SEQUENCE LISTING

<110> Emergent Product Development Gaithersburg Inc.
Blankenship, John W.
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<120> Prostate-Specific Membrane Antigen Binding Proteins and Related Compositions and Methods

<130> 2479.102PC01/EJH

<140> To be assigned
<141> Herewith

<150> 61/478,449
<151> 2011-04-22

<160> 165

<170> PatentIn version 3.5

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<211> 357
<212> DNA
<213> Mus musculus

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tcctgcaagg cttctggata cacattcact gactactaca tgcactgggt gaagcagaac 120

aatggagaga gccttgagtg gattggatat tttaatcctt ataatgatta tactagatac 180

aaccagaatt tcaatggcaa ggccacattg actgtagaca agtcctccag cacagcctac 240

atgcagctca acagcctgac atctgaggac tctgcattct attactgtgc aagatcggat 300

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<210> 2
<211> 111
<212> PRT
<213> Mus musculus

<400> 2

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

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

Tyr Met His Trp Val Lys Gln Asn Asn Gly Glu Ser Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Asn Pro Tyr Asn Asp Tyr Thr Arg Tyr Asn Gln Asn Phe
50 55 60

Asn Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Phe Tyr Tyr Cys
85 90 95

Ala Arg Ser Asp Gly Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln
100 105 110

<210> 3
<211> 327
<212> DNA
<213> Mus musculus

<400> 3
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attaattgca gggcaagtaa gagcattagc aaatatttag cctggtatca agagaaacct 120

gggaaagcta ataagcttct tatccattct ggatccactt tgcaatctgg aattccatca 180

aggttcagtg gcagtggatc tggtacagat ttcactctca ccatcagtag cctggagcct 240

gaagattttg caatgtatta ctgtcaacag catattgaat acccgtggac gttcggtggt 300

ggcaccaaac tggaaattaa acgggct 327

<210> 4
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> modified (mature) murine 107-1A4 VL domain used in construction of chimeric sequences

<400> 4
gatgtccaga taacccagtc tccatcttat cttgctgcat ctcctggaga aaccattact 60

attaattgca gggcaagtaa gagcattagc aaatatttag cctggtatca agagaaacct 120

gggaaagcta ataagctact tatccattct ggatccactt tgcaatctgg aataccatca 180

aggttcagtg gcagtggatc tggtacagat ttcactctca ccatcagtag cctggagcct 240

gaagattttg caatgtatta ctgtcaacag catattgaat acccgtggac gttcggtggt 300

ggcaccaaac tggaaattaa acgggcc 327

<210> 5
<211> 109
<212> PRT
<213> Mus musculus

<400> 5

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

Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
20 25 30

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala
100 105

<210> 6
<211> 33
<212> DNA
<213> Mus musculus

<400> 6
tctggataca cattcactga ctactacatg cac 33

<210> 7
<211> 30
<212> DNA
<213> Mus musculus

<400> 7
tattttaatc cttataatga ttatactaga 30

<210> 8
<211> 42
<212> DNA
<213> Mus musculus

<400> 8
tgtgcaagat cggatggtta ctacgatgct atggactact gg 42

<210> 9
<211> 11
<212> PRT
<213> Mus musculus

<400> 9

Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His
1 5 10

<210> 10
<211> 10
<212> PRT
<213> Mus musculus

<400> 10

Tyr Phe Asn Pro Tyr Asn Asp Tyr Thr Arg
1 5 10

<210> 11
<211> 14

<212> PRT
<213> Mus musculus

<400> 11

Cys Ala Arg Ser Asp Gly Tyr Tyr Asp Ala Met Asp Tyr Trp
1 5 10

<210> 12
<211> 18
<212> DNA
<213> Mus musculus

<400> 12
aagagcatta gcaaatat 18

<210> 13
<211> 9
<212> DNA
<213> Mus musculus

<400> 13
tctggatcc 9

<210> 14
<211> 27
<212> DNA
<213> Mus musculus

<400> 14
caacagcata ttgaataccc gtggacg 27

<210> 15
<211> 6
<212> PRT
<213> Mus musculus

<400> 15

Lys Ser Ile Ser Lys Tyr
1 5

<210> 16
<211> 3
<212> PRT
<213> Mus musculus

<400> 16

Ser Gly Ser
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<210> 17
<211> 9
<212> PRT
<213> Mus musculus

<400> 17

Gln Gln His Ile Glu Tyr Pro Trp Thr
1 5

<210> 18
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> murine scFv (VH-VL orientation)

<400> 18
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tcctgcaagg cttctggata cacattcact gactactaca tgcactgggt gaagcagaac 120

aatggagaga gccttgagtg gattggatat tttaatcctt ataatgatta tactagatac 180

aaccagaatt tcaatggcaa ggccacattg actgtagaca agtcctccag cacagcctac 240

atgcagctca acagcctgac atctgaggac tctgcattct attactgtgc aagatcggat 300

ggttactacg atgctatgga ctactggggt caaggaacct cagtcaccgt ctcctcaggc 360

ggcggcggaa gcggcggtgg cggcagcagc ggcggcggcg gcagcgatgt ccagataacc 420

cagtctccat cttatcttgc tgcatctcct ggagaaacca ttactattaa ttgcagggca 480

agtaagagca ttagcaaata tttagcctgg tatcaagaga aacctgggaa agctaataag 540

ctacttatcc attctggatc cactttgcaa tctggaatac catcaaggtt cagtggcagt 600

ggatctggta cagatttcac tctcaccatc agtagcctgg agcctgaaga ttttgcaatg 660

tattactgtc aacagcatat tgaatacccg tggacgttcg gtggtggcac caaactggaa 720

attaaacggg cctcg 735

<210> 19
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> murine scFv (VH-VL orientation)

<400> 19

Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
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Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met His Trp Val Lys Gln Asn Asn Gly Glu Ser Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Asn Pro Tyr Asn Asp Tyr Thr Arg Tyr Asn Gln Asn Phe
50 55 60

Asn Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Phe Tyr Tyr Cys

85 90 95

Ala Arg Ser Asp Gly Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Ser Gly Gly Gly Gly Ser Asp Val Gln Ile Thr Gln Ser Pro Ser
130 135 140

Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala
145 150 155 160

Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly
165 170 175

Lys Ala Asn Lys Leu Leu Ile His Ser Gly Ser Thr Leu Gln Ser Gly
180 185 190

Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln
210 215 220

Gln His Ile Glu Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
225 230 235 240

Ile Lys Arg Ala Ser
245

<210> 20
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> murine scFv (VL-VH orientation)

<400> 20
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attaattgca gggcaagtaa gagcattagc aaatatttag cctggtatca agagaaacct 120

gggaaagcta ataagctact tatccattct ggatccactt tgcaatctgg aataccatca 180

aggttcagtg gcagtggatc tggtacagat ttcactctca ccatcagtag cctggagcct 240

gaagattttg caatgtatta ctgtcaacag catattgaat acccgtggac gttcggtggt 300

ggcaccaaac tggaaattaa acgggccggc ggcggcggaa gcggcggtgg cggcagcagc 360

ggcggcggcg gcagcgagat ccagctgcaa cagtctggac ctgagctggt gaagcctggg 420

gcttcagtga agatgtcctg caaggcttct ggatacacat tcactgacta ctacatgcac 480

tgggtgaagc agaacaatgg agagagcctt gagtggattg gatattttaa tccttataat 540

gattatacta gatacaacca gaatttcaat ggcaaggcca cattgactgt agacaagtcc 600

tccagcacag cctacatgca gctcaacagc ctgacatctg aggactctgc attctattac 660

tgtgcaagat cggatggtta ctacgatgct atggactact ggggtcaagg aacctcagtc 720

accgtctcct cg 732

<210> 21
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> murine scFv (VL-VH orientation)

<400> 21

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

Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
20 25 30

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Gly Gly Gly
100 105 110

Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Gly Gly Ser Glu Ile Gln
115 120 125

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

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

Trp Val Lys Gln Asn Asn Gly Glu Ser Leu Glu Trp Ile Gly Tyr Phe
165 170 175

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

Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu
195 200 205

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

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

Thr Val Ser Ser

<210> 22
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized VL domain

<400> 22
gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 120

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 180

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 300

gggaccaagg tggaaatcaa acga 324

<210> 23
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized VL domain

<400> 23

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

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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
            100                 105
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<210> 24
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized VH domain #1

<400> 24

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gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaagatc      60

tcctgcaagg cttctggata cacattcact gactactaca tgcactgggt gcaacaggcc     120

cctggaaaag ggcttgagtg gatgggatat tttaatcctt ataatgatta tactagatac     180

gcagagaagt tccagggcag agtcaccata accgcggaca cgtctacaga cacagcctac     240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc aagatcggat     300

ggttactacg atgctatgga ctactggggt caaggaacca cagtcaccgt ctcctcg        357
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<210> 25
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized VH domain #1

<400> 25

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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 Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30

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

Gly Tyr Phe Asn Pro Tyr Asn Asp Tyr Thr Arg Tyr Ala Glu Lys Phe
    50                  55                  60

Gln Gly 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 Asp Gly Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110
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Thr Thr Val Thr Val Ser Ser
115

<210> 26
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized VH domain #2

<400> 26
caggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggcttc agtgaaggtc 60

tcctgcaagg cttctggata cacattcact gactactaca tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatat tttaatcctt ataatgatta tactagatac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtctatcag cacagcctac 240

atggagctga gcagcctgag atctgacgac acggccgtgt attactgtgc aagatcggat 300

ggttactacg atgctatgga ctactggggt caaggaacca cagtcaccgt ctcctcg 357

<210> 27
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized VH domain #2

<400> 27

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 Asp Tyr
20 25 30

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

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

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

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

Ala Arg Ser Asp Gly Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 28
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized scFv A (VL-VH#1 orientation)

<400> 28
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atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 120

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 180

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 300

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 360

ggtggctctg aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggctaca 420

gtgaagatct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 480

caacaggccc ctggaaaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 540

actagatacg cagagaagtt ccagggcaga gtcaccataa ccgcggacac gtctacagac 600

acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgca 660

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 720

tcctcg 726

<210> 29
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized scFv B (VL-VH#2 orientation)

<400> 29
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atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 120

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 180

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 300

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 360

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 420

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 480

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 540

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc 600

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca 660

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 720

tcctcg 726

<210> 30
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized scFv A (VL-VH#1 orientation)

<400> 30

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

<210> 31
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized scFv B (VL-VH#2 orientation)

<400> 31

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

<210> 32
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized scFv A (VH#1-VL orientation)

<400> 32
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tcctgcaagg cttctggata cacattcact gactactaca tgcactgggt gcaacaggcc 120

cctggaaaag ggcttgagtg gatgggatat tttaatcctt ataatgatta tactagatac 180

gcagagaagt tccagggcag agtcaccata accgcggaca cgtctacaga cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc aagatcggat 300

ggttactacg atgctatgga ctactggggt caaggaacca cagtcaccgt ctcctcaggt 360

ggcggagggt ctgggggtgg cggatccgga ggtggtggct ctgatatcca gatgacccag 420

tctccatccg ccatgtctgc atctgtagga gacagagtca ccatcacttg ccgggcgagt 480

aagagcatta gcaaatattt agcctggttt cagcagaaac cagggaaagt tcctaagctc 540

cgcatccatt ctggatctac tttgcaatca ggggtcccat ctcggttcag tggcagtgga 600

tctgggacag aatttactct caccatcagc agcctgcagc ctgaagattt tgcaacttat 660

tactgtcaac agcatattga tacccgtgg acgttcggcc aagggaccaa ggtggaaatc 720

aaacgagcct cg 732

<210> 33
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized scFv B (VH#2-VL orientation)

<400> 33
caggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggcttc agtgaaggtc 60

tcctgcaagg cttctggata cacattcact gactactaca tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatat tttaatcctt ataatgatta tactagatac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtctatcag cacagcctac 240

atggagctga gcagcctgag atctgacgac acggccgtgt attactgtgc aagatcggat 300

ggttactacg atgctatgga ctactggggt caaggaacca cagtcaccgt ctcctcaggt 360

ggcggagggt ctgggggtgg cggatccgga ggtggtggct ctgatatcca gatgacccag 420

tctccatccg ccatgtctgc atctgtagga gacagagtca ccatcacttg ccgggcgagt 480

aagagcatta gcaaatattt agcctggttt cagcagaaac cagggaaagt tcctaagctc 540

cgcatccatt ctggatctac tttgcaatca ggggtcccat ctcggttcag tggcagtgga 600

tctgggacag aatttactct caccatcagc agcctgcagc ctgaagattt tgcaacttat 660

tactgtcaac agcatattga atacccgtgg acgttcggcc aagggaccaa ggtggaaatc 720

aaacgcgcct cg 732

<210> 34
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized scFv A (VH#1-VL orientation)

<400> 34

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 Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

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

Gly Tyr Phe Asn Pro Tyr Asn Asp Tyr Thr Arg Tyr Ala Glu Lys Phe
50 55 60

Gln Gly 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 Asp Gly Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ala
130 135 140

Met Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser

145 150 155 160

Lys Ser Ile Ser Lys Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys
165 170 175

Val Pro Lys Leu Arg Ile His Ser Gly Ser Thr Leu Gln Ser Gly Val
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
195 200 205

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

His Ile Glu Tyr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Arg Ala Ser

<210> 35
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized scFv B (VH#2-VL orientation)

<400> 35

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 Asp Tyr
20 25 30

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

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

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

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

Ala Arg Ser Asp Gly Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ala
130 135 140

Met Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Lys Ser Ile Ser Lys Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys
165 170 175

Val Pro Lys Leu Arg Ile His Ser Gly Ser Thr Leu Gln Ser Gly Val
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
195 200 205

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

His Ile Glu Tyr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225 230 235 240

Lys Arg Ala Ser

<210> 36
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC085 chimeric SMIP (murine VL-VH scFv - human Fc)

<400> 36
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gatgtccaga taacccagtc tccatcttat cttgctgcat ctcctggaga aaccattact 120

attaattgca gggcaagtaa gagcattagc aaatatttag cctggtatca agagaaacct 180

gggaaagcta ataagctact tatccattct ggatccactt tgcaatctgg aataccatca 240

aggttcagtg gcagtggatc tggtacagat ttcactctca ccatcagtag cctggagcct 300

gaagattttg caatgtatta ctgtcaacag catattgaat acccgtggac gttcggtggt 360

ggcaccaaac tggaaattaa acgggccggc ggcggcggaa gcggcggtgg cggcagcagc 420

ggcggcggcg gcagcgagat ccagctgcaa cagtctggac ctgagctggt gaagcctggg 480

gcttcagtga agatgtcctg caaggcttct ggatacacat tcactgacta ctacatgcac 540

tgggtgaagc agaacaatgg agagagcctt gagtggattg gatattttaa tccttataat 600

gattatacta gatacaacca gaatttcaat ggcaaggcca cattgactgt agacaagtcc 660

tccagcacag cctacatgca gctcaacagc ctgacatctg aggactctgc attctattac 720

tgtgcaagat cggatggtta ctacgatgct atggactact ggggtcaagg aacctcagtc 780

accgtctcct cgagtgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 840

gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 960

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080

caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 1140

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atga 1494

<210> 37
<211> 1497
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC092 chimeric SMIP (murine VH-VL scFv - human Fc)

<400> 37
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagatccagc tgcaacagtc tggacctgag ctggtgaagc ctggggcttc agtgaagatg 120

tcctgcaagg cttctggata cacattcact gactactaca tgcactgggt gaagcagaac 180

aatggagaga gccttgagtg gattggatat tttaatcctt ataatgatta tactagatac 240

aaccagaatt tcaatggcaa ggccacattg actgtagaca agtcctccag cacagcctac 300

atgcagctca acagcctgac atctgaggac tctgcattct attactgtgc aagatcggat 360

ggttactacg atgctatgga ctactggggt caaggaacct cagtcaccgt ctcctcaggc 420

ggcggcggaa gcggcggtgg cggcagcagc ggcggcggcg gcagcgatgt ccagataacc 480

cagtctccat cttatcttgc tgcatctcct ggagaaacca ttactattaa ttgcagggca 540

agtaagagca ttagcaaata tttagcctgg tatcaagaga aacctgggaa agctaataag 600

ctacttatcc attctggatc cactttgcaa tctggaatac catcaaggtt cagtggcagt 660

ggatctggta cagatttcac tctcaccatc agtagcctgg agcctgaaga ttttgcaatg 720

tattactgtc aacagcatat tgaatacccg tggacgttcg gtggtggcac caaactggaa 780

attaaacggg cctcgagtga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc 840

ccagcacctg aagccgcggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac 900

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 960

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1020

aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 1080

caccaggact ggctgaatgg caaggcgtac gcgtgcgcgg tctccaacaa agccctccca 1140

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 1200

accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc 1260

aaaggcttct atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1320

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1380

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1440

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaatga 1497

<210> 38
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC085 chimeric SMIP (murine VL-VH scFv - human Fc)

<400> 38

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

Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
20 25 30

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Gly Gly Gly
100 105 110

Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Gly Gly Ser Glu Ile Gln
115 120 125

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

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

Trp Val Lys Gln Asn Asn Gly Glu Ser Leu Glu Trp Ile Gly Tyr Phe

165 170 175

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

Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu
195 200 205

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

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

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

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu
260 265 270

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
290 295 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335

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

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

435 440 445

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 39
<211> 478
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC092 chimeric SMIP (murine VH-VL scFv - human Fc)

<400> 39

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

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

Tyr Met His Trp Val Lys Gln Asn Asn Gly Glu Ser Leu Glu Trp Ile
35 40 45

Gly Tyr Phe Asn Pro Tyr Asn Asp Tyr Thr Arg Tyr Asn Gln Asn Phe
50 55 60

Asn Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Phe Tyr Tyr Cys
85 90 95

Ala Arg Ser Asp Gly Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Ser Gly Gly Gly Gly Ser Asp Val Gln Ile Thr Gln Ser Pro Ser
130 135 140

Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala
145 150 155 160

Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly
165 170 175

Lys Ala Asn Lys Leu Leu Ile His Ser Gly Ser Thr Leu Gln Ser Gly
180 185 190

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Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln
    210                 215                 220

Gln His Ile Glu Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
225                 230                 235                 240

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

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly 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 His Glu Asp Pro Glu Val
    290                 295                 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305                 310                 315                 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
                325                 330                 335

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

Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
        355                 360                 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
    370                 375                 380

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385                 390                 395                 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                405                 410                 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            420                 425                 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
        435                 440                 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
    450                 455                 460
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Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 40
<211> 1488
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC188 humanized SMIP (human VL-VH#1 scFv-Fc)

<400> 40
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

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 ccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agccccatc 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 gtaaatga 1488

<210> 41
<211> 1488
<212> DNA

<213> Artificial Sequence

<220>
<223> TSC189 humanized SMIP (human VL-VH#2 scFv-Fc)

<400> 41
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 ccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agccccatc 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 gtaaatga 1488

<210> 42
<211> 475
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC188 humanized SMIP (human VL-VH#1 scFv-Fc)

<400> 42

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
465 470 475

<210> 43
<211> 475
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC189 humanized SMIP (human VL-VH#2 scFv-Fc)

<400> 43

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
465 470 475

<210> 44
<211> 1794
<212> DNA
<213> Artificial Sequence

<220>
<223> chimeric TSC084 Interceptor (murine VL-VH 107-1A4 scFv-Fc-CH1)

<400> 44
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gatgtccaga taacccagtc tccatcttat cttgctgcat ctcctggaga aaccattact 120

attaattgca gggcaagtaa gagcattagc aaatatttag cctggtatca agagaaacct 180

gggaaagcta ataagctact tatccattct ggatccactt tgcaatctgg aataccatca 240

aggttcagtg gcagtggatc tggtacagat ttcactctca ccatcagtag cctggagcct 300

gaagattttg caatgtatta ctgtcaacag catattgaat acccgtggac gttcggtggt 360

ggcaccaaac tggaaattaa acgggccggc ggcggcggaa gcggcggtgg cggcagcagc 420

ggcggcggcg gcagcgagat ccagctgcaa cagtctggac ctgagctggt gaagcctggg 480

gcttcagtga agatgtcctg caaggcttct ggatacacat tcactgacta ctacatgcac 540

tgggtgaagc agaacaatgg agagagcctt gagtggattg gatattttaa tccttataat 600

gattatacta gatacaacca gaatttcaat ggcaaggcca cattgactgt agacaagtcc 660

tccagcacag cctacatgca gctcaacagc ctgacatctg aggactctgc attctattac 720

tgtgcaagat cggatggtta ctacgatgct atggactact ggggtcaagg aacctcagtc 780

accgtctcct cgagcgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 840

gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 960

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080

caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 1140

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atctagagcc 1500

tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 1560

acagcggccc tgggctgcct ggtcaaggac tacttccccg agccggtgac ggtgtcgtgg 1620

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 1680

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 1740

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt ttga 1794

<210> 45
<211> 1821
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC093 Interceptor (Cris7 scFv-Fc-CkYAE)

<400> 45
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 gaccctgag gtcacatgcg tggtggtgga cgtgagccac 960

gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 1020

acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 1080

ctgcaccagg actggctgaa tggcaaggcg tacgcgtgcg cggtctccaa caaagccctc 1140

ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg 1200

tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 1260

gtcaaaggct tctatccaag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1320

aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1380

aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1440

catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaatct 1500

agaactgtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 1560

ggaactgcct ctgttgtgtg cctgctgaat tacttctatc ccagagaggc caaagtacag 1620

tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgccac agagcaggac 1680

agcaaggaca gcacctacag cctcagcagc gagctgacgc tgagcaaagc agactacgag 1740

aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 1800

agcttcaaca ggggagagtg a 1821

<210> 46
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC084 Interceptor (murine VL-VH 107-1A4 scFv-Fc-CH1)

<400> 46

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

Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
20 25 30

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Gly Gly Gly
100 105 110

Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Gly Gly Ser Glu Ile Gln
115 120 125

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

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

Trp Val Lys Gln Asn Asn Gly Glu Ser Leu Glu Trp Ile Gly Tyr Phe
165 170 175

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

Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu
195 200 205

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

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

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

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu
260 265 270

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
290 295 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335

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

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Arg Ala
465 470 475 480

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
485 490 495

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
515 520 525

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
530 535 540

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
545 550 555 560

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
565 570 575

Val

<210> 47
<211> 586
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC093 Interceptor (Cris7 scFv-Fc-CkYAE)

<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 Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln
130 135 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
145 150 155 160

Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys
165 170 175

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

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
195 200 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr

210 215 220

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

Leu Gln Ile Thr Arg Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His
245 250 255

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val
260 265 270

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
275 280 285

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
290 295 300

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
305 310 315 320

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
325 330 335

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

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

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
370 375 380

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
385 390 395 400

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
405 410 415

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
420 425 430

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
435 440 445

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
450 455 460

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser
465 470 475 480

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu

485 490 495

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Tyr Phe
500 505 510

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
515 520 525

Ser Gly Asn Ser Gln Glu Ser Ala Thr Glu Gln Asp Ser Lys Asp Ser
530 535 540

Thr Tyr Ser Leu Ser Ser Glu Leu Thr Leu Ser Lys Ala Asp Tyr Glu
545 550 555 560

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
565 570 575

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
580 585

<210> 48
<211> 2283
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized TSC194 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-Cris7 scFv)

<400> 48
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 ttccccccaa 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 agccccccatc 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

cagtctgggg gcggagtggt gcagcctggg cggtcactga ggctgtcctg caaggcttct 1620

ggctacacct ttactagatc tacgatgcac tgggtaaggc aggcccctgg aaagggtctg 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 aagcccggca aggccccaa aagatggatt 2100

tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 2160

accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc 2220

cagcagtgga gtcgtaaccc acccacgttc ggaggggggga ccaagctaca aattacacga 2280

taa 2283

<210> 49
<211> 740
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized TSC194 Scorpion (huVL-VH#2 107-1A4 scFv-Fc-Cris7 scFv)

<400> 49

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

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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 Gln 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 Lys 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
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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 Arg
740

<210> 50
<211> 2283
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized TSC199 Scorpion (huVL-VH#1 107-1A4 scFv-Fc-Cris7 scFv)

<400> 50
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

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

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accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

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cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct 1500

tccctgaata caggaactca gatggcaggt cattctccga attctcaggt ccagctggtg 1560

cagtctgggg gcggagtggt gcagcctggg cggtcactga ggctgtcctg caaggcttct 1620

ggctacacct ttactagatc tacgatgcac tgggtaaggc aggcccctgg aaagggtctg 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

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ccaagcagcc tgtctgcaag cgtgggggac agggtcacca tgacctgcag tgccagctca 2040

agtgtaagtt acatgaactg gtaccagcag aagcccggca aggcccccaa aagatggatt 2100

tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 2160

accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc 2220

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taa 2283

<210> 51
<211> 740
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized TSC199 Scorpion (huVL-VH#1 107-1A4 scFv-Fc-Cris7 scFv)

<400> 51

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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
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 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 Gln 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 Lys 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 Arg
740

<210> 52
<211> 1800
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC125 Interceptor (Cris7 scFv-Fc-CH1)

<400> 52
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 gaccctgag 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> 53
<211> 1809
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized TSC192 Interceptor (huVL-VH#2 107-1A4 scFv-Fc-CkYAE)

<400> 53
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 ttcccccccaa 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> 54
<211> 1809
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized TSC193 Interceptor (huVL-VH#1 107-1A4 scFv-Fc-CkYAE)

<400> 54
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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
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acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgca 720
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tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840
gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960
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ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260
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gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440
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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> 55
<211> 1788
<212> DNA

<213> Artificial Sequence

<220>
<223> humanized TSC195 Interceptor (huVL-VH#2 107-1A4 scFv-Fc-CH1)

<400> 55
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180

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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 ccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agccccatc 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> 56

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

<220>
<223> humanized TSC196 Interceptor (huVL-VH#1 107-1A4 scFv-Fc-CH1)

<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

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 ccctgaggt 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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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> 57
<211> 579
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC125 Interceptor (Cris7 scFv-Fc-CH1)

<400> 57

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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 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> 58
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized TSC192 Interceptor (huVL-VH#2 107-1A4 scFv-Fc-CkYAE)

<400> 58

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> 59
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized TSC193 Interceptor (huVL-VH#1 107-1A4 scFv-Fc-CkYAE)

<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

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> 60

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

<220>
<223> humanized TSC195 Interceptor (huVL-VH#2 107-1A4 scFv-Fc-CH1)

<400> 60

```
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
```

<210> 61
<211> 575
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized TSC196 Interceptor (huVL-VH#1 107-1A4 scFv-Fc-CH1)

<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
            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 Ala Ser Thr
465 470 475 480

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
485 490 495

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
500 505 510

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
515 520 525

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
530 535 540

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
545 550 555 560

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
565 570 575

<210> 62
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker H7

<400> 62

Gly Cys Pro Pro Cys Pro Asn Ser
1 5

<210> 63
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker H75

<400> 63

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> 64

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

<220>
<223> Linker H81

<400> 64

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

<210> 65
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker H83

<400> 65

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

<210> 66
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker H91

<400> 66

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> 67
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker H94

<400> 67

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

Pro Asn Ser

<210> 68
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker H98

<400> 68

Ser Ser Leu Asn Thr Gly Thr Gln Pro Asn Ser
1 5 10

<210> 69
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC210-humanized SMIP (human VH#2-VL scFv-Fc)

<400> 69
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

caggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggcttc agtgaaggtc 120

tcctgcaagg cttctggata cacattcact gactactaca tgcactgggt gcgacaggcc 180

cctggacaag ggcttgagtg gatgggatat tttaatcctt ataatgatta tactagatac 240

gcacagaagt tccagggcag agtcaccatg accagggaca cgtctatcag cacagcctac 300

atggagctga gcagcctgag atctgacgac acggccgtgt attactgtgc aagatcggat 360

ggttactacg atgctatgga ctactggggt caaggaacca cagtcaccgt ctcctcaggt 420

ggcggagggt ctgggggtgg cggatccgga ggtggtggct ctgatatcca gatgacccag 480

tctccatccg ccatgtctgc atctgtagga gacagagtca ccatcacttg ccgggcgagt 540

aagagcatta gcaaatattt agcctggttt cagcagaaac cagggaaagt tcctaagctc 600

cgcatccatt ctggatctac tttgcaatca ggggtcccat ctcggttcag tggcagtgga 660

tctgggacag aatttactct caccatcagc agcctgcagc ctgaagattt tgcaacttat 720

tactgtcaac agcatattga atacccgtgg acgttcggcc aagggaccaa ggtggaaatc 780

aaacgcgcct cgagtgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 840

gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 960

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080

caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 1140

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atga 1494

<210> 70
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC210-humanized SMIP (human VH#2-VL scFv-Fc)

<400> 70

```
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 Asp Tyr
            20                  25                  30

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

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

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

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

Ala Arg Ser Asp Gly Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ala
    130                 135                 140

Met Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Lys Ser Ile Ser Lys Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys
                165                 170                 175

Val Pro Lys Leu Arg Ile His Ser Gly Ser Thr Leu Gln Ser Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
        195                 200                 205

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

His Ile Glu Tyr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
```

225 230 235 240

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

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu
260 265 270

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
290 295 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335

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

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 71
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC211 humanized SMIP (human VH#1-VL scFv-Fc)

<400> 71
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaagatc 120

tcctgcaagg cttctggata cacattcact gactactaca tgcactgggt gcaacaggcc 180

cctggaaaag ggcttgagtg gatgggatat tttaatcctt ataatgatta tactagatac 240

gcagagaagt tccagggcag agtcaccata accgcggaca cgtctacaga cacagcctac 300

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc aagatcggat 360

ggttactacg atgctatgga ctactggggt caaggaacca cagtcaccgt ctcctcaggt 420

ggcggagggt ctgggggtgg cggatccgga ggtggtggct ctgatatcca gatgacccag 480

tctccatccg ccatgtctgc atctgtagga gacagagtca ccatcacttg ccgggcgagt 540

aagagcatta gcaaatattt agcctggttt cagcagaaac cagggaaagt tcctaagctc 600

cgcatccatt ctggatctac tttgcaatca ggggtcccat ctcggttcag tggcagtgga 660

tctgggacag aatttactct caccatcagc agcctgcagc ctgaagattt tgcaacttat 720

tactgtcaac agcatattga atacccgtgg acgttcggcc aagggaccaa ggtggaaatc 780

aaacgagcct cgagtgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 840

gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 960

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080

caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 1140

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atga 1494

<210> 72
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC211 humanized SMIP (human VH#1-VL scFv-Fc)

<400> 72

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 Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30

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

Gly Tyr Phe Asn Pro Tyr Asn Asp Tyr Thr Arg Tyr Ala Glu Lys Phe
    50                  55                  60

Gln Gly 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 Asp Gly Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ala
    130                 135                 140

Met Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Lys Ser Ile Ser Lys Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys
                165                 170                 175

Val Pro Lys Leu Arg Ile His Ser Gly Ser Thr Leu Gln Ser Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
        195                 200                 205

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

His Ile Glu Tyr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225                 230                 235                 240

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

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu
            260                 265                 270

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275                 280                 285
```

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
290 295 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335

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

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 73
<211> 2289
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized TSC212 Scorpion (hu VH#2-VL 107-1A4 scFv-Fc Cris7 scFv)

<400> 73
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

caggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggcttc agtgaaggtc 120

tcctgcaagg cttctggata cacattcact gactactaca tgcactgggt gcgacaggcc 180

cctggacaag ggcttgagtg gatgggatat tttaatcctt ataatgatta tactagatac 240

gcacagaagt tccagggcag agtcaccatg accagggaca cgtctatcag cacagcctac 300

atggagctga gcagcctgag atctgacgac acggccgtgt attactgtgc aagatcggat 360

ggttactacg atgctatgga ctactggggt caaggaacca cagtcaccgt ctcctcaggt 420

ggcggagggt ctgggggtgg cggatccgga ggtggtggct ctgatatcca gatgacccag 480

tctccatccg ccatgtctgc atctgtagga gacagagtca ccatcacttg ccgggcgagt 540

aagagcatta gcaaatattt agcctggttt cagcagaaac cagggaaagt tcctaagctc 600

cgcatccatt ctggatctac tttgcaatca ggggtcccat ctcggttcag tggcagtgga 660

tctgggacag aatttactct caccatcagc agcctgcagc ctgaagattt tgcaacttat 720

tactgtcaac agcatattga atacccgtgg acgttcggcc aagggaccaa ggtggaaatc 780

aaacgcgcct cgagtgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 840

gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 960

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080

caggactggc tgaatggcaa ggcgtacgcg tgcgcggtct ccaacaaagc cctcccagcc 1140

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtca gaggcacaac 1500

aattcttccc tgaatacagg aactcagatg gcaggtcatt ctccgaattc tcaggtccag 1560

ctggtgcagt ctgggggcgg agtggtgcag cctgggcggt cactgaggct gtcctgcaag 1620

gcttctggct acacctttac tagatctacg atgcactggg taaggcaggc ccctggaaag 1680

ggtctggaat ggattggata cattaatcct agcagtgctt atactaatta caatcagaaa 1740

ttcaaggaca ggttcacaat cagcgcagac aaatccaaga gcacagcctt cctgcagatg 1800

gacagcctga ggcccgagga caccggcgtc tatttctgtg cacggcccca agtccactat 1860

gattacaacg ggtttcctta ctggggccaa gggactcccg tcactgtctc tagcggtggc 1920

ggagggtctg ggggtggcgg atccggaggt ggtggctctg cacaagacat ccagatgacc 1980

cagtctccaa gcagcctgtc tgcaagcgtg ggggacaggg tcaccatgac ctgcagtgcc 2040

agctcaagtg taagttacat gaactggtac cagcagaagc ccggcaaggc ccccaaaaga 2100

tggatttatg actcatccaa actggcttct ggagtccctg ctcgcttcag tggcagtggg 2160

tctgggaccg actataccct cacaatcagc agcctgcagc ccgaagattt cgccacttat 2220

tactgccagc agtggagtcg taacccaccc acgttcggag gggggaccaa gctacaaatt 2280

acacgataa 2289

<210> 74
<211> 742
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized TSC212 Scorpion (huVH#2-VL 107-1A4 scFV-Fc-Cris7 scFV)

<400> 74

```
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 Asp Tyr
            20                  25                  30

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

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

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

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

Ala Arg Ser Asp Gly Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ala
    130                 135                 140

Met Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Lys Ser Ile Ser Lys Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys
                165                 170                 175

Val Pro Lys Leu Arg Ile His Ser Gly Ser Thr Leu Gln Ser Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220
```

His Ile Glu Tyr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225 230 235 240

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

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu
260 265 270

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
290 295 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335

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

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn
465 470 475 480

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

Ser Gln Val Gln Leu Val Gln 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 Lys 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 Arg
740

<210> 75
<211> 2289
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized TSC213 Scorpion (huVH#1-VL 107-1A4 scFv-FcCris7 scFv)

<400> 75
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaagatc 120

tcctgcaagg cttctggata cacattcact gactactaca tgcactgggt gcaacaggcc 180

cctggaaaag ggcttgagtg gatgggatat tttaatcctt ataatgatta tactagatac 240

gcagagaagt tccagggcag agtcaccata accgcggaca cgtctacaga cacagcctac 300

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc aagatcggat 360

ggttactacg atgctatgga ctactggggt caaggaacca cagtcaccgt ctcctcaggt 420

ggcggagggt ctgggggtgg cggatccgga ggtggtggct ctgatatcca gatgacccag 480

tctccatccg ccatgtctgc atctgtagga gacagagtca ccatcacttg ccgggcgagt 540

aagagcatta gcaaatattt agcctggttt cagcagaaac cagggaaagt tcctaagctc 600

cgcatccatt ctggatctac tttgcaatca ggggtcccat ctcggttcag tggcagtgga 660

tctgggacag aatttactct caccatcagc agcctgcagc ctgaagattt tgcaacttat 720

tactgtcaac agcatattga atacccgtgg acgttcggcc aagggaccaa ggtggaaatc 780

aaacgagcct cgagtgagcc caaatcttct gacaaaactc acacatgccc accgtgccca 840

gcacctgaag ccgcgggtgc accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 960

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cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtca gaggcacaac 1500

aattcttccc tgaatacagg aactcagatg gcaggtcatt ctccgaattc tcaggtccag 1560

ctggtgcagt ctgggggcgg agtggtgcag cctgggcggt cactgaggct gtcctgcaag 1620

gcttctggct acacctttac tagatctacg atgcactggg taaggcaggc ccctggaaag 1680

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tggatttatg actcatccaa actggcttct ggagtccctg ctcgcttcag tggcagtggg 2160

tctgggaccg actatacccct cacaatcagc agcctgcagc ccgaagattt cgccacttat 2220

tactgccagc agtggagtcg taacccaccc acgttcggag gggggaccaa gctacaaatt 2280

acacgataa 2289

<210> 76
<211> 742
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized TSC213 Scorpion (huVH#1-VL 107-1A4 scFv-Fc-Cris7 scFv)

<400> 76

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 Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

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

Gly Tyr Phe Asn Pro Tyr Asn Asp Tyr Thr Arg Tyr Ala Glu Lys Phe
50 55 60

Gln Gly 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 Asp Gly Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ala
130 135 140

Met Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Lys Ser Ile Ser Lys Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys
165 170 175

Val Pro Lys Leu Arg Ile His Ser Gly Ser Thr Leu Gln Ser Gly Val
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
195 200 205

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

His Ile Glu Tyr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225 230 235 240

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

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu
260 265 270

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
290 295 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335

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

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn
465 470 475 480

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

Ser Gln Val Gln Leu Val Gln 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 Lys 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 Arg
740

<210> 77
<211> 2289
<212> DNA
<213> Artificial Sequence

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

<400> 77
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 ttccccccaa aacccaagga caccctcatg 900

atctcccgga ccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agccccatc 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 aggcccccaa 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> 78
<211> 742
<212> PRT
<213> Artificial Sequence

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

<400> 78

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

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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
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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
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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> 79
<211> 2268
<212> DNA
<213> Artificial Sequence

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

<400> 79
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 agccccccatc 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> 80
<211> 1335
<212> PRT
<213> Artificial Sequence

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

<400> 80

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 Glu Val Gln Ile Pro Leu
465 470 475 480

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

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

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

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

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

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

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

Tyr Asn Gly Phe Pro Tyr Trp Gly Asp Ile Gln Met Thr Gln Ser Pro
595 600 605

Ser Ala Met Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
610 615 620

Ala Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Phe Gln Gln Lys Pro
625 630 635 640

Gly Lys Val Pro Lys Leu Arg Ile His Ser Gly Ser Thr Leu Gln Ser
645 650 655

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
660 665 670

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
675 680 685

Gln Gln His Ile Glu Tyr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val
690 695 700

Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
705 710 715 720

Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
725 730 735

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
740 745 750

Thr Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
755 760 765

Glu Trp Met Gly Tyr Phe Asn Pro Tyr Asn Asp Tyr Thr Arg Tyr Ala
770 775 780

Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
785 790 795 800

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val
805 810 815

Tyr Tyr Cys Ala Arg Ser Asp Gly Tyr Tyr Asp Ala Met Asp Tyr Trp
820 825 830

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser
835 840 845

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
850 855 860

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
865 870 875 880

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
885 890 895

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
900 905 910

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
915 920 925

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
930 935 940

Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
945 950 955 960

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
965 970 975

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
980 985 990

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
995 1000 1005

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
1010 1015 1020

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
1025 1030 1035

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
1040 1045 1050

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
1055 1060 1065

Leu Ser Leu Ser Pro Gly Glu Val Gln Ile Pro Leu Thr Glu Ser
1070 1075 1080

Tyr Ser Pro Asn Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly
1085 1090 1095

Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser
1100 1105 1110

Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala
1115 1120 1125

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser
1130 1135 1140

Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile
1145 1150 1155

Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser
1160 1165 1170

Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln
1175 1180 1185

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr
1190 1195 1200

Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1205 1210 1215

Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser
1220 1225 1230

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr
1235 1240 1245

Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
1250 1255 1260

Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys
1265 1270 1275

Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
1280 1285 1290

Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
1295 1300 1305

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe
1310 1315 1320

Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
1325 1330 1335

<210> 81
<211> 2274
<212> DNA
<213> Artificial Sequence

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

<400> 81
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 caccttttact 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> 82
<211> 737
<212> PRT
<213> Artificial Sequence

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

<400> 82

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

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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 Ser Leu Asn Thr Gly
465                 470                 475                 480
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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> 83
<211> 2286
<212> DNA
<213> Artificial Sequence

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

<400> 83
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 ccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agccccatc 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 gggggggacca agctacaaat tacatcctcc 2280

agctaa 2286

<210> 84
<211> 1478
<212> PRT
<213> Artificial Sequence

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

<400> 84

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 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

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

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

Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Arg
    770                 775                 780

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

Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
                805                 810                 815

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

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly
        835                 840                 845

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
    850                 855                 860

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

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp
                885                 890                 895

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

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

Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
    930                 935                 940

Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Asp
945                 950                 955                 960
```

```
Gly Tyr Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
                965                 970                 975

Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            980                 985                 990

Pro Cys Pro Ala Pro Glu Ala Ala  Gly Ala Pro Ser Val  Phe Leu Phe
        995                 1000                1005

Pro Pro  Lys Pro Lys Asp Thr  Leu Met Ile Ser Arg  Thr Pro Glu
    1010                1015                1020

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

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

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

Ser Val  Leu Thr Val Leu His  Gln Asp Trp Leu Asn  Gly Lys Ala
    1070                1075                1080

Tyr Ala  Cys Ala Val Ser Asn  Lys Ala Leu Pro Ala  Pro Ile Glu
    1085                1090                1095

Lys Thr  Ile Ser Lys Ala Lys  Gly Gln Pro Arg Glu  Pro Gln Val
    1100                1105                1110

Tyr Thr  Leu Pro Pro Ser Arg  Asp Glu Leu Thr Lys  Asn Gln Val
    1115                1120                1125

Ser Leu  Thr Cys Leu Val Lys  Gly Phe Tyr Pro Ser  Asp Ile Ala
    1130                1135                1140

Val Glu  Trp Glu Ser Asn Gly  Gln Pro Glu Asn Asn  Tyr Lys Thr
    1145                1150                1155

Thr Pro  Pro Val Leu Asp Ser  Asp Gly Ser Phe Phe  Leu Tyr Ser
    1160                1165                1170

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

Ser Cys  Ser Val Met His Glu  Ala Leu His Asn His  Tyr Thr Gln
    1190                1195                1200

Lys Ser  Leu Ser Leu Ser Pro  Gly Asn Ser Leu Ala  Asn Gln Glu
    1205                1210                1215
```

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

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

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

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

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

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

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

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

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

Gly Gly  Gly Ser Gly Gly Gly  Gly Ser Gly Gly Gly  Gly Ser Ala
    1355                 1360                 1365

Gln Asp  Ile Gln Met Thr Gln  Ser Pro Ser Ser Leu  Ser Ala Ser
    1370                 1375                 1380

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

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

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

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

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

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

Ile Thr Ser Ser Ser
1475

<210> 85
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> secretory signal sequence

<400> 85

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> 86
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> HuM291 VL amino acid sequence

<400> 86

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> 87
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> HuM291 VH amino acid sequence

<400> 87

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> 88
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> sss(s)-hIgG1 hinge

<400> 88

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

<210> 89
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> csc(s)-hIgG1 hinge

<400> 89

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

<210> 90
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> ssc(s)-hIgG1 hinge

<400> 90

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

<210> 91
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> scc(s)-hIgG1 hinge

<400> 91

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

<210> 92
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> css(s)-hIgG1 hinge

<400> 92

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

<210> 93
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> scs(s)-hIgG1 hinge

<400> 93

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

<210> 94
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> ccc(s)-hIgG1 hinge

<400> 94

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

<210> 95
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> ccc(p)-hIgG1 hinge

<400> 95

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

<210> 96
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> sss(p)-hIgG1 hinge

<400> 96

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

<210> 97
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> csc(p)-hIgG1 hinge

<400> 97

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

<210> 98
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> ssc(p)-hIgG1 hinge

<400> 98

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

<210> 99
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> scc(p)-hIgG1 hinge

<400> 99

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

<210> 100
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> css(p)-hIgG1 hinge

<400> 100

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

<210> 101
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> scs(p)-hIgG1 hinge

<400> 101

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

<210> 102
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Scppcp

<400> 102

Ser Cys Pro Pro Cys Pro
1 5

<210> 103
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> STD1

<400> 103

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> 104
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> STD2

<400> 104

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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> 105
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> H1

<400> 105

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Asn Ser
1
```

<210> 106
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> H2

<400> 106

```
Gly Gly Gly Gly Ser Gly Asn Ser
1               5
```

<210> 107
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> H3

<400> 107

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

<210> 108
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> H4

<400> 108

```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser
1               5                   10
```

<210> 109
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H5

<400> 109

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

<210> 110
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> H6

<400> 110

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

Asn Ser

<210> 111
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> (G4S)3

<400> 111

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

<210> 112
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> (GAS)4

<400> 112

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

Ser

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

<220>
<223> H16

<400> 113

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

<210> 114
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H17

<400> 114

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

<220>
<223> H18

<400> 115

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

<210> 116
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H19

<400> 116

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

<220>
<223> H20

<400> 117

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

<210> 118
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H21

<400> 118

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> 119
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H22

<400> 119

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

<210> 120
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H23

<400> 120

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

<220>
<223> H24

<400> 121

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

<210> 122
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H25

<400> 122

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

<220>
<223> H26

<400> 123

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

<210> 124
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H27

<400> 124

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

<220>
<223> H28

<400> 125

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

<210> 126
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> H30

<400> 126

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

<210> 127
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H32

<400> 127

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

<210> 128
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H33

<400> 128

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> 129
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> H36

<400> 129

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

<210> 130
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> H40

<400> 130

Gly Cys Pro Pro Cys Pro Ala Asn Ser
1 5

<210> 131
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> H41

<400> 131

Gly Cys Pro Pro Cys Pro Ala Asn Ser
1 5

<210> 132
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> H42

<400> 132

Gly Cys Pro Pro Cys Pro Asn Ser
1 5

<210> 133
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> H44

<400> 133

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

<210> 134
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> H45

<400> 134

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

<210> 135
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> H46

<400> 135

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

<210> 136
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H47

<400> 136

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

<210> 137
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> H48

<400> 137

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

<210> 138
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H50

<400> 138

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

<210> 139
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H51

<400> 139

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

<210> 140
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> H52

<400> 140

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

<210> 141
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> H53

<400> 141

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

<210> 142
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> H54

<400> 142

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

Pro Asn Ser

<210> 143
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H55

<400> 143

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

<210> 144
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> H56

<400> 144

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

<210> 145
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> H57

<400> 145

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

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

<220>
<223> H58

<400> 146

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

<210> 147
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H59

<400> 147

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

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

<220>
<223> H60

<400> 148

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

<210> 149
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H61

<400> 149

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> 150
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H62

<400> 150

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

<220>
<223> H63

<400> 151

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

<220>
<223> peptide linker

<400> 152

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

<210> 153
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> VL amino acid

<400> 153

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> 154
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> VH amino acid

<400> 154

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser
            20                  25                  30

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

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

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

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

Ala Ser Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ala
        115                 120
```

<210> 155
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge region H-105

<400> 155

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

<210> 156
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge Region H106 (NKG2A derived)

<400> 156

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

His Ser

<210> 157
<211> 2250
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized TSC95 Scorpion (hu VL-VH#2 107-1A4 scFv-Fc-DRA222 scFv, with H9 linker)

<400> 157
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 agccccatc 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> 158
<211> 729
<212> PRT
<213> Artificial Sequence

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

<400> 158

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 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> 159
<211> 2283
<212> DNA
<213> Artificial Sequence

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

<400> 159
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 agccccccatc 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

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acctttacta gatctacgat gcactgggta aggcaggccc ctggacaagg tctggaatgg 1680

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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> 160
<211> 740
<212> PRT
<213> Artificial Sequence

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

<400> 160

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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 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 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

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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> 161
<211> 2274
<212> DNA
<213> Artificial Sequence

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

<400> 161

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 ttccccccaa 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 agccccccatc 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 caccttttact 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> 162
<211> 737
<212> PRT
<213> Artificial Sequence

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

<400> 162

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

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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> 163
<211> 2280
<212> DNA
<213> Artificial Sequence

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

<400> 163
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> 164
<211> 739
<212> PRT
<213> Artificial Sequence

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

<400> 164

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 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> 165
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<220>
<221> REPEAT
<222> (1)..(5)
<223> n=5

<400> 165

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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
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