480

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
                485                 490                 495

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu
            500                 505                 510

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
        515                 520                 525

Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
    530                 535                 540

Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
545                 550                 555                 560
```

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
565 570 575

Ser Phe Asn Arg Gly Glu
580

<210> 215
<211> 1788
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC195

<400> 215
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc 660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca 720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg 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

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatctag agcctccacc 1500

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 1560

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> 216
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC195

<400> 216

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
100 105 110

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

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser
130 135 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145 150 155 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
165 170 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
180 185 190

```
Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
        195                 200                 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
    210                 215                 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225                 230                 235                 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
                245                 250                 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala 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 Ala Tyr Ala Cys Ala 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
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<210> 217
<211> 1806
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC219

<400> 217

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cgaggacagg tccagctggt ggagtctggg ggcggagtgg tgcagcctgg gcggtcactg      120

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caggcccctg gacaaggtct ggaatggatt ggatacatta atcctagcag tgcttatact      240

aattacaatc agaaattcaa ggacaggttc acaatcagcg cagacaaatc caagagcaca      300

gccttcctgc agatggacag cctgaggccc gaggacaccg gcgtctattt ctgtgcacgg      360

ccccaagtcc actatgatta caacgggttt ccttactggg gccaagggac tcccgtcact      420

gtctctagcg gtggcggagg gtctgggggt ggcggatccg gaggtggtgg ctctgcacaa      480

gacatccaga tgacccagtc tccaagcagc ctgtctgcaa gcgtggggga cagggtcacc      540

atgacctgca gtgccagctc aagtgtaagt tacatgaact ggtaccagca gaagccgggc      600

aaggccccca aaagatggat ttatgactca tccaaactgg cttctggagt ccctgctcgc      660

ttcagtggca gtgggtctgg gaccgactat accctcacaa tcagcagcct gcagcccgaa      720

gatttcgcca cttattactg ccagcagtgg agtcgtaacc cacccacgtt cggaggggggg      780

accaagctac aaattacatc ctcgagtgag cccaaatctt ctgacaaaac tcacacatgc      840

ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag tcttcctctt ccccccaaaa      900
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cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 960

agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 1020

gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 1080

accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 1140

gccctcccag cccccatcga 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

gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1500

aaatctagag 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> 218
<211> 579
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC219

<400> 218

Gln Val Gln Leu Val Glu 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 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 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 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 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> 219
<211> 1809
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC220

<400> 219
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

caggtccagc ttgtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 120

tcctgcaagg cttctggata caccttcact agatctacga tgcactgggt gcgccaggcc 180

cccggacaaa ggcttgagtg gatgggatac attaatccta gcagtgctta tactaattac 240

aatcagaaat tcaaggacag agtcaccatt accagggaca catccgcgag cacagcctac 300

atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagaccccaa 360

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc 420

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga 480

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc 540

accctctcct gcagtgccag ctcaagtgta agttacatga actggtacca acagaaacct 600

ggccaggctc ccaggctcct catctatgac tcatccaaac tggcttctgg catcccagcc 660

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 720

gaagattttg cagtttatta ctgtcagcag tggagtcgta acccacccac tttcggcgga 780

gggaccaagg tggagatcaa atcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggcgt acgcgtgcgc ggtctccaac 1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

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ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 1740

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aaagtttga 1809

<210> 220
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC220

<400> 220

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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 Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        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 Val Thr Ile Thr Arg Asp Thr 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 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 Gly Gly Gly Gly Ser Glu Ile Val
    130                 135                 140

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145                 150                 155                 160

Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ser Ser
            180                 185                 190

Lys Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala
    210                 215                 220

Val Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            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

Ala Tyr Ala Cys Ala 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> 221
<211> 1827
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC222

<400> 221
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cgaggacagg tccagctggt ggagtctggg ggcggagtgg tgcagcctgg gcggtcactg 120

aggctgtcct gcaaggcttc tggctacacc tttactagat ctacgatgca ctgggtaagg 180

caggcccctg gacaaggtct ggaatggatt ggatacatta atcctagcag tgcttatact 240

aattacaatc agaaattcaa ggacaggttc acaatcagcg cagacaaatc caagagcaca 300

gccttcctgc agatggacag cctgaggccc gaggacaccg gcgtctattt ctgtgcacgg 360

ccccaagtcc actatgatta caacgggttt ccttactggg gccaagggac tcccgtcact 420

gtctctagcg gtggcggagg gtctgggggt ggcggatccg gaggtggtgg ctctgcacaa 480

gacatccaga tgacccagtc tccaagcagc ctgtctgcaa gcgtggggga cagggtcacc 540

atgacctgca gtgccagctc aagtgtaagt tacatgaact ggtaccagca gaagccgggc 600

aaggccccca aaagatggat ttatgactca tccaaactgg cttctggagt ccctgctcgc 660

ttcagtggca gtgggtctgg gaccgactat accctcacaa tcagcagcct gcagcccgaa 720

gatttcgcca cttattactg ccagcagtgg agtcgtaacc cacccacgtt cggaggggg 780

accaagctac aaattacatc ctcgagtgag cccaaatctt ctgacaaaac tcacacatgc 840

ccaccgtgcc cagcacctga agccgcgggt gcaccgtcag 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 aaggcgtacg cgtgcgcggt ctccaacaaa 1140

gccctcccag cccccatcga 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

gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1500

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> 222
<211> 586
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC222

<400> 222

Gln Val Gln Leu Val Glu 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 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 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 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> 223
<211> 1830
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC223

<400> 223
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caggtccagc ttgtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 120

tcctgcaagg cttctggata caccttcact agatctacga tgcactgggt gcgccaggcc 180

cccggacaaa ggcttgagtg gatgggatac attaatccta gcagtgctta tactaattac 240

aatcagaaat tcaaggacag agtcaccatt accagggaca catccgcgag cacagcctac 300

atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagaccccaa 360

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc 420

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga 480

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc 540

accctctcct gcagtgccag ctcaagtgta agttacatga actggtacca acagaaacct 600

ggccaggctc ccaggctcct catctatgac tcatccaaac tggcttctgg catcccagcc 660

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 720

gaagattttg cagtttatta ctgtcagcag tggagtcgta acccacccac tttcggcgga 780

gggaccaagg tggagatcaa atcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttcccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggcgt acgcgtgcgc ggtctccaac 1140

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500

ggtaaatcta gaactgtggc tgcaccatct gtcttcatct tcccgccatc tgatgagcag 1560

ttgaaatctg gaactgcctc tgttgtgtgc ctgctgaatt acttctatcc cagagaggcc 1620

aaagtacagt ggaaggtgga taacgccctc caatcgggta actcccagga gagtgccaca 1680

gagcaggaca gcaaggacag cacctacagc ctcagcagcg agctgacgct gagcaaagca 1740

gactacgaga aacacaaagt ctacgcctgc gaagtcaccc atcagggcct gagctcgccc 1800

gtcacaaaga gcttcaacag gggagagtga 1830

<210> 224
<211> 589
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC223

<400> 224

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 Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

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

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Lys Asp Arg Val Thr Ile Thr Arg Asp Thr 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 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 Gly Gly Gly Gly Ser Glu Ile Val
    130                 135                 140

Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
145                 150                 155                 160

Thr Leu Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr
                165                 170                 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ser Ser
            180                 185                 190

Lys Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala
    210                 215                 220

Val Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly
225                 230                 235                 240

Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            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
```

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Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Ala Tyr Ala Cys Ala 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 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
                485                 490                 495

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
            500                 505                 510

Asn Tyr Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
        515                 520                 525

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser
    530                 535                 540

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala
545                 550                 555                 560

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
                565                 570                 575

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
            580                 585
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<210> 225
<211> 1803
<212> DNA

<213> Artificial Sequence

<220>
<223> TSC254

<400> 225
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gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 420

ggtggctctg aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggctaca 480

gtgaagatct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540

caacaggccc ctggaaaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 600

actagatacg cagagaagtt ccagggcaga gtcaccataa ccgcggacac gtctacagac 660

acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgca 720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg 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

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

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aactctgcct ccaccaaggg cccatcggtc ttcccctgg caccctcctc caagagcacc 1560

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tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 1740

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tga 1803

<210> 226
<211> 580
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC254

<400> 226

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
            100                 105                 110

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

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Thr Val Lys Ile Ser
    130                 135                 140

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145                 150                 155                 160

Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
                165                 170                 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Glu Lys Phe Gln Gly Arg Val Thr
            180                 185                 190

Ile Thr Ala Asp Thr Ser Thr Asp Thr Ala Tyr Met Glu Leu Ser Ser
        195                 200                 205

Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
    210                 215                 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
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225 230 235 240

Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
245 250 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala 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 Ala Tyr Ala Cys Ala 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 Ser Ser Leu Asn Thr Pro
465 470 475 480

Asn Ser 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> 227
<211> 1845
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC258

<400> 227
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cgaggacagg tccagctggt ggagtctggg ggcggagtgg tgcagcctgg gcggtcactg 120

aggctgtcct gcaaggcttc tggctacacc tttactagat ctacgatgca ctgggtaagg 180

caggcccctg gacaaggtct ggaatggatt ggatacatta atcctagcag tgcttatact 240

aattacaatc agaaattcaa ggacaggttc acaatcagcg cagacaaatc caagagcaca 300

gccttcctgc agatggacag cctgaggccc gaggacaccg gcgtctattt ctgtgcacgg 360

ccccaagtcc actatgatta caacgggttt ccttactggg gccaagggac tcccgtcact 420

gtctctagcg gtggcggagg gtctgggggt ggcggatccg gaggtggtgg ctctgcacaa 480

gacatccaga tgacccagtc tccaagcagc ctgtctgcaa gcgtggggga cagggtcacc 540

atgacctgca gtgccagctc aagtgtaagt tacatgaact ggtaccagca gaagccgggc 600

aaggccccca aaagatggat ttatgactca tccaaactgg cttctggagt ccctgctcgc 660

ttcagtggca gtgggtctgg gaccgactat accctcacaa tcagcagcct gcagcccgaa 720

gatttcgcca cttattactg ccagcagtgg agtcgtaacc cacccacgtt cggaggggg 780

accaagctac aaattacatc ctcgagtgag cccaaatctt ctgacaaaac tcacacatgc 840

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cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 960

agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 1020

gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 1080

accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 1140

gccctcccag cccccatcga 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

gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1500

tcttccctga atacaccgaa ctctaggact gtggctgcac catctgtctt catcttcccg 1560

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaattacttc 1620

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 1680

caggagagtg ccacagagca ggacagcaag gacagcacct acagcctcag cagcgagctg 1740

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 1800

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtga 1845

<210> 228
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC258

<400> 228

Gln Val Gln Leu Val Glu 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 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 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 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 Ser Ser
465                 470                 475                 480

Leu Asn Thr Pro Asn Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile
                485                 490                 495

Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
            500                 505                 510

Cys Leu Leu Asn Tyr Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
        515                 520                 525

Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu
    530                 535                 540

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu
545                 550                 555                 560

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
                565                 570                 575

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
            580                 585                 590
```

<210> 229
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence from Figure 3

<220>
<221> misc_feature
<223> Xaa is a position that was not a consensus in Figure 3 with Ala and Phe being equally prevalent at that position and Val occuring in 1 out of 7 of the sequences

<220>
<221> misc_feature
<222> (68)..(68)
<223> Xaa can be any naturally occurring amino acid

<400> 229

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Lys Pro Gly Ala
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 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 Arg Xaa Thr Ile Thr Ala Asp Lys Ser Lys 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> 230
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence from Figure 4

<400> 230

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 Met 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 Trp
35 40 45

Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Tyr 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 Arg Asn Pro
85 90 95

Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr
100 105

<210> 231
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence from Figure 5

<220>
<221> misc_feature
<223> This is the consensus seqeunce from figure 5. X represents where there was no consequence, so X could equally be one of the amino acids shown in that position in the other sequences

<220>
<221> misc_feature
<222> (50)..(50)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (52)..(52)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (54)..(55)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (57)..(58)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (74)..(74)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (84)..(84)
<223> Xaa can be any naturally occurring amino acid

<400> 231

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 Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Xaa Ile Xaa Pro Xaa Xaa Ala Xaa Xaa Asn Tyr Ala Gln Lys Phe
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Xaa Ser Lys Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg

<210> 232
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> IGKV1-5*01

<400> 232

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 Ile
35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser
85 90 95

<210> 233
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence from Figure 6

<220>
<221> misc_feature
<223> This is the consensus seqeunce from figure 6. X represents where there was no consequence, so X could equally be one of the amino acids shown in that position in the other sequences

<220>
<221> misc_feature
<222> (24)..(24)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature

<222> (27)..(27)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (31)..(31)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (34)..(34)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (46)..(47)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (53)..(53)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (55)..(55)
<223> Xaa can be any naturally occurring amino acid

<400> 233

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 Xaa Ala Ser Xaa Ser Ile Ser Xaa Trp
            20   25   30

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

Tyr Asp Ala Ser Xaa Leu Xaa Ser Gly Val Pro Ala Arg Phe Ser Gly
    50   55   60

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp
                85   90

<210> 234
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> IGKJ1*01

<400> 234

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
1   5   10

<210> 235
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> IGKJ2*01

<400> 235

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 236
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> IGKJ3*01

<400> 236

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
1 5 10

<210> 237
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> IGKJ4*01

<400> 237

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 238
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> IGKJ5*01

<400> 238

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
1 5 10

<210> 239
<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> Figure 7 consensus sequence

<400> 239

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 Leu Leu 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

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 Ala 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 Gln Glu Asp Pro Glu Val
    290                 295                 300

Gln 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 Phe Asn Ser Thr Tyr Arg Val Val Ser Val
                325                 330                 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys
            340                 345                 350

Ala Val Ser Asn Lys Gly Leu Pro Ser Ser 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 Gln Glu Glu Met 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
            420
```

<210> 240
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> DRA161

<400> 240

```
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 Arg Thr Ser Pro Lys Ser Ser Asp Lys Thr His
                245                 250                 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Ala 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 Gln Glu Asp Pro Glu Val
    290                 295                 300

Gln 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 Phe Ala 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 Gly Leu Pro Ser Ser 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 Gln Glu Glu Met 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 Arg Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Glu 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
465 470 475

<210> 241
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence of Figure 8

<400> 241

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 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 Ala 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 Gln Glu Asp Pro Glu Val
    290                 295                 300

Gln 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 Phe Ala 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 Gly Leu Pro Ser Ser 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 Gln Glu Glu Met 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 Arg Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Glu 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
465 470 475

<210> 242
<211> 1800
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC125

<400> 242
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> 243
<211> 579
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC125 mature protein

<400> 243

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 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> 244
<211> 2310
<212> DNA
<213> Artificial Sequence

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atgaactggg tgaagcagag gcctggacag ggtcttgagt ggattggaca gatttggcct 600

ggagatggtg atactaacta caatggaaag ttcaagggta aagccactct gactgcagac 660

gaatcctcca gcacagccta catgcaactc agcagcctag catctgagga ctctgcggtc 720

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gtcactgtct ctagcggtgg cggagggtct gggggtggcg gatccggagg tggtggctct 1980

gcacaagaca tccagatgac ccagtctcca agcagcctgt ctgcaagcgt gggggacagg 2040

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gctcgcttca gtggcagtgg gtctgggacc gactataccc tcacaatcag cagcctgcag 2220

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<211> 749
<212> PRT
<213> Artificial Sequence

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<223> TSC129a mature protein

<400> 245

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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
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```
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 Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln
                485                 490                 495
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Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu Val Gln Ser Gly
            500                 505                 510

Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala
        515                 520                 525

Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala
    530                 535                 540

Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
545                 550                 555                 560

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala
                565                 570                 575

Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro
            580                 585                 590

Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp
        595                 600                 605

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser
    610                 615                 620

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
625                 630                 635                 640

Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
                645                 650                 655

Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
            660                 665                 670

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
        675                 680                 685

Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
    690                 695                 700

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
705                 710                 715                 720

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro
                725                 730                 735

Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Arg
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<210> 246
<211> 1806
<212> DNA
<213> Artificial Sequence

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<223> TSC218 DNA

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aggctgtcct gcaaggcttc tggctacacc tttactagat ctacgatgca ctgggtaagg 180

caggcccctg gacaaggtct ggaatggatt ggatacatta atcctagcag tgcttatact 240

aattacaatc agaaattcaa ggacaggttc acaatcagcg cagacaaatc caagagcaca 300

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gtctctagcg gtggcggagg gtctgggggt ggcggatccg gaggtggtgg ctctgcacaa 480

gacatccaga tgacccagtc tccaagcagc ctgtctgcaa gcgtggggga cagggtcacc 540

atgacctgca gtgccagctc aagtgtaagt tacatgaact ggtaccagca gaagccgggc 600

aaggccccca aactcctcat ttatgactca tccaaactgg cttctggagt ccctgctcgc 660

ttcagtggca gtgggtctgg gaccgactat accctcacaa tcagcagcct gcagcccgaa 720

gatttcgcca cttattactg ccagcagtgg agtcgtaacc cacccacttt cggcggaggg 780

accaaggtgg agatcaaatc ctcgagtgag cccaaatctt ctgacaaaac tcacacatgc 840

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gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 1080

accgtcctgc accaggactg gctgaatggc aaggcgtacg cgtgcgcggt ctccaacaaa 1140

gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagaacca 1200

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ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1380

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acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 1680

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 1740

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<212> PRT
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            20                  25                  30


Thr Met His Trp Val Arg 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 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 Leu Leu 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
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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 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
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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> 248
<211> 1827
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC221 DNA

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ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1380

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tacgagaaac acaaagtcta cgcctgcgaa gtcacccatc agggcctgag ctcgcccgtc 1800

acaaagagct tcaacagggg agagtga 1827

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

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<223> TSC221 mature protein

<400> 249

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Thr Met His Trp Val Arg 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 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 Leu Leu 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

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
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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> 250
<211> 2283
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC194 DNA

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

His Ser Gly Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
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Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Ile Glu Tyr Pro Trp
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
100 105 110

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

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val
145 150 155 160

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Phe Asn Pro
165 170 175

Tyr Asn Asp Tyr Thr Arg Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr
180 185 190

Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser
195 200 205

Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp Gly
210 215 220

Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225 230 235 240

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Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro
                245                 250                 255

Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
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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 Ala Tyr Ala Cys Ala 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
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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 Gln Arg His Asn Asn Ser
465                 470                 475                 480

Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln
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Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
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Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr
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Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly
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Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
545                 550                 555                 560

Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe Leu
                565                 570                 575

Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala
            580                 585                 590

Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln
        595                 600                 605

Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
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Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser
625                 630                 635                 640

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                645                 650                 655

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            660                 665                 670

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        675                 680                 685

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
    690                 695                 700

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