SEQUENCE LISTING

<110> APTEVO RESEARCH AND DEVELOPMENT LLC
Tan, Philip
Blankenship, John W.

<120> CD3 BINDING POLYPEPTIDES

<130> APVO-052/01WO

<150> US 62/221,190
<151> 2015-09-21

<160> 222

<170> PatentIn version 3.5

<210> 1
<211> 1560
<212> DNA
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<220>
<223> Fc DRA222 (TSC311 or TSC312) CD3-binding domain

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acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

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tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt ggagtctggg 840

ggcggagtgg tgcagcctgg gcggtcactg aggctgtcct gcaaggcttc tggctacacc 900

tttactagat ctacgatgca ctgggtaagg caggcccctg gacaaggtct ggaatggatt 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacaggttc 1020

acaatcagcg cagacaaatc caagagcaca gccttcctgc agatggacag cctgaggccc 1080

gaggacaccg gcgtctattt ctgtgcacgg ccccaagtcc actatgatta caacgggttt 1140

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ctgtctgcaa gcgtggggga cagggtcacc atgacctgca gtgccagctc aagtgtaagt 1320

tacatgaact ggtaccagca gaagccgggc aaggccccca aaagatggat ttatgactca 1380

tccaaactgg cttctggagt ccctgctcgc ttcagtggca gtgggtctgg gaccgactat 1440

accctcacaa tcagcagcct gcagcccgaa gatttcgcca cttattactg ccagcagtgg 1500

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<210> 2
<211> 499
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc DRA222 (TSC311 or TSC312) CD3-binding domain

<400> 2

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
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Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln

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65                  70                  75                  80

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285
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Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe
305                 310                 315                 320

Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
385                 390                 395                 400

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser
                405                 410                 415

Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
            420                 425                 430

Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro
        435                 440                 445

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
    450                 455                 460

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp
465                 470                 475                 480

Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr
                485                 490                 495
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Ser Ser Ser

<210> 3
<211> 1569
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H7L1 (TSC313) CD3-binding domain

<400> 3
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ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg 840

gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc 900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc 1020

accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct 1080

gacgacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

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ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccaagcagcc tgtctgcaag cgtgggggac agggtcacca tgacctgcag tgccagctca 1320

agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcccccaa aagatggatt 1380

tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1440

accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc 1500

cagcagtgga gtcgtaaccc acccacgttc ggaggggggga ccaagctaca aattacatcc 1560

tccagctaa 1569

<210> 4
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H7L1 (TSC313) CD3-binding domain

<400> 4

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320
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Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
                485                 490                 495

Gln Ile Thr Ser Ser Ser
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<210> 5
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> H7L4 (TSC314) CD3-binding domain

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ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg 840

gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc 900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc 1020

accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct 1080

gacgacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

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tatgactcat ccaaactggc ttctggcatc ccagccaggt tcagtggcag tgggtctggg 1440

acagacttca ctctcaccat cagcagccta gagcctgaag attttgcagt ttattactgt 1500

cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 6
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H7L4 (TSC314) CD3-binding domain

<400> 6

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser

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145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365
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Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
385                 390                 395                 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
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<210> 7
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H7L5 (TSC315) CD3-binding domain

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ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg 840

gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc 900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

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accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct 1080

gacgacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

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ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gctcctgatc 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg 1440

acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt 1500

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tcctccagct aa 1572

<210> 8
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H7L5 (TSC315) CD3-binding domain

<400> 8

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50   55   60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100   105   110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130   135   140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145   150   155   160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180   185   190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400
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Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
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<210> 9
<211> 1569
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H8L1 (TSC316) CD3-binding domain

<400> 9

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atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt       60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg      120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg      180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc       420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      480
```

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg 840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc 900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgctaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccaagcagcc tgtctgcaag cgtgggggac agggtcacca tgacctgcag tgccagctca 1320

agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcccccaa aagatggatt 1380

tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1440

accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc 1500

cagcagtgga gtcgtaaccc acccacgttc ggaggggggga ccaagctaca aattacatcc 1560

tccagctaa 1569

<210> 10
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H8L1 (TSC316) CD3-binding domain

<400> 10

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
```

```
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445
```

```
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
                485                 490                 495

Gln Ile Thr Ser Ser Ser
            500
```

<210> 11
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H8L4 (TSC317) CD3-binding domain

<400> 11

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atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt       60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg      120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg      180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc       420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc      660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780
```

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg 840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc 900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgctaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacacagtct 1260

ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca 1320

agtgtaagtt acatgaactg gtaccaacag aaacctggcc aggctcccag gctcctcatc 1380

tatgactcat ccaaactggc ttctggcatc ccagccaggt tcagtggcag tgggtctggg 1440

acagacttca ctctcaccat cagcagccta gagcctgaag attttgcagt ttattactgt 1500

cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 12
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H8L4 (TSC317) CD3-binding domain

<400> 12

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

```
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270
```

```
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
385                 390                 395                 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
465                 470                 475                 480
```

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 13
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H8L5 (TSC318) CD3-binding domain

<400> 13
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg 840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc 900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgctaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gctcctgatc 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg 1440

acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 14
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H8L5 (TSC318) CD3-binding domain

<400> 14

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

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

```
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
```

```
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 15
<211> 1569

<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H9L1 (TSC319) CD3-binding domain

<400> 15
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagcttgt gcagtctggg 840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcttc tggctacacc 900

tttactagat ctacgatgca ttgggtgcgc caggcccccg gacaaaggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc 1020

accattacca gggacacatc cgcgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaagacacgg ctgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccaagcagcc tgtctgcaag cgtgggggac agggtcacca tgacctgcag tgccagctca 1320

agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcccccaa aagatggatt 1380

tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1440

accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc 1500

cagcagtgga gtcgtaaccc acccacgttc ggaggggggga ccaagctaca aattacatcc 1560

tccagctaa 1569

<210> 16
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H9L1 (TSC319) CD3-binding domain

<400> 16

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

```
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350
```

```
Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
                485                 490                 495

Gln Ile Thr Ser Ser Ser
            500
```

<210> 17
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H9L4 (TSC320) CD3-binding domain

<400> 17
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagcttgt gcagtctggg 840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcttc tggctacacc 900

tttactagat ctacgatgca ttgggtgcgc caggcccccg gacaaaggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc 1020

accattacca gggacacatc cgcgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaagacacgg ctgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacacagtct 1260

ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca 1320

agtgtaagtt acatgaactg gtaccaacag aaacctggcc aggctcccag gctcctcatc 1380

tatgactcat ccaaactggc ttctggcatc ccagccaggt tcagtggcag tgggtctggg 1440

acagacttca ctctcaccat cagcagccta gagcctgaag attttgcagt ttattactgt 1500

cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 18

<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H9L4 (TSC320) CD3-binding domain

<400> 18

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


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


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


Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60


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


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


Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110


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


Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140


Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160


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

```
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
```

385 390 395 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 19
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H9L5 (TSC321) CD3-binding domain

<400> 19
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagcttgt gcagtctggg 840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcttc tggctacacc 900

tttactagat ctacgatgca ttgggtgcgc caggcccccg gacaaaggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc 1020

accattacca gggacacatc cgcgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaagacacgg ctgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gctcctgatc 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg 1440

acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 20
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H9L5 (TSC321) CD3-binding domain

<400> 20

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

```
1               5                   10                  15

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220
```

```
Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430
```

```
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 21
<211> 1569
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H10L1 (TSC322) CD3-binding domain

<400> 21

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atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt       60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg      120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg      180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc       420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc      660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720
```

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc 900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccaagcagcc tgtctgcaag cgtgggggac agggtcacca tgacctgcag tgccagctca 1320

agtgtaagtt acatgaactg gtaccagcag aagccgggca aggcccccaa aagatggatt 1380

tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 1440

accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc 1500

cagcagtgga gtcgtaaccc acccacgttc ggaggggggga ccaagctaca aattacatcc 1560

tccagctaa 1569

<210> 22
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H10L1 (TSC322) CD3-binding domain

<400> 22

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

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

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

```
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255
```

```
Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
    450                 455                 460

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

465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
485 490 495

Gln Ile Thr Ser Ser Ser
500

<210> 23
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H10L4 (TSC323) CD3-binding domain

<400> 23
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc 900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacacagtct 1260

ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca 1320

agtgtaagtt acatgaactg gtaccaacag aaacctggcc aggctcccag gctcctcatc 1380

tatgactcat ccaaactggc ttctggcatc ccagccaggt tcagtggcag tgggtctggg 1440

acagacttca ctctcaccat cagcagccta gagcctgaag attttgcagt ttattactgt 1500

cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 24
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H10L4 (TSC323) CD3-binding domain

<400> 24

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln

```
                85                  90                  95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300
```

```
Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
385                 390                 395                 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 25
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H10L5 (TSC324) CD3-binding domain

<400> 25
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcgtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc 900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gctcctgatc 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg 1440

acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 26
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H10L5 (TSC324) CD3-binding domain

<400> 26

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

```
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335
```

```
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 27
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H7L6 (TSC334) CD3-binding domain

<400> 27

atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg 840

gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc 900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc 1020

accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct 1080

gacgacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg 1440

acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 28
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H7L6 (TSC334) CD3-binding domain

<400> 28

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr

```
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380
```

```
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 29
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H7L7 (TSC335) CD3-binding domain

<400> 29
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg 840

gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc 900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc 1020

accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct 1080

gacgacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacgcagtct 1260

ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca 1320

agtgtaagtt acatgaactg gtaccagcag aaacctggcc tggcgcccag gagatggatt 1380

tatgactcat ccaaactggc ttctggcatc ccagacaggt tcagtggcag tgggtctggg 1440

acagacttca ctctcaccat cagcagactg gagcctgaag attttgcagt gtattactgt 1500

cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 30
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H7L7 (TSC335) CD3-binding domain

<400> 30

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

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

```
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
385                 390                 395                 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                405                 410                 415
```

```
Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Leu Ala Pro Arg Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
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<210> 31
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H7L8 (TSC336) CD3-binding domain

<400> 31

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atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt       60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg      120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg      180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc       420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600
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cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg 840

gctgaggtga agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc 900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagggtc 1020

accatgacca gggacacgtc catcagcaca gcctacatgg agctgagcag gctgagatct 1080

gacgacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440

acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 32
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H7L8 (TSC336) CD3-binding domain

<400> 32

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

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

```
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
```

```
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460
```

```
Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480


Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495


Glu Ile Lys Arg Ser Ser Ser
            500


<210>  33
<211>  1572
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Fc H8L6 (TSC337) CD3-binding domain

<400>  33
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt       60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg      120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg      180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc       420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc      660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg      840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc      900
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ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgctaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg 1440

acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 34
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H8L6 (TSC337) CD3-binding domain

<400> 34

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

```
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285
```

```
Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495
```

Glu Ile Lys Arg Ser Ser Ser
500

<210> 35
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H8L7 (TSC338) CD3-binding domain

<400> 35
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg 840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc 900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgctaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacgcagtct 1260

ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca 1320

agtgtaagtt acatgaactg gtaccagcag aaacctggcc tggcgcccag gagatggatt 1380

tatgactcat ccaaactggc ttctggcatc ccagacaggt tcagtggcag tgggtctggg 1440

acagacttca ctctcaccat cagcagactg gagcctgaag attttgcagt gtattactgt 1500

cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 36
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H8L7 (TSC338) CD3-binding domain

<400> 36

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
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325 330 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
355 360 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
370 375 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
385 390 395 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Leu Ala Pro Arg Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 37
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>

<223> Fc H8L8 (TSC339) CD3-binding domain

<400> 37

atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tgcagctggt gcagtctggg 840

gctgaggtga agaagcctgg ggcctcagtg aaggtttcct gcaaggcatc tggatacacc 900

ttcaccagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

accatgacca gggacacgtc cacgagcaca gtctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgctaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440

acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 38
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H8L8 (TSC339) CD3-binding domain

<400> 38

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365
```

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Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 39
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H10L6 (TSC340) CD3-binding domain

<400> 39
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc 900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagtggcag tggatctggg 1440

acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 40
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H10L6 (TSC340) CD3-binding domain

<400> 40

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50   55   60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100   105   110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130   135   140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145   150   155   160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180   185   190

```
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
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405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 41
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H10L7 (TSC341) CD3-binding domain

<400> 41
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc 900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg aaattgtgtt gacgcagtct 1260

ccagccaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag tgccagctca 1320

agtgtaagtt acatgaactg gtaccagcag aaacctggcc tggcgcccag gagatggatt 1380

tatgactcat ccaaactggc ttctggcatc ccagacaggt tcagtggcag tgggtctggg 1440

acagacttca ctctcaccat cagcagactg gagcctgaag attttgcagt gtattactgt 1500

cagcagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 42
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H10L7 (TSC341) CD3-binding domain

<400> 42

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

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

```
            20                  25                  30

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240
```

```
Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
385                 390                 395                 400

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Leu Ala Pro Arg Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445
```

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
450 455 460

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 43
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc H10L8 (TSC342) CD3-binding domain

<400> 43
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc 900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440

acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 44
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> Fc H10L8 (TSC342) CD3-binding domain

<400> 44

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

```
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270
```

```
Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
```

485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 45
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC370 CD3-binding domain

<400> 45
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatatacc 900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440

acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 46
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC370 CD3-binding domain

<400> 46

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala

```
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320
```

```
Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 47
<211> 1572
<212> DNA

<213> Artificial Sequence

<220>
<223> TSC371 CD3-binding domain

<400> 47
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc 900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggata 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440

acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 48
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC371 CD3-binding domain

<400> 48

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

```
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160


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


Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190


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


Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220


Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240


Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255


Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270


Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285


Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
    290                 295                 300


Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320


Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335


Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            340                 345                 350
```

```
Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 49
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC372 CD3-binding domain

<400> 49
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc 900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tgacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440

acagaattca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 50
<211> 503

<212> PRT
<213> Artificial Sequence

<220>
<223> TSC372 CD3-binding domain

<400> 50

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

```
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400
```

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
405 410 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
420 425 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
435 440 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
450 455 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465 470 475 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
485 490 495

Glu Ile Lys Arg Ser Ser Ser
500

<210> 51
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC390 CD3-binding domain

<400> 51
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840

cctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatatacc 900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440

acagagttca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 52
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC390 CD3-binding domain

<400> 52

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220
```

```
Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430
```

```
Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 53
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC391 CD3-binding domain

<400> 53

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atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt       60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg      120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg      180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc       420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc      660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720
```

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840

cctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatatacc 900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggata 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tcacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440

acagagttca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 54
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC391 CD3-binding domain

<400> 54

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

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

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

```
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
```

```
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480
```

```
Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 55
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC392 CD3-binding domain

<400> 55

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atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt       60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg      120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg      180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc       420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc      660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat      780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg      840

cctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatatacc      900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggatg      960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc     1020
```

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tgacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440

acagagttca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 56
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC392 CD3-binding domain

<400> 56

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

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

```
Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
            100                 105                 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Tyr Ile Asn
    290                 295                 300
```

```
Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
```

<210> 57
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC393 CD3-binding domain

<400> 57
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840

gctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatatacc 900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggata 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tgacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440

acagagttca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 58
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC393 CD3-binding domain

<400> 58

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

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Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400

Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                405                 410                 415

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495

Glu Ile Lys Arg Ser Ser Ser
            500
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<210> 59
<211> 1572
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC394 CD3-binding domain

<400> 59
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gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 120

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 180

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 240

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 300

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 360

ggcaaggcat acgcatgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 420

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 480

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 540

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 600

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 660

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 720

tacacgcaga agagcctctc cctgtctccg ggtcagaggc acaacaattc ttccctgaat 780

acaggaactc agatggcagg tcattctccg aattctcagg tccagctggt gcaatctggg 840

cctgaggtga agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggatatacc 900

ttcagcagat ctacgatgca ctgggtgcga caggcccctg gacaagggct tgagtggata 960

ggatacatta atcctagcag tgcttatact aattacaatc agaaattcaa ggacagagtc 1020

acgattaccg cggacaaatc cacgagcaca gcctacatgg agctgagcag cctgagatct 1080

gaggacacgg ccgtgtatta ctgtgcgaga ccccaagtcc actatgatta caacgggttt 1140

ccttactggg gccaaggaac cctggtcacc gtctcctcag gtggaggcgg ttcaggcgga 1200

ggtggatccg gcggtggcgg atcgggtggc ggcggatctg acatccagat gacccagtct 1260

ccttccaccc tgtctgcatc tgtaggagac agagtcacca tgacttgcag tgccagctca 1320

agtgtaagtt acatgaactg gtatcagcag aaaccaggga aagcccctaa gagatggatt 1380

tatgactcat ccaaactggc ttctggggtc ccatcaaggt tcagcggcag tggatctggg 1440

acagagttca ctctcaccat cagcagcctg cagcctgatg attttgcaac ttattactgc 1500

caacagtgga gtcgtaaccc acccactttc ggcggaggga ccaaggtgga gatcaaacgg 1560

tcctccagct aa 1572

<210> 60
<211> 503
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC394 CD3-binding domain

<400> 60

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

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

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

Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

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

```
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser Ser Leu Asn
225                 230                 235                 240

Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln Val Gln Leu
                245                 250                 255

Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
            260                 265                 270

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp
        275                 280                 285

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
    290                 295                 300

Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val
305                 310                 315                 320

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                325                 330                 335

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

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380
```

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Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
385                 390                 395                 400


Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                405                 410                 415


Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430


Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        435                 440                 445


Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
    450                 455                 460


Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480


Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val
                485                 490                 495


Glu Ile Lys Arg Ser Ser Ser
            500


<210>  61
<211>  2301
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  TSC408 Anti-PSMA X anti-CD3 bispecific molecule

<400>  61
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
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gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc 660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca 720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc 1140

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1200

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260

tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1320

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct 1500

tccctgaata caggaactca gatggcaggt cattctccga attctcaggt ccagctggtg 1560

caatctgggc ctgaggtgaa gaagcctggg tcctcggtga aggtctcctg caaggcttct 1620

ggatatacct tcagcagatc tacgatgcac tgggtgcgac aggcccctgg acaagggctt 1680

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gacagagtca cgattaccgc ggacaaatcc acgagcacag cctacatgga gctgagcagc 1800

ctgagatctg aggacacggc cgtgtattac tgtgcgagac cccaagtcca ctatgattac 1860

aacgggtttc cttactgggg ccaaggaacc ctggtcaccg tctcctcagg tggaggcggt 1920

tcaggcggag gtggatccgg cggtggcgga tcgggtggcg gcggatctga catccagatg 1980

acccagtctc cttccaccct gtctgcatct gtaggagaca gagtcaccat cacttgcagt 2040

gccagctcaa gtgtaagtta catgaactgg tatcagcaga aaccagggaa agcccctaag 2100

agatggattt atgactcatc caaactggct tctggggtcc catcaaggtt cagcggcagt 2160

ggatctggga cagagttcac tctcaccatc agcagcctgc agcctgatga ttttgcaact 2220

tattactgcc aacagtggag tcgtaaccca cccactttcg gcggagggac caaggtggag 2280

atcaaacggt cctccagcta a 2301

<210> 62
<211> 746
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC408 Anti-PSMA X anti-CD3 bispecific molecule

<400> 62

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 Pro Asn Ser Gln
                485                 490                 495

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

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

Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met
                565                 570                 575

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr 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 Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    610                 615                 620

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

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

Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
            660                 665                 670

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

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

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

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

Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
            740                 745
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<210> 63
<211> 2301
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC409 Anti-PSMA X anti-CD3 bispecific molecule

<400> 63
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gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc 660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca 720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

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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gacagagtca cgattaccgc ggacaaatcc acgagcacag cctacatgga gctgagcagc 1800

ctgagatctg aggacacggc cgtgtattac tgtgcgagac cccaagtcca ctatgattac 1860

aacgggtttc cttactgggg ccaaggaacc ctggtcaccg tctcctcagg tggaggcggt 1920

tcaggcggag gtggatccgg cggtggcgga tcgggtggcg gcggatctga catccagatg 1980

acccagtctc cttccaccct gtctgcatct gtaggagaca gagtcaccat gacttgcagt 2040

gccagctcaa gtgtaagtta catgaactgg tatcagcaga aaccagggaa agcccctaag 2100

agatggattt atgactcatc caaactggct tctggggtcc catcaaggtt cagcggcagt 2160

ggatctggga cagagttcac tctcaccatc agcagcctgc agcctgatga ttttgcaact 2220

tattactgcc aacagtggag tcgtaaccca cccactttcg gcggagggac caaggtggag 2280

atcaaacggt cctccagcta a 2301

<210> 64
<211> 746
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC409 Anti-PSMA X anti-CD3 bispecific molecule

<400> 64

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    290                 295                 300

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 Pro Glu Val Lys Lys Pro Gly Ser Ser
            500                 505                 510

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

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met 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 Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met
                565                 570                 575

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr 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 Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    610                 615                 620

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

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

Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
            660                 665                 670
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Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys
        675                 680                 685

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

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

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

Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
            740                 745
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<210> 65
<211> 2301
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC410 Anti-PSMA X anti-CD3 bispecific molecule

<400> 65

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gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc      120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca      180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct      240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct      300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa      360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt      420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca      480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg      540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat      600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc      660
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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 cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc 1140

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1200

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260

tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1320

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtcagaggca caacaattct 1500

tccctgaata caggaactca gatggcaggt cattctccga attctcaggt ccagctggtg 1560

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aacgggtttc cttactgggg ccaaggaacc ctggtcaccg tctcctcagg tggaggcggt 1920

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acccagtctc cttccaccct gtctgcatct gtaggagaca gagtcaccat gacttgcagt 2040

gccagctcaa gtgtaagtta catgaactgg tatcagcaga aaccagggaa agcccctaag 2100

agatggattt atgactcatc caaactggct tctggggtcc catcaaggtt cagcggcagt 2160

ggatctggga cagagttcac tctcaccatc agcagcctgc agcctgatga ttttgcaact 2220

tattactgcc aacagtggag tcgtaaccca cccactttcg gcggagggac caaggtggag 2280

atcaaacggt cctccagcta a 2301

<210> 66
<211> 746
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC410 Anti-PSMA X anti-CD3 bispecific molecule

<400> 66

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
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```
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 Ala Glu Val Lys Lys Pro Gly Ser Ser
            500                 505                 510

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser 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 Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met
                565                 570                 575

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr 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 Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
610 615 620

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

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

Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
660 665 670

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

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

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

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

Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
740 745

<210> 67
<211> 2301
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC411 Anti-PSMA X anti-CD3 bispecific molecule

<400> 67
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gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc 660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca 720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

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

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gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

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tccctgaata caggaactca gatggcaggt cattctccga attctcaggt ccagctggtg 1560

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acccagtctc cttccaccct gtctgcatct gtaggagaca gagtcaccat gacttgcagt 2040

gccagctcaa gtgtaagtta catgaactgg tatcagcaga aaccagggaa agcccctaag 2100

agatggattt atgactcatc caaactggct tctggggtcc catcaaggtt cagcggcagt 2160

ggatctggga cagagttcac tctcaccatc agcagcctgc agcctgatga ttttgcaact 2220

tattactgcc aacagtggag tcgtaaccca cccactttcg gcggagggac caaggtggag 2280

atcaaacggt cctccagcta a 2301

<210> 68
<211> 746
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC411 Anti-PSMA X anti-CD3 bispecific molecule

<400> 68

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        275                 280                 285
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```
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    290                 295                 300

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

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

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

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

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

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385                 390                 395                 400

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

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

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

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

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

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

```
Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser
            500                 505                 510

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser 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 Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met
                565                 570                 575

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr 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 Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    610                 615                 620

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

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

Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln
            660                 665                 670

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

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

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

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

Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
740 745

<210> 69
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> CAS105 Anti-CD37 X anti-CD3 bispecific molecule

<400> 69
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tcctgtaagg gctccggtta ctcattcact ggctacaata tgaactgggt gcgccagatg 180

cccgggaaag gcctggagtg gatgggcaat attgatcctt attatggtgg tactacctac 240

aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac 300

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tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc 540

accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa 600

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cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc 780

caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac 840

acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc 900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc 1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1200

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260

ctgacctgcc tggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat 1320

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1440

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500

ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct 1560

ccgaattctc aggtccagct ggtggagtct gggggcggag tggtgcagcc tgggcggtca 1620

ctgaggctgt cctgcaaggc ttctggctac acctttacta gatctacgat gcactgggta 1680

aggcaggccc ctggacaagg tctggaatgg attggataca ttaatcctag cagtgcttat 1740

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ggcaaggccc ccaaaagatg gatttatgac tcatccaaac tggcttctgg agtccctgct 2160

cgcttcagtg gcagtgggtc tgggaccgac tataccctca caatcagcag cctgcagccc 2220

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gggaccaagc tacaaattac atcctccagc taa 2313

<210> 70
<211> 750
<212> PRT
<213> Artificial Sequence

<220>
<223> CAS105 Anti-CD37 X anti-CD3 bispecific molecule

<400> 70

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
            20                  25                  30

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

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

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
    130                 135                 140

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

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

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

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

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

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
225                 230                 235                 240

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
            260                 265                 270

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285

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

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

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350

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

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

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415
```

```
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480

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

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

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

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

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

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

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

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

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

```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala
625                 630                 635                 640


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


Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
            660                 665                 670


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


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


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


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


Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
            740                 745                 750


<210>  71
<211>  2325
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Anti-CD37 X TSC445 anti-CD3 bispecific molecule

<400>  71
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt       60

gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt      120

tcctgtaagg gctccggtta ctcattcact ggctacaata tgaactgggt gcgccagatg      180

cccgggaaag gcctggagtg gatgggcaat attgatcctt attatggtgg tactacctac      240

aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac      300

ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc      360
```

ggcccttttcg actcctgggg ccagggcacc ctggtcactg tctcctctgg gggtggaggc 420

tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc 480

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc 540

accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa 600

cctggccagg ctcctaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca 660

gccaggttca gtggcagtgg ctccgggaca gacttcactc tcaccatcag cagcctagag 720

cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc 780

caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac 840

acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc 900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc 1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1200

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260

ctgacctgcc tggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat 1320

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1440

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500

ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct 1560

ccgaattctc aggtccagct ggtgcaatct gggcctgagg tgaagaagcc tgggtcctcg 1620

gtgaaggtct cctgcaaggc ttctggatat accttcagca gatctacgat gcactgggtg 1680

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acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg 1860

agaccccaag tccactatga ttacaacggg tttccttact ggggccaagg aaccctggtc 1920

accgtctcct caggtggagg cggttcaggc ggaggtggat ccggcggtgg cggatcgggt 1980

ggcggcggat ctgacatcca gatgacccag tctccttcca ccctgtctgc atctgtagga 2040

gacagagtca ccatgacttg cagtgccagc tcaagtgtaa gttacatgaa ctggtatcag 2100

cagaaaccag ggaaagcccc taagagatgg atttatgact catccaaact ggcttctggg 2160

gtcccatcaa ggttcagcgg cagtggatct gggacagagt tcactctcac catcagcagc 2220

ctgcagcctg atgattttgc aacttattac tgccaacagt ggagtcgtaa cccacccact 2280

ttcggcggag ggaccaaggt ggagatcaaa cggtcctcca gctaa 2325

<210> 72
<211> 754
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD37 X TSC445 anti-CD3 bispecific molecule

<400> 72

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

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

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

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

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

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

```
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
    130                 135                 140

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

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

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

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

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

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
225                 230                 235                 240

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
            260                 265                 270

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285

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

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

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
                325                 330                 335
```

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Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350

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

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

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480

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

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

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
        515                 520                 525

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

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


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


Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
            580                 585                 590


Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
        595                 600                 605


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


Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640


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


Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
            660                 665                 670


Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
        675                 680                 685


Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
    690                 695                 700


Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
705                 710                 715                 720


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


Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
            740                 745                 750
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Ser Ser

<210> 73
<211> 2325
<212> DNA
<213> Artificial Sequence

<220>
<223> Anti-CD37 X TSC452 anti-CD3 bispecific molecule

<400> 73
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gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt 120

tcctgtaagg gctccggtta ctcattcact ggctacaata tgaactgggt gcgccagatg 180

cccgggaaag gcctggagtg gatgggcaat attgatcctt attatggtgg tactacctac 240

aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac 300

ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc 360

ggcccctttcg actcctgggg ccagggcacc ctggtcactg tctcctctgg gggtggaggc 420

tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc 480

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc 540

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cctggccagg ctcctaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca 660

gccaggttca gtggcagtgg ctccgggaca gacttcactc tcaccatcag cagcctagag 720

cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc 780

caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac 840

acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc 900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc 1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1200

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260

ctgacctgcc tggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat 1320

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1440

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500

ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct 1560

ccgaattctc aggtccagct ggtggagtct gggggcggag tggtgcagcc tgggcggtca 1620

ctgaggctgt cctgcaaggc ttctggctac acctttacta gatctacgat gcactgggta 1680

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ggcggcggat ctgacatcca gatgacccag tctccttcca ccctgtctgc atctgtagga 2040

gacagagtca ccatgacttg cagtgccagc tcaagtgtaa gttacatgaa ctggtatcag 2100

cagaaaccag ggaaagcccc taagagatgg atttatgact catccaaact ggcttctggg 2160

gtcccatcaa ggttcagcgg cagtggatct gggacagagt tcactctcac catcagcagc 2220

ctgcagcctg atgattttgc aacttattac tgccaacagt ggagtcgtaa cccacccact 2280

ttcggcggag ggaccaaggt ggagatcaaa cggtcctcca gctaa 2325

<210> 74
<211> 754
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD37 X TSC452 anti-CD3 bispecific molecule

<400> 74

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

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Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
            20                  25                  30

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

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

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
    130                 135                 140

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

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

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

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

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

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
```

```
225                 230                 235                 240

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
            260                 265                 270

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285

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

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

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350

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

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

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430

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

```
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480

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

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

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

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

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

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

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

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

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
                645                 650                 655
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```
Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
            660                 665                 670

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
        675                 680                 685

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
    690                 695                 700

Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
705                 710                 715                 720

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

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
            740                 745                 750

Ser Ser
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<210> 75
<211> 2322
<212> DNA
<213> Artificial Sequence

<220>
<223> Anti-CD37 X TSC453 anti-CD3 bispecific molecule

<400> 75

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gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt      120

tcctgtaagg gctccggtta ctcattcact ggctacaata tgaactgggt gcgccagatg      180

cccgggaaag gcctggagtg gatgggcaat attgatcctt attatggtgg tactacctac      240

aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac      300

ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc      360

ggcccttttcg actcctgggg ccagggcacc ctggtcactg tctcctctgg gggtggaggc      420

tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc      480
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tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc 540

accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa 600

cctggccagg ctcctaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca 660

gccaggttca gtggcagtgg ctccgggaca gacttcactc tcaccatcag cagcctagag 720

cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc 780

caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac 840

acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc 900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc 1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1200

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260

ctgacctgcc tggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat 1320

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1440

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500

ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct 1560

ccgaattctc aggtccagct ggtgcaatct gggcctgagg tgaagaagcc tgggtcctcg 1620

gtgaaggtct cctgcaaggc ttctggatat accttcagca gatctacgat gcactgggtg 1680

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acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg 1860

agaccccaag tccactatga ttacaacggg tttccttact ggggccaagg aaccctggtc 1920

accgtctcct caggtggagg cggttcaggc ggaggtggat ccggaggtgg tggctctggt 1980

ggcggcggat ctgacatcca gatgacccag tctccaagca gcctgtctgc aagcgtgggg 2040

gacagggtca ccatgacctg cagtgccagc tcaagtgtaa gttacatgaa ctggtaccag 2100

cagaagccgg gcaaggcccc caaaagatgg atttatgact catccaaact ggcttctgga 2160

gtccctgctc gcttcagtgg cagtgggtct gggaccgact ataccctcac aatcagcagc 2220

ctgcagcccg aagatttcgc cacttattac tgccagcagt ggagtcgtaa cccacccacg 2280

ttcggagggg ggaccaagct acaaattaca tcctccagct aa 2322

<210> 76
<211> 753
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD37 X TSC453 anti-CD3 bispecific molecule

<400> 76

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

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

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

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

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

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

```
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
    130                 135                 140

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

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

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

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

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

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
225                 230                 235                 240

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
            260                 265                 270

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285

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

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

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
```

```
            340                 345                 350

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

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

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480

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

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

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
        515                 520                 525

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

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

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

Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
            580                 585                 590

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
        595                 600                 605

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640

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

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
            660                 665                 670

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
        675                 680                 685

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg
    690                 695                 700

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser
705                 710                 715                 720

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg
                725                 730                 735

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser
            740                 745                 750

Ser
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<210> 77
<211> 2325
<212> DNA
<213> Artificial Sequence

<220>
<223> Anti-CD37 X TSC454 anti-CD3 bispecific molecule

<400> 77
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gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt 120

tcctgtaagg gctccggtta ctcattcact ggctacaata tgaactgggt gcgccagatg 180

cccgggaaag gcctggagtg gatgggcaat attgatcctt attatggtgg tactacctac 240

aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac 300

ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc 360

ggcccctttcg actcctgggg ccagggcacc ctggtcactg tctcctctgg gggtggaggc 420

tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc 480

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc 540

accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa 600

cctggccagg ctcctaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca 660

gccaggttca gtggcagtgg ctccgggaca gacttcactc tcaccatcag cagcctagag 720

cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc 780

caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac 840

acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc 900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc 1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1200

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260

ctgacctgcc tggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat 1320

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1440

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500

ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct 1560

ccgaattctc aggtccagct ggtgcaatct gggcctgagg tgaagaagcc tgggtcctcg 1620

gtgaaggtct cctgcaaggc ttctggatat accttcagca gatctacgat gcactgggtg 1680

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acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg 1860

agaccccaag tccactatga ttacaacggg tttccttact ggggccaagg aaccctggtc 1920

accgtctcct caggtggagg cggttcaggc ggaggtggat ccggcggtgg cggatcgggt 1980

ggcggcggat ctgacatcca gatgacccag tctccttcca ccctgtctgc atctgtagga 2040

gacagagtca ccatgacttg cagtgccagc tcaagtgtaa gttacatgaa ctggtatcag 2100

cagaaaccag ggaaagcccc taagagatgg atttatgact catccaaact ggcttctggg 2160

gtcccatcaa ggttcagcgg cagtggatct gggacagatt tcactctcac catcagcagc 2220

ctgcagcctg atgattttgc aacttattac tgccaacagt ggagtcgtaa cccacccact 2280

ttcggcggag ggaccaaggt ggagatcaaa cggtcctcca gctaa 2325

<210> 78
<211> 754
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD37 X TSC454 anti-CD3 bispecific molecule

<400> 78

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

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

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

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
    130                 135                 140

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

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

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

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

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

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
225                 230                 235                 240
```

```
Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
                245                 250                 255

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
            260                 265                 270

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285

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

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

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350

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

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

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
```

```
    450                 455                 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480

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

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

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
        515                 520                 525

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

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

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

Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
            580                 585                 590

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
        595                 600                 605

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640

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

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
            660                 665                 670
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```
Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
        675                 680                 685

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
    690                 695                 700

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
705                 710                 715                 720

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

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
            740                 745                 750

Ser Ser
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<210> 79
<211> 2325
<212> DNA
<213> Artificial Sequence

<220>
<223> Anti-CD37 X TSC455 anti-CD3 bispecific molecule

<400> 79

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gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggagagtc tctgaagatt      120

tcctgtaagg gctccggtta ctcattcact ggctacaata tgaactgggt gcgccagatg      180

cccgggaaag gcctggagtg gatgggcaat attgatcctt attatggtgg tactacctac      240

aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac      300

ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc      360

ggcccttttcg actcctgggg ccagggcacc ctggtcactg tctcctctgg gggtggaggc      420

tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc      480

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc      540
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accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa 600

cctggccagg ctcctaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca 660

gccaggttca gtggcagtgg ctccgggaca gacttcactc tcaccatcag cagcctagag 720

cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc 780

caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac 840

acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc 900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc 1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1200

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260

ctgacctgcc tggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat 1320

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1440

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500

ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct 1560

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gtgaaggtct cctgcaaggc ttctggatat accttcagca gatctacgat gcactgggtg 1680

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acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg 1860

agaccccaag tccactatga ttacaacggg tttccttact ggggccaagg aaccctggtc 1920

accgtctcct caggtggagg cggttcaggc ggaggtggat ccggcggtgg cggatcgggt 1980

ggcggcggat ctgacatcca gatgacccag tctccttcca ccctgtctgc atctgtagga 2040

gacagagtca ccatgacttg cagtgccagc tcaagtgtaa gttacatgaa ctggtatcag 2100

cagaaaccag ggaaagcccc taagagatgg atttatgact catccaaact ggcttctggg 2160

gtcccatcaa ggttcagcgg cagtggatct gggacagagt atactctcac catcagcagc 2220

ctgcagcctg atgattttgc aacttattac tgccaacagt ggagtcgtaa cccacccact 2280

ttcggcggag ggaccaaggt ggagatcaaa cggtcctcca gctaa 2325

<210> 80
<211> 754
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD37 X TSC455 anti-CD3 bispecific molecule

<400> 80

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

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

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

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
130 135 140

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

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

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

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

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

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
225                 230                 235                 240

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
            260                 265                 270

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285

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

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

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350
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```
Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
        355                 360                 365

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

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480

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

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

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
        515                 520                 525

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

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

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

Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
            580                 585                 590

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
        595                 600                 605

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640

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

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
            660                 665                 670

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
        675                 680                 685

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
    690                 695                 700

Phe Ser Gly Ser Gly Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Ser
705                 710                 715                 720

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

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
            740                 745                 750

Ser Ser
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<210> 81
<211> 2325

<212> DNA
<213> Artificial Sequence

<220>
<223> Anti-CD37 X TSC456 anti-CD3 bispecific molecule

<400> 81
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tcctgtaagg gctccggtta ctcattcact ggctacaata tgaactgggt gcgccagatg 180

cccgggaaag gcctggagtg gatgggcaat attgatcctt attatggtgg tactacctac 240

aaccggaagt tcaagggcca ggtcactatc tccgccgaca agtccatcag caccgcctac 300

ctgcaatgga gcagcctgaa ggcctcggac accgccatgt attactgtgc acgctcagtc 360

ggcccttttcg actcctgggg ccagggcacc ctggtcactg tctcctctgg gggtggaggc 420

tctggtggcg gtggctctgg cggaggtgga tccggtggcg gcggatctgg cgggggtggc 480

tctgaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg cgaaagagcc 540

accctctcct gccgagcaag tgaaaatgtt tacagctact tagcctggta ccaacagaaa 600

cctggccagg ctcctaggct cctcatctat tttgcaaaaa ccttagcaga aggtattcca 660

gccaggttca gtggcagtgg ctccgggaca gacttcactc tcaccatcag cagcctagag 720

cctgaagatt ttgcagttta ttactgtcaa catcattccg ataatccgtg gacattcggc 780

caagggacca aggtggaaat caaatcctcg agtgagccca aatcttctga caaaactcac 840

acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc 900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg catacgcgtg cgcggtctcc 1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1200

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260

ctgacctgcc tggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat 1320

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1440

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500

ccgggtcaga ggcacaacaa ttcttccctg aatacaggaa ctcagatggc aggtcattct 1560

ccgaattctc aggtccagct ggtgcaatct gggcctgagg tgaagaagcc tgggtcctcg 1620

gtgaaggtct cctgcaaggc ttctggatat accttcagca gatctacgat gcactgggtg 1680

cgacaggccc ctggacaagg gcttgagtgg ataggataca ttaatcctag cagtgcttat 1740

actaattaca atcagaaatt caaggacaga gtcacgatta ccgcggacaa atccacgagc 1800

acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg 1860

agaccccaag tccactatga ttacaacggg tttccttact ggggccaagg aaccctggtc 1920

accgtctcct caggtggagg cggttcaggc ggaggtggat ccggcggtgg cggatcgggt 1980

ggcggcggat ctgacatcca gatgacccag tctccttcca ccctgtctgc atctgtagga 2040

gacagagtca ccatgacttg cagtgccagc tcaagtgtaa gttacatgaa ctggtatcag 2100

cagaaaccag ggaaagcccc taagagatgg atttatgact catccaaact ggcttctggg 2160

gtcccatcaa ggttcagcgg cagtggatct gggacagatt atactctcac catcagcagc 2220

ctgcagcctg atgattttgc aacttattac tgccaacagt ggagtcgtaa cccacccact 2280

ttcggcggag ggaccaaggt ggagatcaaa cggtcctcca gctaa 2325

<210> 82
<211> 754
<212> PRT
<213> Artificial Sequence

<220>
<223> Anti-CD37 X TSC456 anti-CD3 bispecific molecule

<400> 82

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

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

```
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe
    50                  55                  60

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
    130                 135                 140

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

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

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

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

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

Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe Gly
225                 230                 235                 240

Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser Ser
                245                 250                 255
```

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
            260                 265                 270

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
        275                 280                 285

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

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

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            340                 345                 350

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

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

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
                405                 410                 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            420                 425                 430

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
    450                 455                 460
```

```
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465                 470                 475                 480

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

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

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
        515                 520                 525

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

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

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

Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
            580                 585                 590

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr
        595                 600                 605

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
625                 630                 635                 640

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

Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser
            660                 665                 670

Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
```

675 680 685

Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg
690 695 700

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser
705 710 715 720

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

Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
740 745 750

Ser Ser

<210> 83
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC455 CD3 scFv CD3-binding domain

<400> 83

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

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

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

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

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
    130                 135                 140

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

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

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

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

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

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

Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
                245                 250
```

<210> 84
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC456 CD3 scFv CD3-binding domain

<400> 84

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

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

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

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

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
    130                 135                 140

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

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

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

Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
        195                 200                 205
```

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

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

Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
                245                 250
```

<210> 85
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> DRA222 CD3 scFv CD3-binding domain

<400> 85

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

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

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

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

Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65                  70                  75                  80

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
                85                  90                  95

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

Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
```

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

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

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

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

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

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

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

Leu Gln Ile Thr Ser Ser Ser
                245
```

<210> 86
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC455 and TSC456 variable heavy domain CD3-binding domain

<400> 86

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

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

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

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


Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


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


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


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  87
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  DRA222 variable heavy domain CD3-binding domain

<400>  87

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


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


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


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


Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe
65                  70                  75                  80


Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
```

85 90 95

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

Gln Gly Thr Pro Val Thr Val Ser Ser
115 120

<210> 88
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC455 variable light domain CD3-binding domain

<400> 88

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

Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

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

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

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

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

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

<210> 89
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC456 variable light domain CD3-binding domain

<400> 89

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

Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            20   25   30

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

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

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

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

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

<210> 90
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> DRA222 variable light domain CD3-binding domain

<400> 90

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

Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
            20   25   30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr

```
        35                  40                  45

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

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

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

Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser
            100                 105
```

<210> 91
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7 and DRA222 VH CDR1 (Kabat) CD3-binding domain

<400> 91

```
Arg Ser Thr Met His
1               5
```

<210> 92
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7 and DRA222 VH CDR2 (Kabat) CD3-binding domain

<400> 92

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

<210> 93
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Cris7 and DRA222 VH CDR3 (Kabat) CD3-binding domain

<400> 93

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

<210> 94
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7 and DRA222 VL CDR1 (Kabat) CD3-binding domain

<400> 94

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

<210> 95
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7 and DRA222 VL CDR2 (Kabat) CD3-binding domain

<400> 95

Asp Ser Ser Lys Leu Ala Ser
1   5

<210> 96
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7 and DRA222 VL CDR3 (Kabat) CD3-binding domain

<400> 96

Gln Gln Trp Ser Arg Asn Pro Pro Thr
1   5

<210> 97
<211> 2304
<212> DNA

<213> Artificial Sequence

<220>
<223> ROR133 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 97
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc 180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc 240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc 300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc 360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc 420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc 480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac 540

gactacccca tctcctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc 600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc 660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc 720

gccgtgtact attgcgcccg gggctactcc acctactacg gcgacttcaa catctggggc 780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct 1560

caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 1620

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 1680

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 1740

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 1800

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc 2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 2220

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 2280

ctacaaatta catcctccag ctaa 2304

<210> 98
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR133 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 98

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 Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
20 25 30

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

```
Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

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

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

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
            100                 105                 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

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

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

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

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Gly Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255
```

```
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

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

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

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

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

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

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
```

```
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
            740                 745
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<210> 99
<211> 2316
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR193 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 99

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gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc      120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc      180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc      240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc      300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc      360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc      420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc      480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac      540

gactacccca tctcctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc      600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc      660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc      720

gccgtgtact attgcgcccg gggctactcc acctactacg gcgacttcaa catctggggc      780
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cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

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ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

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caggtccagc tggtgcaatc tgggcctgag gtgaagaagc ctgggtcctc ggtgaaggtc 1620

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gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc 1920

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tctgacatcc agatgaccca gtctccttcc accctgtctg catctgtagg agacagagtc 2040

accatgactt gcagtgccag ctcaagtgta agttacatga actggtatca gcagaaacca 2100

gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca 2160

aggttcagcg gcagtggatc tgggacagag tatactctca ccatcagcag cctgcagcct 2220

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gggaccaagg tggagatcaa acggtcctcc agctaa 2316

<210> 100
<211> 751
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR193 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 100

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 Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
20 25 30

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

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

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

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

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

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

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145 150 155 160

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

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Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Gly Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

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

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

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

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

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

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

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

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

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

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

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

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
            580                 585                 590

Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
```

595 600 605

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625 630 635 640

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

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
660 665 670

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
740 745 750

<210> 101
<211> 2304
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR134 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 101
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gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc 180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc 240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc 300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc 360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc 420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc 480

ctggtgcagc ccggcggctc cctgcggctg tcctgcaccg cctccggctc cgacatcaac 540

gactacccca tctcctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc 600

atcaactccg gcggctccac ctggtacgcc gactcggtga agggccggtt caccatctcc 660

cggcactcct ccaagaacac cctgtacctg cagatgaact ccctgcgggc cgaggacacc 720

gccgtgtact tctgcgcccg gggctactcc acctactacg gcgacttcaa catctggggc 780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

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cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 1740

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ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc 2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 2220

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 2280

ctacaaatta catcctccag ctaa 2304

<210> 102
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR134 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 102

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 Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
20 25 30

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

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

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

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

```
Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
            100                 105                 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

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

Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

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

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Asp Ser
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg His Ser Ser Lys Asn Thr Leu
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Gly Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

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

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

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

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

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

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 103
<211> 2316
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR189 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 103
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gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc 180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc 240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc 300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc 360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc 420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc 480

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gccgtgtact tctgcgcccg gggctactcc acctactacg gcgacttcaa catctggggc 780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

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cctggacaag ggcttgagtg gataggatac attaatccta gcagtgctta tactaattac 1740

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atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaccccaa 1860

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc 1920

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga 1980

tctgacatcc agatgaccca gtctccttcc accctgtctg catctgtagg agacagagtc 2040

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gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca 2160

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gggaccaagg tggagatcaa acggtcctcc agctaa 2316

<210> 104
<211> 751
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR189 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 104

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

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Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
            20                  25                  30

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

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

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

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

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
            100                 105                 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

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

Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

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

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Asp Ser
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg His Ser Ser Lys Asn Thr Leu
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
    210                 215                 220
```

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Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Gly Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

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

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

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

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

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

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

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

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

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

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

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

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
            580                 585                 590

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

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640
```

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

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
            660                 665                 670

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
            740                 745                 750
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<210> 105
<211> 2304
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR154 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 105
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc 180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc 240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc 300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc 360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc 420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc 480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac 540

gactacccca tcacctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc 600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc 660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc 720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc 780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct 1560

caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 1620

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 1680

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 1740

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 1800

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc 2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 2220

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 2280

ctacaaatta catcctccag ctaa 2304

<210> 106
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR154 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 106

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

Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
20 25 30

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

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

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

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

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

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

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    130                 135                 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

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

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350
```

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

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

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

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

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

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560
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```
Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys
                565                 570                 575

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

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

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

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

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

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

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

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

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

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

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
            740                 745
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<210> 107
<211> 2316
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR185 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 107
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gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc 180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc 240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc 300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc 360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc 420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc 480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac 540

gactacccca tcacctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc 600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc 660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc 720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc 780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

aaagccctcc cagccccca cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

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cctggacaag ggcttgagtg gataggatac attaatccta gcagtgctta tactaattac 1740

aatcagaaat tcaaggacag agtcacgatt accgcggaca aatccacgag cacagcctac 1800

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaccccaa 1860

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc 1920

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga 1980

tctgacatcc agatgaccca gtctccttcc accctgtctg catctgtagg agacagagtc 2040

accatgactt gcagtgccag ctcaagtgta agttacatga actggtatca gcagaaacca 2100

gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca 2160

aggttcagcg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct 2220

gatgattttg caacttatta ctgccaacag tggagtcgta acccacccac tttcggcgga 2280

gggaccaagg tggagatcaa acggtcctcc agctaa 2316

<210> 108
<211> 751
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR185 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 108

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 Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
20 25 30

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

```
Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

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

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

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
            100                 105                 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

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

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
```

```
            260                 265                 270

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

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

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

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

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

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

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480
```

```
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

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

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

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

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

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

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
            580                 585                 590

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

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640

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

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
            660                 665                 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
        675                 680                 685
```

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
            740                 745                 750
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<210> 109
<211> 2304
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR179 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 109
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gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc 180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc 240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc 300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ctggacctcc 360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc 420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc 480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac 540

gactacccca tcacctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc 600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc 660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc 720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc 780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

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ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct 1560

caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 1620

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 1680

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 1740

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 1800

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc 2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 2220

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 2280

ctacaaatta catcctccag ctaa 2304

<210> 110

<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR179 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 110

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 Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
20 25 30

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

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

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

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

Tyr Trp Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

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

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145 150 155 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
165 170 175

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Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

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

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

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

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

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

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
405 410 415

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
450 455 460

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
485 490 495

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
            740                 745
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<210> 111
<211> 2316
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR186 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 111
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gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc 180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc 240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc 300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ctggacctcc 360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc 420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc 480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac 540

gactacccca tcacctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc 600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc 660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc 720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc 780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440

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ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct 1560

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cctggacaag ggcttgagtg gataggatac attaatccta gcagtgctta tactaattac 1740

aatcagaaat tcaaggacag agtcacgatt accgcggaca aatccacgag cacagcctac 1800

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaccccaa 1860

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc 1920

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga 1980

tctgacatcc agatgaccca gtctccttcc accctgtctg catctgtagg agacagagtc 2040

accatgactt gcagtgccag ctcaagtgta agttacatga actggtatca gcagaaacca 2100

gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca 2160

aggttcagcg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct 2220

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gggaccaagg tggagatcaa acggtcctcc agctaa 2316

<210> 112
<211> 751
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR186 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 112

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 Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
20 25 30

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

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

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

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

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Tyr Trp Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
            100                 105                 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

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

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300
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```
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

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

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

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

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

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

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
```

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        515                 520                 525

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

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

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

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
            580                 585                 590

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

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640

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

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
            660                 665                 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
        675                 680                 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    690                 695                 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705                 710                 715                 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
                725                 730                 735
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Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
740 745 750

<210> 113
<211> 2304
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR181 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 113
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gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc 180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc 240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc 300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc 360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc 420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc 480

ctggtgcagc ccggcggctc cctgcggctg tcctgcaccg tgtccggcac cgacatcaac 540

gactacccca tctcctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc 600

atcaactccg gcggctccac ctggtacgcc gactcggtga agggccggtt caccatctcc 660

cggcactcct ccaagaacac cctgtacctg cagatgaact ccctgcgggc cgaggacacc 720

gccgtgtact tctgcgcccg gggctactcc acctactacc gggacttcaa catctggggc 780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

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caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 1620

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 1680

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 1740

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 1800

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc 2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 2220

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 2280

ctacaaatta catcctccag ctaa 2304

<210> 114
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR181 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 114

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
            20                  25                  30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
                85                  90                  95

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
            100                 105                 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Gly Ser Leu Arg Leu Ser Cys Thr Val Ser Gly Thr Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Asp Ser
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg His Ser Ser Lys Asn Thr Leu
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
    210                 215                 220
```

```
Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
        275                 280                 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
385                 390                 395                 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430
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Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
            500                 505                 510

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560

Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys
                565                 570                 575

Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
            580                 585                 590

Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
        595                 600                 605

Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile
625                 630                 635                 640

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
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645 650 655

Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
660 665 670

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser
675 680 685

Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
690 695 700

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
705 710 715 720

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly
725 730 735

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
740 745

<210> 115
<211> 2316
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR191 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 115
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gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc 180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc 240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc 300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc 360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc 420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc 480

ctggtgcagc ccggcggctc cctgcggctg tcctgcaccg tgtccggcac cgacatcaac 540

gactacccca tctcctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc 600

atcaactccg gcggctccac ctggtacgcc gactcggtga agggccggtt caccatctcc 660

cggcactcct ccaagaacac cctgtacctg cagatgaact ccctgcgggc cgaggacacc 720

gccgtgtact tctgcgcccg gggctactcc acctactacc gggacttcaa catctggggc 780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

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ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct 1560

caggtccagc tggtgcaatc tgggcctgag gtgaagaagc ctgggtcctc ggtgaaggtc 1620

tcctgcaagg cttctggata taccttcagc agatctacga tgcactgggt gcgacaggcc 1680

cctggacaag ggcttgagtg gataggatac attaatccta gcagtgctta tactaattac 1740

aatcagaaat tcaaggacag agtcacgatt accgcggaca aatccacgag cacagcctac 1800

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaccccaa 1860

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc 1920

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga 1980

tctgacatcc agatgaccca gtctccttcc accctgtctg catctgtagg agacagagtc 2040

accatgactt gcagtgccag ctcaagtgta agttacatga actggtatca gcagaaacca 2100

gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca 2160

aggttcagcg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct 2220

gatgattttg caacttatta ctgccaacag tggagtcgta acccacccac tttcggcgga 2280

gggaccaagg tggagatcaa acggtcctcc agctaa 2316

<210> 116
<211> 751
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR191 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 116

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 Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
35 40 45

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
85 90 95

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

```
Gly Gly Ser Leu Arg Leu Ser Cys Thr Val Ser Gly Thr Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                165                 170                 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Asp Ser
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg His Ser Ser Lys Asn Thr Leu
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
        275                 280                 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350
```

```
Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
385                 390                 395                 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
            500                 505                 510

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560
```

```
Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
                565                 570                 575

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
            580                 585                 590

Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
        595                 600                 605

Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
                645                 650                 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
            660                 665                 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
        675                 680                 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    690                 695                 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705                 710                 715                 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
                725                 730                 735

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
            740                 745                 750
```

<210> 117
<211> 2304
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR182 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 117
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc 180

ggccagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgcccgac 240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctggaggcc 300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc 360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc 420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc 480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac 540

gactacccca tcacctgggt gcggcaggcc cccggccagg gcctggagtg gatcggcttc 600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc 660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc 720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc 780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct 1560

caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 1620

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 1680

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 1740

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 1800

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc 2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 2220

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 2280

ctacaaatta catcctccag ctaa 2304

<210> 118
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR182 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 118

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 Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
35 40 45

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser Gly

```
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Ala
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
                85                  90                  95

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
            100                 105                 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
                165                 170                 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270
```

```
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
        275                 280                 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
385                 390                 395                 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480
```

```
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
            500                 505                 510

Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560

Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys
                565                 570                 575

Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
            580                 585                 590

Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
        595                 600                 605

Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile
625                 630                 635                 640

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
                645                 650                 655

Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp
            660                 665                 670

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser
        675                 680                 685
```

```
Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser
    690                 695                 700

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
705                 710                 715                 720

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly
                725                 730                 735

Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
            740                 745
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<210> 119
<211> 2316
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR192 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 119

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atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt       60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc      120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc      180

ggccagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgcccgac      240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctggaggcc      300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc      360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc      420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc      480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac      540

gactacccca tcacctgggt gcggcaggcc cccggccagg gcctggagtg gatcggcttc      600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc      660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc      720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc      780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca      840
```

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct 1560

caggtccagc tggtgcaatc tgggcctgag gtgaagaagc ctgggtcctc ggtgaaggtc 1620

tcctgcaagg cttctggata taccttcagc agatctacga tgcactgggt gcgacaggcc 1680

cctggacaag ggcttgagtg gataggatac attaatccta gcagtgctta tactaattac 1740

aatcagaaat tcaaggacag agtcacgatt accgcggaca aatccacgag cacagcctac 1800

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaccccaa 1860

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc 1920

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga 1980

tctgacatcc agatgaccca gtctccttcc accctgtctg catctgtagg agacagagtc 2040

accatgactt gcagtgccag ctcaagtgta agttacatga actggtatca gcagaaacca 2100

gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca 2160

aggttcagcg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct 2220

gatgattttg caacttatta ctgccaacag tggagtcgta acccacccac tttcggcgga 2280

gggaccaagg tggagatcaa acggtcctcc agctaa 2316

<210> 120
<211> 751

<212> PRT
<213> Artificial Sequence

<220>
<223> ROR192 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 120

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 Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
35 40 45

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Ala
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
85 90 95

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145 150 155 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
165 170 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp

```
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205

Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
        275                 280                 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
385                 390                 395                 400
```

```
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
            500                 505                 510

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525

Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540

Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560

Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
                565                 570                 575

Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
            580                 585                 590

Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
        595                 600                 605
```

```
Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
                645                 650                 655

Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
            660                 665                 670

Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
        675                 680                 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    690                 695                 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705                 710                 715                 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
                725                 730                 735

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
            740                 745                 750
```

<210> 121
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> sss(s)-hIgG1 hinge

<400> 121

```
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Ser
1               5                   10                  15
```

<210> 122
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> csc(s)-hIgG1 hinge

<400> 122

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Ser
1   5   10   15

<210> 123
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> ssc(s)-hIgG1 hinge

<400> 123

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Ser
1   5   10   15

<210> 124
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> scc(s)-hIgG1 hinge

<400> 124

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Ser
1   5   10   15

<210> 125
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> css(s)-hIgG1 hinge

<400> 125

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Ser
1   5   10   15

<210> 126
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> scs(s)-hIgG1 hinge

<400> 126

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Ser
1   5   10   15

<210> 127
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> ccc(s)-hIgG1 hinge

<400> 127

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Ser
1   5   10   15

<210> 128
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> ccc(p)-hIgG1 hinge

<400> 128

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
1   5   10   15

<210> 129
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> sss(p)-hIgG1 hinge

<400> 129

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
1   5   10   15

<210> 130
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> csc(p)-hIgG1 hinge

<400> 130

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
1   5   10   15

<210> 131
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> ssc(p)-hIgG1 hinge

<400> 131

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro
1   5   10   15

<210> 132
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> scc(p)-hIgG1 hinge

<400> 132

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1   5   10   15

<210> 133
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> css(p)-hIgG1 hinge

<400> 133

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Pro
1 5 10 15

<210> 134
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> scs(p)-hIgG1 hinge

<400> 134

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Pro
1 5 10 15

<210> 135
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Scppcp linker

<400> 135

Ser Cys Pro Pro Cys Pro
1 5

<210> 136
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> STD1 linker

<400> 136

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> 137
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> STD2 linker

<400> 137

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> 138
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> H1 linker

<400> 138

Asn Ser
1

<210> 139
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> H2 linker

<400> 139

Gly Gly Gly Gly Ser Gly Asn Ser
1   5

<210> 140
<211> 10
<212> PRT

<213> Artificial Sequence

<220>
<223> H3 linker

<400> 140

Asn Tyr Gly Gly Gly Gly Ser Gly Asn Ser
1   5   10

<210> 141
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> H4 linker

<400> 141

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser
1   5   10

<210> 142
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H5 linker

<400> 142

Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser
1   5   10   15

<210> 143
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> H6 linker

<400> 143

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1   5   10   15

Asn Ser

<210> 144
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> H7 linker

<400> 144

Gly Cys Pro Pro Cys Pro Asn Ser
1   5

<210> 145
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> (G4S)3 linker

<400> 145

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1   5   10   15

<210> 146
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> H105 linker

<400> 146

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1   5   10   15

<210> 147
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> (G4S)4 linker

<400> 147

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 148
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H75 (NKG2A quadruple mutant) linker

<400> 148

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> 149
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> H83 (NKG2A derived) linker

<400> 149

Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser
1 5 10 15

<210> 150
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> H106 (NKG2A derived) linker

<400> 150

Gln Arg His Asn Asn Ser Ser Leu Asn Thr Gly Thr Gln Met Ala Gly
1   5   10   15

His Ser

<210> 151
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> H81 (NKG2D derived) linker

<400> 151

Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr Ser Pro Asn Ser
1   5   10

<210> 152
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H91 (NKG2D derived) linker

<400> 152

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> 153
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> H94 linker

<400> 153

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1   5   10   15

Pro Asn Ser

<210> 154
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H16 hinge

<400> 154

Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
1 5 10 15

<210> 155
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H17 hinge

<400> 155

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> 156
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H18 hinge

<400> 156

Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
1 5 10 15

<210> 157
<211> 20

<212> PRT
<213> Artificial Sequence

<220>
<223> H19 hinge

<400> 157

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> 158
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H20 hinge

<400> 158

Leu Lys Ile Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Asn Ser
1   5   10   15

<210> 159
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H21 hinge

<400> 159

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> 160
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H22 hinge

<400> 160

Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Asn Ser
1   5   10   15

<210> 161
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H23 hinge

<400> 161

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> 162
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H24 hinge

<400> 162

Arg Glu Gln Leu Ala Glu Val Thr Leu Ser Leu Lys Ala Asn Ser
1   5   10   15

<210> 163
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H25 hinge

<400> 163

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> 164
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H26 hinge

<400> 164

Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
1   5   10   15

<210> 165
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H27 hinge

<400> 165

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> 166
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H28 hinge

<400> 166

Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Ser Asn Ser
1   5   10   15

<210> 167

<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H30 hinge

<400> 167

Leu Pro Pro Glu Thr Gln Glu Ser Gln Glu Val Thr Leu Asn Ser
1   5   10   15

<210> 168
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H32 hinge

<400> 168

Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro Asn Ser
1   5   10   15

<210> 169
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> H33 hinge

<400> 169

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> 170
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> H36 hinge

<400> 170

Gly Cys Pro Pro Cys Pro Gly Gly Gly Gly Ser Asn Ser
1 5 10

<210> 171
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> H40 hinge

<400> 171

Gly Cys Pro Pro Cys Pro Ala Asn Ser
1 5

<210> 172
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> H41 hinge

<400> 172

Gly Cys Pro Pro Cys Pro Ala Asn Ser
1 5

<210> 173
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> H42 hinge

<400> 173

Gly Cys Pro Pro Cys Pro Asn Ser
1 5

<210> 174
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> H44 hinge

<400> 174

Gly Gly Gly Ala Ser Cys Pro Pro Cys Pro Gly Asn Ser
1   5   10

<210> 175
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> H45 hinge

<400> 175

Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Gly Asn Ser
1   5   10

<210> 176
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> H46 hinge

<400> 176

Gly Gly Gly Ala Ser Cys Pro Pro Cys Ala Asn Ser
1   5   10

<210> 177
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H47 hinge

<400> 177

Leu Ser Val Lys Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
1   5   10   15

<210> 178
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> H48 hinge

<400> 178

Ala Asp Phe Leu Thr Pro Ser Ile Gly Asn Ser
1   5   10

<210> 179
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H50 hinge

<400> 179

Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
1   5   10   15

<210> 180
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H51 hinge

<400> 180

Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Gly Asn Ser
1   5   10   15

<210> 181
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> H52 hinge

<400> 181

Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ser
1   5   10

<210> 182
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> H53 hinge

<400> 182

Ser Gln Pro Glu Ile Val Pro Ile Ser Cys Pro Pro Cys Pro Asn Ser
1   5   10   15

<210> 183
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> H54 hinge

<400> 183

Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Ser Cys Pro Pro Cys
1   5   10   15

Pro Asn Ser

<210> 184
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H55 hinge

<400> 184

Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
1   5   10   15

<210> 185
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> H56 hinge

<400> 185

Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Ser
1   5   10

<210> 186
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> H57 hinge

<400> 186

Val Ser Glu Arg Pro Phe Pro Pro Asn Ser
1   5   10

<210> 187
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H58 hinge

<400> 187

Lys Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys Pro Asn Ser
1   5   10   15

<210> 188
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> H59 hinge

<400> 188

Lys Pro Phe Phe Thr Cys Gly Ser Ala Asp Thr Cys Pro Asn Ser
1   5   10   15

<210> 189
<211> 15
<212> PRT

<213> Artificial Sequence

<220>
<223> H60 hinge

<400> 189

Gln Tyr Asn Cys Pro Gly Gln Tyr Thr Phe Ser Met Pro Asn Ser
1 5 10 15

<210> 190
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H61 hinge

<400> 190

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> 191
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> H62 hinge

<400> 191

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> 192
<211> 20
<212> PRT
<213> Artificial Sequence

<220>

<223> H63 hinge

<400> 192

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> 193
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> ((Gly4Ser)3) linker

<400> 193

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1   5   10   15

<210> 194
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> (Gly4Ser)n linker

<220>
<221> MISC_FEATURE
<222> (6)..(25)
<223> amino acid residues may be absent

<400> 194

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1   5   10   15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
            20   25

<210> 195
<211> 20
<212> PRT

<213> Artificial Sequence

<220>
<223> secretory signal sequence

<400> 195

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> 196
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> H111 linker

<400> 196

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

Pro Gly Ser

<210> 197
<211> 751
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric bispecific anti-CD123 (VLVH) x anti-CD3 (TSC456) scFv-Fc-scFv CD3-binding domain

<400> 197

Asp Ile Met Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
1 5 10 15

Glu Lys Phe Thr Met Thr Cys Lys Ser Ser Gln Ser Leu Phe Phe Gly
20 25 30

Ser Thr Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

```
        35                  40                  45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ala
65                  70                  75                  80

Ile Ser Ser Val Met Pro Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

Tyr Tyr Asn Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100                 105                 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
    130                 135                 140

Lys Pro Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Asp Tyr Ser
145                 150                 155                 160

Ile Thr Ser Gly Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn
                165                 170                 175

Lys Leu Glu Trp Met Gly Tyr Ile Ser Tyr Asp Gly Ser Asn Asn Tyr
            180                 185                 190

Asn Pro Ser Leu Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys
        195                 200                 205

Asn Gln Phe Phe Leu Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala
    210                 215                 220

Thr Tyr Tyr Cys Ser Arg Gly Glu Gly Phe Tyr Phe Asp Ser Trp Gly
225                 230                 235                 240

Gln Gly Thr Thr Leu Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255
```

```
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
        275                 280                 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
385                 390                 395                 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460
```

```
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495


Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys
            500                 505                 510


Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
        515                 520                 525


Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
    530                 535                 540


Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr
545                 550                 555                 560


Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
                565                 570                 575


Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
            580                 585                 590


Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe
        595                 600                 605


Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
    610                 615                 620


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640


Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
                645                 650                 655


Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr
            660                 665                 670
```

```
Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile
        675                 680                 685

Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    690                 695                 700

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
705                 710                 715                 720

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro
                725                 730                 735

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser Ser
            740                 745                 750
```

<210> 198
<211> 753
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric bispecific anti-CD123 (VHVL) x anti-CD3 (TSC456) scFv-Fc-scFv CD3-binding domain

<400> 198

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Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Ser
1               5                   10                  15

Leu Ser Leu Thr Cys Ser Val Thr Asp Tyr Ser Ile Thr Ser Gly Tyr
            20                  25                  30

Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp Met
        35                  40                  45

Gly Tyr Ile Ser Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu Lys
    50                  55                  60

Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe Leu
65                  70                  75                  80

Lys Leu Ser Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ser
                85                  90                  95
```

```
Arg Gly Glu Gly Phe Tyr Phe Asp Ser Trp Gly Gln Gly Thr Thr Leu
            100                 105                 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Met Met Ser Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ala Val Ser Val Gly Glu Lys Phe Thr Met Thr Cys Lys
145                 150                 155                 160

Ser Ser Gln Ser Leu Phe Phe Gly Ser Thr Gln Lys Asn Tyr Leu Ala
                165                 170                 175

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp
            180                 185                 190

Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly
        195                 200                 205

Ser Gly Thr Asp Phe Thr Leu Ala Ile Ser Ser Val Met Pro Glu Asp
    210                 215                 220

Leu Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn Tyr Pro Trp Thr Phe
225                 230                 235                 240

Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Ser Ser Glu Pro Lys Ser
                245                 250                 255

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
            260                 265                 270

Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
        275                 280                 285

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
    290                 295                 300
```

```
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
305                 310                 315                 320

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
                325                 330                 335

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            340                 345                 350

Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
        355                 360                 365

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
    370                 375                 380

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
385                 390                 395                 400

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
                405                 410                 415

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            420                 425                 430

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
        435                 440                 445

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
    450                 455                 460

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
465                 470                 475                 480

Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                485                 490                 495

Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu
            500                 505                 510
```

```
Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly
        515                 520                 525

Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly
    530                 535                 540

Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr
545                 550                 555                 560

Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys
                565                 570                 575

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
            580                 585                 590

Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn
        595                 600                 605

Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
    610                 615                 620

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
625                 630                 635                 640

Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala
                645                 650                 655

Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val
            660                 665                 670

Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg
        675                 680                 685

Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe
    690                 695                 700

Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu
705                 710                 715                 720

Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn
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725 730 735

Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser Ser
740 745 750

Ser

<210> 199
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7 and DRA222 VH CDR1 (IMGT) CD3-binding domain

<400> 199

Gly Tyr Thr Phe Thr Arg Ser Thr
1 5

<210> 200
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7 and DRA222 VH CDR2 (IMGT) CD3-binding domain

<400> 200

Ile Asn Pro Ser Ser Ala Tyr Thr
1 5

<210> 201
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7 and DRA222 VH CDR3 (IMGT) CD3-binding domain

<400> 201

Gln Gln Trp Ser Arg Asn Pro Pro Thr
1 5

<210> 202
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7 and DRA222 VL CDR1 (IMGT) CD3-binding domain

<400> 202

Ala Ser Ser Ser Val Ser Tyr
1 5

<210> 203
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7 and DRA222 VL CDR2 (IMGT) CD3-binding domain

<400> 203

Asp Ser Ser
1

<210> 204
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Cris7 and DRA222 VL CDR3 (IMGT) CD3-binding domain

<400> 204

Gln Gln Trp Ser Arg Asn Pro Pro Thr
1 5

<210> 205
<211> 2286
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC471 Anti-PSMA X anti-CD3 bispecific molecule

<400> 205
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gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540

cgacaggccc ctggacaagg gcttgagtgg atgggatatt ttaatcctta taatgattat 600

actagatacg cacagaagtt ccagggcaga gtcaccatga ccagggacac gtctatcagc 660

acagcctaca tggagctgag cagcctgaga tctgacgaca cggccgtgta ttactgtgca 720

agatcggatg gttactacga tgctatggac tactggggtc aaggaaccac agtcaccgtc 780

tcctcgagtg agcccaaatc ttctgacaaa actcacacat gcccaccgtg cccagcacct 840

gaagccgcgg gtgcaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 900

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggaata caagtgcgcg 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 gttccggagg tggcggttcg 1500

ggaggtggcg ggtcaggagg tgggggctct ccttcacagg tgcagctggt gcagtctggt 1560

cctgaggtga aaaagcctgg ctccagcgtg aaggtgtcct gcaaggccag cggatacacc 1620

tttagccggt ccaccatgca ttgggtgagg caggctcctg gacagggcct ggagtggatc 1680

ggctacatca accccagcag cgcttatacc aactacaatc agaagtttaa ggaccgggtg 1740

accatcaccg ccgataagtc caccagcacc gcctacatgg agctgtccag cctgaggagc 1800

gaggataccg ccgtgtacta ttgcgcccgg ccccaggtcc attacgacta caacggcttc 1860

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ccctccaccc tgtccgctag cgtgggcgat cgggtgacca tgacctgcag cgccagcagc 2040

tccgtgtcct acatgaactg gtaccagcag aagcccggca aggctcccaa gaggtggatt 2100

tacgactcca gcaagctggc ctctggtgtc cccagcaggt tctctggtag cggcagcggc 2160

acagactaca ccctgaccat ctcctccctg cagcccgacg atttcgccac ctactattgc 2220

cagcagtggt cccggaatcc ccctaccttt ggcggcggca ccaaggtgga gatcaagagg 2280

agctaa 2286

<210> 206
<211> 741
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC471 Anti-PSMA X anti-CD3 bispecific molecule

<400> 206

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 Glu Tyr Lys 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 Ser Gln Val Gln Leu
                485                 490                 495

Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
```

```
            500                 505                 510

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser 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 Val
545                 550                 555                 560

Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
                565                 570                 575

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln
            580                 585                 590

Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu
        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 Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
625                 630                 635                 640

Pro Ser Thr 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 Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
    690                 695                 700

Leu Thr Ile Ser Ser Leu Gln Pro Asp 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 Val
                725                 730                 735


Glu Ile Lys Arg Ser
            740
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<210> 207
<211> 2307
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR243 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 207

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gacatccaga tgacccagtc cccttcctcc ctgtccgcta gcgtgggcga tagggtgacc      120

atcaactgcc aggcctccca gtccattgac tccaatctgg cctggttcca gcagaagccc      180

ggacagcccc ccaagctgct gatttacagg gcctccaacc tggcttccgg cgtgcctgac      240

aggttctccg gatccggcag cggcaccgac ttcaccctga ccatctcctc cctggaggcc      300

gaggatgtcg ccacctacta ctgtctgggc ggcgtgggcg ctgtgagcta tcggacctcc      360

ttcggcggcg gcaccaaggt ggagatcaag ggcggcggcg gcagcggcgg cggcggcagc      420

ggcggcggag gctccggcgg cggcggcagc gaggtgcagc tggtggaaag cggaggaggc      480

ctggtgcagc ctggaaggtc cctgaggctg tcctgcacag ccagcggctc cgacatcaac      540

gactacccca tcacctgggt gaggcaggct cctggccagg gcctggaatg gatcggcttt      600

atcaacagcg gcggcagcac ctggtatgct tcctgggtga agggccggtt caccattagc      660

agggacgact ccaagtccat tgcctacctg cagatgaact ccctgaagac cgaggacacc      720

gccgtgtact actgcgccag gggctacagc acctattacc gggactttaa catctggggc      780

cagggcacac tggtcaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca      840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccccа      900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac      960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat     1020
```

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

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tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500

ggttccggag gagggggttc aggtggggga ggttctggcg gcgggggaag cccttcacag 1560

gtgcaactgg tgcagagtgg acccgaggtt aaaaaaccag ggtcctccgt taaggttagc 1620

tgcaaagcct ctggctacac attttccagg agtacaatgc actgggtgag gcaggctcct 1680

ggacagggac tcgagtggat cgggtatatc aacccatcta gcgcctatac caattacaac 1740

caaaagttta aggaccgagt taccattacc gctgacaaat ccaccagtac agcttatatg 1800

gagctgtcat ctcttaggtc cgaggacact gctgtttatt actgcgctcg tcctcaggtt 1860

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gatattcaga tgactcagtc tcctagcact ctcagcgcca gcgtgggggga tcgtgtgaca 2040

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aaagcaccta agcgctggat ctatgactct tccaagctgg caagtggtgt cccctcacgg 2160

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accaaagtgg agatcaagag gtcatga 2307

<210> 208
<211> 748
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR243 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 208

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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 Asn Cys Gln Ala Ser Gln Ser Ile Asp Ser Asn
            20                  25                  30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Ala
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val Gly Ala Val Ser
                85                  90                  95

Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly
            100                 105                 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
    130                 135                 140

Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Ser Asp Ile Asn
145                 150                 155                 160

Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
                165                 170                 175

Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp Tyr Ala Ser Trp
            180                 185                 190

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala
        195                 200                 205
```

```
Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr
    210                 215                 220

Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe Asn Ile Trp Gly
225                 230                 235                 240

Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp
                245                 250                 255

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala
            260                 265                 270

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
        275                 280                 285

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
    290                 295                 300

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
305                 310                 315                 320

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                325                 330                 335

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
            340                 345                 350

Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        355                 360                 365

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    370                 375                 380

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
385                 390                 395                 400

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                405                 410                 415
```

```
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            420                 425                 430

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        435                 440                 445

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    450                 455                 460

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
465                 470                 475                 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                485                 490                 495

Ser Pro Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
            500                 505                 510

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        515                 520                 525

Ser Arg Ser Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    530                 535                 540

Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn
545                 550                 555                 560

Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
                565                 570                 575

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            580                 585                 590

Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro
        595                 600                 605

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    610                 615                 620

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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625 630 635 640

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
645 650 655

Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
660 665 670

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
675 680 685

Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
690 695 700

Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
705 710 715 720

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro Pro Thr
725 730 735

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ser
740 745

<210> 209
<211> 2289
<212> DNA
<213> Artificial Sequence

<220>
<223> TSC266 Anti-PSMA X anti-CD3 bispecific molecule

<400> 209
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gatatccaga tgacccagtc tccatccgcc atgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtaa gagcattagc aaatatttag cctggtttca gcagaaacca 180

gggaaagttc ctaagctccg catccattct ggatctactt tgcaatcagg ggtcccatct 240

cggttcagtg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 300

gaagattttg caacttatta ctgtcaacag catattgaat acccgtggac gttcggccaa 360

gggaccaagg tggaaatcaa acgaggtggc ggagggtctg ggggtggcgg atccggaggt 420

ggtggctctc aggtccagct ggtacagtct ggggctgagg tgaagaagcc tggggcttca 480

gtgaaggtct cctgcaaggc ttctggatac acattcactg actactacat gcactgggtg 540

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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 cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 960

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 1020

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac 1080

tggctgaatg gcaaggcgta cgcgtgcgcg gtctccaaca aagccctccc agcccccatc 1140

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1200

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260

tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1320

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

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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 aagccgggca aggcccccaa aagatggatt 2100

tatgactcat ccaaactggc ttctggagtc cctgctcgct tcagtggcag tgggtctggg 2160

accgactata ccctcacaat cagcagcctg cagcccgaag atttcgccac ttattactgc 2220

cagcagtgga gtcgtaaccc acccacgttc ggaggggggga ccaagctaca aattacatcc 2280

tccagctaa 2289

<210> 210
<211> 742
<212> PRT
<213> Artificial Sequence

<220>
<223> TSC266 Anti-PSMA X anti-CD3 bispecific molecule

<400> 210

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
```

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Leu His Gln Asp Trp Leu Asn Gly Lys Ala Tyr Ala Cys Ala Val Ser
            340                 345                 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
        355                 360                 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
    370                 375                 380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385                 390                 395                 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                405                 410                 415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
            420                 425                 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        435                 440                 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    450                 455                 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Arg His Asn Asn Ser
465                 470                 475                 480

Ser Leu Asn Thr Gly Thr Gln Met Ala Gly His Ser Pro Asn Ser Gln
                485                 490                 495

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
            500                 505                 510

Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Ser Thr
        515                 520                 525

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
    530                 535                 540
```

```
Tyr Ile Asn Pro Ser Ser Ala Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
545                 550                 555                 560

Asp Arg Phe Thr Ile Ser Ala Asp Lys Ser Lys Ser Thr Ala Phe Leu
                565                 570                 575

Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala
            580                 585                 590

Arg Pro Gln Val His Tyr Asp Tyr Asn Gly Phe Pro Tyr Trp Gly Gln
        595                 600                 605

Gly Thr Pro Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    610                 615                 620

Gly Ser Gly Gly Gly Gly Ser Ala Gln Asp Ile Gln Met Thr Gln Ser
625                 630                 635                 640

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys
                645                 650                 655

Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
            660                 665                 670

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser
        675                 680                 685

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
    690                 695                 700

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
705                 710                 715                 720

Gln Gln Trp Ser Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
                725                 730                 735

Gln Ile Thr Ser Ser Ser
            740
```

<210> 211

<211> 2301
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR206 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 211
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc 180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc 240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc 300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc 360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc 420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc 480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac 540

gactacccca tcacctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc 600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc 660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc 720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc 780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct 1560

caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 1620

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 1680

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 1740

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 1800

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc 2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 2220

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 2280

ctacaaatta catcctccag c 2301

<210> 212
<211> 767
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR206 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 212

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser

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        35                  40                  45

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro
    50                  55                  60

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
            100                 105                 110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
        115                 120                 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
145                 150                 155                 160

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
                165                 170                 175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
            180                 185                 190

Lys Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
        195                 200                 205

Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
    210                 215                 220

Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
225                 230                 235                 240

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe
                245                 250                 255
```

```
Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
            260                 265                 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        275                 280                 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    290                 295                 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
305                 310                 315                 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                325                 330                 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            340                 345                 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        355                 360                 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
    370                 375                 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385                 390                 395                 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
                405                 410                 415

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            420                 425                 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        435                 440                 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
    450                 455                 460
```

```
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465                 470                 475                 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                485                 490                 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            500                 505                 510

Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly
        515                 520                 525

Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala
    530                 535                 540

Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala
545                 550                 555                 560

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
                565                 570                 575

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala
            580                 585                 590

Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro
        595                 600                 605

Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp
    610                 615                 620

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser
625                 630                 635                 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                645                 650                 655

Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            660                 665                 670
```

```
Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
        675                 680                 685

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
    690                 695                 700

Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
705                 710                 715                 720

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
                725                 730                 735

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro
            740                 745                 750

Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
        755                 760                 765
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<210> 213
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR207 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 213

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atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt       60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc      120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc      180

ggcaagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgccctcc      240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctgcagccc      300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc      360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc      420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc      480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac      540

gactacccca tcacctgggt gcggcaggcc cccggcaagg gcctggagtg gatcggcttc      600
```

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc 660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc 720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc 780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

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cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

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cctggacaag ggcttgagtg gataggatac attaatccta gcagtgctta tactaattac 1740

aatcagaaat tcaaggacag agtcacgatt accgcggaca aatccacgag cacagcctac 1800

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaccccaa 1860

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc 1920

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga 1980

tctgacatcc agatgaccca gtctccttcc accctgtctg catctgtagg agacagagtc 2040

accatgactt gcagtgccag ctcaagtgta agttacatga actggtatca gcagaaacca 2100

gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca 2160

aggttcagcg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct 2220

gatgattttg caacttatta ctgccaacag tggagtcgta acccacccac tttcggcgga 2280

gggaccaagg tggagatcaa acggtcctcc agc 2313

<210> 214
<211> 771
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR207 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 214

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser
35 40 45

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro
50 55 60

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
100 105 110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
115 120 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly

```
145                 150                 155                 160

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
                165                 170                 175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
            180                 185                 190

Lys Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
        195                 200                 205

Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
    210                 215                 220

Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
225                 230                 235                 240

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe
                245                 250                 255

Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
            260                 265                 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        275                 280                 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    290                 295                 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
305                 310                 315                 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                325                 330                 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            340                 345                 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        355                 360                 365
```

```
Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
    370                 375                 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385                 390                 395                 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
                405                 410                 415

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            420                 425                 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        435                 440                 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
    450                 455                 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465                 470                 475                 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                485                 490                 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            500                 505                 510

Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly
        515                 520                 525

Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
    530                 535                 540

Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala
545                 550                 555                 560

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
                565                 570                 575
```

```
Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala
            580                 585                 590

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
        595                 600                 605

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp
    610                 615                 620

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
625                 630                 635                 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                645                 650                 655

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
            660                 665                 670

Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser
        675                 680                 685

Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    690                 695                 700

Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser
705                 710                 715                 720

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
                725                 730                 735

Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
            740                 745                 750

Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
        755                 760                 765

Ser Ser Ser
    770
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<210> 215
<211> 2301
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR208 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 215
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gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc 180

ggccagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgcccgac 240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctggaggcc 300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc 360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc 420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc 480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac 540

gactacccca tcacctgggt gcggcaggcc cccggccagg gcctggagtg gatcggcttc 600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc 660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc 720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc 780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct 1560

caggtccagc tggtggagtc tgggggcgga gtggtgcagc ctgggcggtc actgaggctg 1620

tcctgcaagg cttctggcta cacctttact agatctacga tgcactgggt aaggcaggcc 1680

cctggacaag gtctggaatg gattggatac attaatccta gcagtgctta tactaattac 1740

aatcagaaat tcaaggacag gttcacaatc agcgcagaca aatccaagag cacagccttc 1800

ctgcagatgg acagcctgag gcccgaggac accggcgtct atttctgtgc acggccccaa 1860

gtccactatg attacaacgg gtttccttac tggggccaag ggactcccgt cactgtctct 1920

agcggtggcg gagggtctgg gggtggcgga tccggaggtg gtggctctgc acaagacatc 1980

cagatgaccc agtctccaag cagcctgtct gcaagcgtgg gggacagggt caccatgacc 2040

tgcagtgcca gctcaagtgt aagttacatg aactggtacc agcagaagcc gggcaaggcc 2100

cccaaaagat ggatttatga ctcatccaaa ctggcttctg gagtccctgc tcgcttcagt 2160

ggcagtgggt ctgggaccga ctataccctc acaatcagca gcctgcagcc cgaagatttc 2220

gccacttatt actgccagca gtggagtcgt aacccaccca cgttcggagg ggggaccaag 2280

ctacaaatta catcctccag c 2301

<210> 216
<211> 767
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR208 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 216

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

```
Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser
        35                  40                  45

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
    50                  55                  60

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Asp
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

Ser Leu Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
            100                 105                 110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
        115                 120                 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
145                 150                 155                 160

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
                165                 170                 175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
            180                 185                 190

Gln Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
        195                 200                 205

Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
    210                 215                 220

Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
225                 230                 235                 240

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe
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                245                 250                 255

Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
            260                 265                 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        275                 280                 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    290                 295                 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
305                 310                 315                 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                325                 330                 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            340                 345                 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        355                 360                 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
    370                 375                 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385                 390                 395                 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
                405                 410                 415

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            420                 425                 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        435                 440                 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
    450                 455                 460
```

```
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465                 470                 475                 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                485                 490                 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            500                 505                 510

Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Glu Ser Gly
        515                 520                 525

Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala
    530                 535                 540

Ser Gly Tyr Thr Phe Thr Arg Ser Thr Met His Trp Val Arg Gln Ala
545                 550                 555                 560

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
                565                 570                 575

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala
            580                 585                 590

Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro
        595                 600                 605

Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Pro Gln Val His Tyr Asp
    610                 615                 620

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser
625                 630                 635                 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                645                 650                 655

Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            660                 665                 670
```

```
Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
        675                 680                 685

Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp
    690                 695                 700

Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
705                 710                 715                 720

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
                725                 730                 735

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Arg Asn Pro
            740                 745                 750

Pro Thr Phe Gly Gly Gly Thr Lys Leu Gln Ile Thr Ser Ser Ser
        755                 760                 765
```

<210> 217
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR209 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 217
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gacatccaga tgacccagtc cccctcctcc ctgtccgcct ccgtgggcga ccgggtgacc 120

atcaactgcc aggcctccca gtccatcgac tccaacctgg cctggttcca gcagaagccc 180

ggccagcccc ccaagctgct gatctaccgg gcctccaacc tggcctccgg cgtgcccgac 240

cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcctc cctggaggcc 300

gaggacgtgg ccacctacta ctgcctgggc ggcgtgggcg ccgtgtccta ccggacctcc 360

ttcggcggcg gcaccaaggt ggagatcaag ggtggaggcg gttcaggcgg aggtggatcc 420

ggcggtggcg gctccggtgg cggcggatct gaggtgcagc tggtggagtc cggcggcggc 480

ctggtgcagc ccggccggtc cctgcggctg tcctgcaccg cctccggctc cgacatcaac 540

gactacccca tcacctgggt gcggcaggcc cccggccagg gcctggagtg gatcggcttc 600

atcaactccg gcggctccac ctggtacgcc tcctgggtga agggccggtt caccatctcc 660

cgggacgact ccaagtccat cgcctacctg cagatgaact ccctgaagac cgaggacacc 720

gccgtgtact attgcgcccg gggctactcc acctactacc gggacttcaa catctggggc 780

cagggcaccc tggtgaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500

ggttctggtg gaggcggttc aggcggaggt ggctccggcg gtggcggatc gccgggctct 1560

caggtccagc tggtgcaatc tgggcctgag gtgaagaagc ctgggtcctc ggtgaaggtc 1620

tcctgcaagg cttctggata taccttcagc agatctacga tgcactgggt gcgacaggcc 1680

cctggacaag ggcttgagtg gataggatac attaatccta gcagtgctta tactaattac 1740

aatcagaaat tcaaggacag agtcacgatt accgcggaca aatccacgag cacagcctac 1800

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaccccaa 1860

gtccactatg attacaacgg gtttccttac tggggccaag gaaccctggt caccgtctcc 1920

tcaggtggag gcggttcagg cggaggtgga tccggcggtg gcggatcggg tggcggcgga 1980

tctgacatcc agatgaccca gtctccttcc accctgtctg catctgtagg agacagagtc 2040

accatgactt gcagtgccag ctcaagtgta agttacatga actggtatca gcagaaacca 2100

gggaaagccc ctaagagatg gatttatgac tcatccaaac tggcttctgg ggtcccatca 2160

aggttcagcg gcagtggatc tgggacagat tatactctca ccatcagcag cctgcagcct 2220

gatgattttg caacttatta ctgccaacag tggagtcgta acccacccac tttcggcgga 2280

gggaccaagg tggagatcaa acggtcctcc agc 2313

<210> 218
<211> 771
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR209 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 218

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser
35 40 45

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
50 55 60

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Asp
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
100 105 110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
115 120 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

```
Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
145                 150                 155                 160

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
                165                 170                 175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
            180                 185                 190

Gln Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
        195                 200                 205

Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
    210                 215                 220

Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
225                 230                 235                 240

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe
                245                 250                 255

Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
            260                 265                 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        275                 280                 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    290                 295                 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
305                 310                 315                 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                325                 330                 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            340                 345                 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
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        355                 360                 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
    370                 375                 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385                 390                 395                 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
                405                 410                 415

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            420                 425                 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        435                 440                 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
    450                 455                 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465                 470                 475                 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                485                 490                 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            500                 505                 510

Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly
        515                 520                 525

Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
    530                 535                 540

Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala
545                 550                 555                 560

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
                565                 570                 575
```

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Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala
            580                 585                 590

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
        595                 600                 605

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp
    610                 615                 620

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
625                 630                 635                 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                645                 650                 655

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
            660                 665                 670

Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser
        675                 680                 685

Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    690                 695                 700

Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser
705                 710                 715                 720

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
                725                 730                 735

Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
            740                 745                 750

Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
        755                 760                 765

Ser Ser Ser
    770
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<210> 219
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> ROR231 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 219
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gacatccaga tgacccaatc cccttctagt ctctccgcta gcgtcggaga ccgcgtgacc 120

atcaattgtc aagcatctca gagtattgac agcaatctcg cctggtttca gcagaagcca 180

ggaaagccac ccaagctcct gatttatagg gctagcaacc tggcttctgg tgtccctagt 240

aggttcagcg gctctgggag tggcacagac ttcaccctga ccattagtag tctgcagccc 300

gaagatgtcg ctacctatta ctgcctcgga ggagtgggtg ccgtttctta tcgcacctca 360

tttggaggtg gcaccaaagt ggagatcaaa ggtggtggcg gctccggggg tggcgggtca 420

gggggggggag ggtctggagg cggcggatca gaagttcagc tggtggaatc tggaggaggt 480

ctggtgcagc caggcaggtc cctccggctg agctgcactg catccggctc tgacattaat 540

gactacccta tcacctgggt gaggcaggcc cccggtaaag gcctggagtg gatcgggttc 600

atcaattctg gtggatctac ttggtacgca agctgggtga aaggacgctt cacaattagt 660

agagacgact ctaagtctat cgcatatctg cagatgaata gcttgaagac agaggacacc 720

gccgtgtact attgtgcaag aggatactcc acttactacc gcgatttcaa tatctggggc 780

cagggaaccc tggtgacagt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260

acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 1380

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ggttccggag gcggcggctc cggcggcggc ggcagcggcg gcggcggcag ccccggatcc 1560

caggtgcagc tggtgcagtc tggtcctgag gtgaaaaagc ctggctccag cgtgaaggtg 1620

tcctgcaagg ccagcggata cacctttagc cggtccacca tgcattgggt gaggcaggct 1680

cctggacagg gcctggagtg gatcggctac atcaacccca gcagcgctta taccaactac 1740

aatcagaagt ttaaggaccg ggtgaccatc accgccgata agtccaccag caccgcctac 1800

atggagctgt ccagcctgag gagcgaggat accgccgtgt actattgcgc ccggccccag 1860

gtccattacg actacaacgg cttcccctat tggggccagg gaaccctggt gaccgtgtcc 1920

agcggaggcg gcggcagcgg cggcggcggc agcggcggag gaggcagcgg cggaggaggc 1980

tccgacattc agatgaccca gtccccctcc accctgtccg ctagcgtggg cgatcgggtg 2040

accatgacct gcagcgccag cagctccgtg tcctacatga actggtacca gcagaagccc 2100

ggcaaggctc ccaagaggtg gatttacgac tccagcaagc tggcctctgg tgtccccagc 2160

aggttctctg gtagcggcag cggcacagac tacaccctga ccatctcctc cctgcagccc 2220

gacgatttcg ccacctacta ttgccagcag tggtcccgga atccccctac ctttggcggc 2280

ggcaccaagg tggagatcaa gaggagctcc agc 2313

<210> 220
<211> 771
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR231 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 220

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

```
Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser
        35                  40                  45

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Pro Pro
    50                  55                  60

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ser
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
            100                 105                 110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
        115                 120                 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
145                 150                 155                 160

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
                165                 170                 175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
            180                 185                 190

Lys Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
        195                 200                 205

Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
    210                 215                 220

Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
225                 230                 235                 240
```

```
Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe
                245                 250                 255

Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
            260                 265                 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        275                 280                 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    290                 295                 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
305                 310                 315                 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                325                 330                 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            340                 345                 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        355                 360                 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
    370                 375                 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385                 390                 395                 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
                405                 410                 415

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            420                 425                 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        435                 440                 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
```

```
    450                 455                 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465                 470                 475                 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                485                 490                 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            500                 505                 510

Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly
        515                 520                 525

Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
    530                 535                 540

Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala
545                 550                 555                 560

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
                565                 570                 575

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala
            580                 585                 590

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
        595                 600                 605

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp
    610                 615                 620

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
625                 630                 635                 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                645                 650                 655

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
            660                 665                 670
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Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser
        675                 680                 685

Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    690                 695                 700

Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser
705                 710                 715                 720

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
                725                 730                 735

Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
            740                 745                 750

Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
        755                 760                 765

Ser Ser Ser
    770
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<210> 221
<211> 2313
<212> DNA
<213> Artificial Sequence

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<223> ROR233 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 221
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ggacagcccc ccaagctgct gatttacagg gcctccaacc tggcttccgg cgtgcctgac 240

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gaggatgtcg ccacctacta ctgtctgggc ggcgtgggcg ctgtgagcta tcggacctcc 360

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ggcggcggag gctccggcgg cggcggcagc gaggtgcagc tggtggaaag cggaggaggc 480

ctggtgcagc ctggaaggtc cctgaggctg tcctgcacag ccagcggctc cgacatcaac 540

gactacccca tcacctgggt gaggcaggct cctggccagg gcctggaatg gatcggcttt 600

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agggacgact ccaagtccat tgcctacctg cagatgaact ccctgaagac cgaggacacc 720

gccgtgtact actgcgccag gggctacagc acctattacc gggactttaa catctggggc 780

cagggcacac tggtcaccgt gtcctcgagt gagcccaaat cttctgacaa aactcacaca 840

tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttccccca 900

aaacccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960

gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020

aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080

ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140

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ggcaaggctc ccaagaggtg gatttacgac tccagcaagc tggcctctgg tgtccccagc 2160

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ggcaccaagg tggagatcaa gaggagctcc agc 2313

<210> 222
<211> 771
<212> PRT
<213> Artificial Sequence

<220>
<223> ROR233 Anti-ROR1 X anti-CD3 bispecific molecule

<400> 222

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
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Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser
35 40 45

Ile Asp Ser Asn Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
50 55 60

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Asp
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Gly Val
100 105 110

Gly Ala Val Ser Tyr Arg Thr Ser Phe Gly Gly Gly Thr Lys Val Glu
115 120 125

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Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
145                 150                 155                 160

Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly
                165                 170                 175

Ser Asp Ile Asn Asp Tyr Pro Ile Thr Trp Val Arg Gln Ala Pro Gly
            180                 185                 190

Gln Gly Leu Glu Trp Ile Gly Phe Ile Asn Ser Gly Gly Ser Thr Trp
        195                 200                 205

Tyr Ala Ser Trp Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
    210                 215                 220

Lys Ser Ile Ala Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
225                 230                 235                 240

Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Ser Thr Tyr Tyr Arg Asp Phe
                245                 250                 255

Asn Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser Glu Pro
            260                 265                 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        275                 280                 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
    290                 295                 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
305                 310                 315                 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                325                 330                 335
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Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            340                 345                 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        355                 360                 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
    370                 375                 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385                 390                 395                 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
                405                 410                 415

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
            420                 425                 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
        435                 440                 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
    450                 455                 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465                 470                 475                 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
                485                 490                 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            500                 505                 510

Gly Gly Gly Gly Ser Pro Gly Ser Gln Val Gln Leu Val Gln Ser Gly
        515                 520                 525

Pro Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
    530                 535                 540

Ser Gly Tyr Thr Phe Ser Arg Ser Thr Met His Trp Val Arg Gln Ala
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545                 550                 555                 560

Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Ser Ala
                565                 570                 575

Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Arg Val Thr Ile Thr Ala
            580                 585                 590

Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser
        595                 600                 605

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Pro Gln Val His Tyr Asp
    610                 615                 620

Tyr Asn Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
625                 630                 635                 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                645                 650                 655

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu
            660                 665                 670

Ser Ala Ser Val Gly Asp Arg Val Thr Met Thr Cys Ser Ala Ser Ser
        675                 680                 685

Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    690                 695                 700

Lys Arg Trp Ile Tyr Asp Ser Ser Lys Leu Ala Ser Gly Val Pro Ser
705                 710                 715                 720

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
                725                 730                 735

Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
            740                 745                 750

Arg Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
        755                 760                 765
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Ser Ser Ser
    770