SEQUENCE LISTING

<110> Grosmaire et al.

<120> B-Cell Reduction Using CD37-Specific And CD20-Specific Binding Molecules

<130> EMER-012/05SG

<140> National Phase of PCT/US2006/029038
<141> 2006-07-25

<150> US 60/702,499
<151> 2005-07-25

<150> US 60/800,595
<151> 2006-05-16

<160> 226

<170> PatentIn version 3.3

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tctgtgggag agactgtcac catcacatgt cgaacaagtg aaaatgttta cagttatttg 180

gcttggtatc agcagaaaca gggaaaatct cctcagctcc tggtctcttt tgcaaaaacc 240

ttagcagaag gtgtgccatc aaggttcagt ggcagtggat caggcacaca gttttctctg 300

aagatcagca gcctgcagcc tgaagattct ggaagttatt tctgtcaaca tcattccgat 360

aatccgtgga cgttcggtgg aggcaccgaa ctggagatca aaggtggcgg tggctcgggc 420

ggtggtgggt cgggtggcgg cggatcgtca gcggtccagc tgcagcagtc tggacctgag 480

tcggaaaagc ctggcgcttc agtgaagatt tcctgcaagg cttctggtta ctcattcact 540

ggctacaata tgaactgggt gaagcagaat aatggaaaga gccttgagtg gattggaaat 600

attgatcctt attatggtgg tactacctac aaccggaagt tcaagggcaa ggccacattg 660

actgtagaca aatcctccag cacagcctac atgcagctca agagtctgac atctgaggac 720

tctgcagtct attactgtgc aagatcggtc ggccctatgg actactgggg tcaaggaacc 780

tcagtcaccg tctcttcaga tctggagccc aaatcttctg acaaaactca cacatctcca 840

ccgtgcccag cacctgaact cttgggtgga ccgtcagtct tcctcttccc cccaaaaccc 900

aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 960

cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 1020

aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 1080

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 1140

ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1200

gtgtacaccc tgcccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 1260

ctggtcaaag gcttctatcc aagcgacatc gccgtggagt gggagagcaa tgggcaaccg 1320

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1380

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 1440

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tgagtctaga 1510

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<211> 496
<212> PRT
<213> Artificial sequence

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<223> TRU-016 polynucleotide

<400> 2

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Val Ile Ile Ala Arg Gly Val Asp Ile Gln Met Thr Gln Ser Pro Ala
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Ser Leu Ser Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Thr
35 40 45

Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly
50 55 60

Lys Ser Pro Gln Leu Leu Val Ser Phe Ala Lys Thr Leu Ala Glu Gly
65 70 75 80

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu
85 90 95

Lys Ile Ser Ser Leu Gln Pro Glu Asp Ser Gly Ser Tyr Phe Cys Gln
100 105 110

His His Ser Asp Asn Pro Trp Thr Phe Gly Gly Gly Thr Glu Leu Glu
115 120 125

Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Ser Ala Val Gln Leu Gln Gln Ser Gly Pro Glu Ser Glu Lys Pro
145 150 155 160

Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr
165 170 175

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Gly Tyr Asn Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu
            180                 185                 190

Trp Ile Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg
        195                 200                 205

Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr
    210                 215                 220

Ala Tyr Met Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
225                 230                 235                 240

Tyr Cys Ala Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr
                245                 250                 255

Ser Val Thr Val Ser Ser Asp Leu Glu Pro Lys Ser Ser Asp Lys Thr
            260                 265                 270

His Thr Ser Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
        275                 280                 285

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

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
305                 310                 315                 320

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
                325                 330                 335

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
        355                 360                 365

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

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
385                 390                 395                 400

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

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
            420                 425                 430

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
        435                 440                 445

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
    450                 455                 460
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Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
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Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490 495

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ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180

taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240

tctggagtcc ctgctcgctt cagtggcagt gggtctggga cctcttactc tctcacaatc 300

agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360

cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggt 420

ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagtcggtg 480

aggcctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt taccagttac 540

aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600

ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660

gacaaatcct ccagcacagc ctacatgcag ctcagcagcc tgacatctga agactctgcg 720

gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780

ggcacaggga ccacggtcac cgtctctgat caggagccca aatcttgtga caaaactcac 840

acatctccac cgtgctcagc acctgaactc ctgggtggac cgtcagtctt cctcttcccc 900

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 960

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1020

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080

gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1140

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1200

gaaccacagg tgtacaccct gccccatcc 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

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ccgggtaaat gatctaga 1518

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<211> 499
<212> PRT
<213> Artificial sequence

<220>
<223> TRU-015 polynucleotide

<400> 4

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Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95

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

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125

Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
130 135 140

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175

Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240

Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255

Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Cys
260 265 270

Asp Lys Thr His Thr Ser Pro Pro Cys Ser Ala Pro Glu Leu Leu Gly
275 280 285

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
290 295 300

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
305 310 315 320

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
325 330 335

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
340 345 350

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
355 360 365

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

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385 390 395 400

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
405 410 415

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
420 425 430

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

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
465 470 475 480

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

Pro Gly Lys

<210> 5
<211> 1482
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

gggaccggtg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggagagtct 480

ctgaagattt cctgtaaggg atccggttac tcattcactg gctacaatat gaactgggtg 540

cgccagatgc ccgggaaagg cctcgagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctctgat 780

caggagccca aatcttctga caaaactcac acatctccac cgtgcccagc acctgaactc 840

ctgggtggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 900

cggaccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 960

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1020

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1080

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1140

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1200

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 1260

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1320

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1380

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1440

cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 1482

<210> 6
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 6

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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
        35                  40                  45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
    130                 135                 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145                 150                 155                 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
            260                 265                 270
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Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
275 280 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
290 295 300

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
305 310 315 320

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
325 330 335

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

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

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

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

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

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
435 440 445

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

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

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

<210> 7
<211> 1482
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

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ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

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ctgaagattt cctgtaaggg atccggttac tcattcactg gctacaatat gaactgggtg 540

cgccagatgc ccgggaaagg cctcgagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctctgat 780

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cggaccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 960

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aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1140

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1200

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 1260

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1320

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agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1440

cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 1482

<210> 8
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 8

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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
260 265 270

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
275 280 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
290 295 300

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
305 310 315 320

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
325 330 335

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

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

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

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

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

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        435                 440                 445

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

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

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                485                 490
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<210> 9
<211> 1482
<212> DNA
<213> Artificial sequence

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<223> Humanized TRU-016

<400> 9

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gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa    360
gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt    420
gggaccggtg aggtgcagct ggtgcagtct ggagcagagt cgaaaaagcc cggagagtct    480
ctgaagattt cctgtaaggg atccggttac tcattcactg gctacaatat gaactgggtg    540
cgccagatgc ccgggaaagg cctcgagtgg atgggcaata ttgatcctta ttatggtggt    600
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actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

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cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctctgat 780

caggagccca aatcttctga caaaactcac acatctccac cgtgcccagc acctgaactc 840

ctgggtggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 900

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 960

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1020

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1080

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1140

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1200

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 1260

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1320

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1380

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1440

cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 1482

<210> 10
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 10

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

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Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
    130                 135                 140

Val Gln Leu Val Gln Ser Gly Ala Glu Ser Lys Lys Pro Gly Glu Ser
145                 150                 155                 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
            260                 265                 270

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        275                 280                 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    290                 295                 300

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
305                 310                 315                 320

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                325                 330                 335

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

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

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    370                 375                 380
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Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
385 390 395 400

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

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
435 440 445

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

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

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

<210> 11
<211> 1482
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 11
atggaagccc cagctcagct tctcttcctc ctgctactct ggctcccaga taccaccgga 60

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtca aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

gggaccggtg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggagagtct 480

ctgaagattt cctgtaaggg atccggttac tcattcactg gctacaatat gaactgggtg 540

cgccagatgc ccgggaaagg cctcgagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctctgat 780

caggagccca aatcttctga caaaactcac acatctccac cgtgcccagc acctgaactc 840

ctgggtggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 900

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 960

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1020

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1080

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1140

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc 1200

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 1260

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1320

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1380

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1440

cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 1482

<210> 12
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 12

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Gln Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

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Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
            260                 265                 270

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        275                 280                 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    290                 295                 300

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
305                 310                 315                 320

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                325                 330                 335

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

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

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

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

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

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        435                 440                 445
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Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
450 455 460

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

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

<210> 13
<211> 1482
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 13
atggaagccc cagctcagct tctcttcctc ctgctactct ggctcccaga taccaccgga 60

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aagtgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata tccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

gggaccggtg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggagagtct 480

ctgaagattt cctgtaaggg atccggttac tcattcactg gctacaatat gaactgggtg 540

cgccagatgc ccgggaaagg cctcgagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctctgat 780

caggagccca aatcttctga caaaactcac acatctccac cgtgcccagc acctgaactc 840

ctgggtggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 900

cggaccccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 960

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1020

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1080

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1140

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1200

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 1260

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1320

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1380

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1440

cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 1482

<210> 14
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 14

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Ser
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

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Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
            260                 265                 270

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        275                 280                 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    290                 295                 300

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
305                 310                 315                 320

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                325                 330                 335

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

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

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

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

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

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        435                 440                 445

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

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

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                485                 490
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<210> 15
<211> 1482

<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 15
atggaagccc cagctcagct tctcttcctc ctgctactct ggctcccaga taccaccgga 60

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gagcaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

gggaccggtg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggagagtct 480

ctgaagattt cctgtaaggg atccggttac tcattcactg gctacaatat gaactgggtg 540

cgccagatgc ccgggaaagg cctcgagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctctgat 780

caggagccca aatcttctga caaaactcac acatctccac cgtgcccagc acctgaactc 840

ctgggtggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 900

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 960

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1020

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1080

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1140

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1200

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 1260

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1320

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1380

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1440

cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 1482

<210> 16
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 16

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
260 265 270

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
275 280 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
290 295 300

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
305 310 315 320

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
325 330 335

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

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

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

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

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

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
435 440 445

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

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

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

<210> 17
<211> 1479
<212> DNA

<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 17
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gacatccaga tgactcagtc tccagcctcc ctatctgcat ctgtgggaga gactgtcacc 120

atcacatgtc gaacaagtga aaatgtttac agttatttgg cttggtatca gcagaaacag 180
ggaaaatctc ctcagctcct ggtctctttt gcaaaaacct tagcagaagg tgtgccatca 240
aggttcagtg gcagtggatc aggcacacag ttttctctga agatcagcag cctgcagcct 300
gaagattctg gaagttattt ctgtcaacat cattccgata atccgtggac gttcggtgga 360
ggcaccgaac tggagatcaa aggtggcggt ggctcgggcg gtggtgggtc gggtggcggc 420
ggagctagcg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggagagtct 480
ctgaggattt cctgtaaggg atccggttac tcattcactg gctacaatat gaactgggtg 540
cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600
actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660
accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720
cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780
gagcccaaat cttctgacaa aactcacaca tctccaccgt gcccagcacc tgaactcctg 840
ggtggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 900
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440
tacacgcaga agagcctctc cctgtctccg ggtaaatga 1479

<210> 18
<211> 492
<212> PRT
<213> Artificial sequence

<220>

<223> Humanized TRU-016

<400> 18

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 Ala Ser Leu Ser
20 25 30

Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
50 55 60

Gln Leu Leu Val Ser Phe Ala Lys Thr Leu Ala Glu Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Ser Gly Ser Tyr Phe Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gly Gly Thr Glu Leu Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro
260 265 270

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305 310 315 320

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
325 330 335

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

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        355                 360                 365

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                405                 410                 415

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

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        435                 440                 445

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
465                 470                 475                 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                485                 490
```

<210> 19
<211> 1479
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 19

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atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt     60

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc    120

ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct    180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc    240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct    300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa    360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtagtggatc tggaggaggt    420

ggagctagcg cggtccagct gcagcagtct ggacctgagt cggaaaagcc tggcgcttca    480

gtgaagattt cctgcaaggc ttctggttac tcattcactg gctacaatat gaactgggtg    540

aagcagaata atggaaagag ccttgagtgg attggaaata ttgatcctta ttatggtggt    600
```

actacctaca accggaagtt caagggcaag gccacattga ctgtagacaa atcctccagc 660

acagcctaca tgcagctcaa gagtctgaca tctgaggact ctgcagtcta ttactgtgca 720

agatcggtcg gccctatgga ctactggggt caaggaacct cagtcaccgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tctccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaatga 1479

<210> 20
<211> 492
<212> PRT

<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 20

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

```
Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Ser Gly Ser Gly Gly Gly Gly Ala Ser Ala
    130                 135                 140

Val Gln Leu Gln Gln Ser Gly Pro Glu Ser Glu Lys Pro Gly Ala Ser
145                 150                 155                 160

Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
    210                 215                 220

Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
                245                 250                 255

Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro
            260                 265                 270

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        275                 280                 285

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305                 310                 315                 320

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                325                 330                 335

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

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        355                 360                 365

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    370                 375                 380
```

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
435 440 445

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
465 470 475 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 21
<211> 1479
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 21
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

ggagctagcc aggtgcagct ggtggagtct ggtggaggcg tggtccagcc tgggaggtcc 480

ctgagactct cctgtgcagc ctctggattc accttcagtg gctacaatat gaactgggtc 540

cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tctccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaatga 1479

<210> 22
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 22

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
130 135 140

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
145 150 155 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro
260 265 270

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305 310 315 320

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
325 330 335

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

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
355 360 365

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
435 440 445

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
465 470 475 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 23
<211> 1503
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 23
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gcggtccagc tgcagcagtc tggacctgag tcggaaaagc ctggcgcttc agtgaagatt 120

tcctgcaagg cttctggtta ctcattcact ggctacaata tgaactgggt gaagcagaat 180

aatggaaaga gccttgagtg gattggaaat attgatcctt attatggtgg tactacctac 240

aaccggaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac 300

atgcagctca agagtctgac atctgaggac tctgcagtct attactgtgc aagatcggtc 360

ggccctatgg actactgggg tcaaggaacc tcagtcaccg tctcttctgg tggcggtggc 420

tcgggcggtg gtgggtcggg tggcggcgga tcaggaggag gcgggagtgc tagcgaaatt 480

gtgttgacac agtctccagc caccctgtct ttgtctccag gcgaaagagc caccctctcc 540

tgccgaacaa gtgaaaatgt ttacagctac ttagcctggt accaacagaa acctggccag 600

gctcctaggc tcctcatcta ttttgcaaaa accttagcag aaggaattcc agccaggttc 660

agtggcagtg gatccgggac agacttcact ctcaccatca gcagcctaga gcctgaagat 720

tttgcagttt attactgtca acatcattcc gataatccgt ggacattcgg ccaagggacc 780

aaggtggaaa tcaaaggctc gagcgagccc aaatcttctg acaaaactca cacatctcca 840

ccgtgcccag cacctgaact cctgggtgga ccgtcagtct tcctcttccc cccaaaaccc 900

aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 960

cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 1020

aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 1080

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 1140

ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1200

gtgtacaccc tgcccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 1260

ctggtcaaag gcttctatcc aagcgacatc gccgtggagt gggagagcaa tgggcagccg 1320

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1380

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 1440

atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa 1500

tga 1503

<210> 24
<211> 500
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 24

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Ala Val Gln Leu Gln Gln Ser Gly Pro Glu Ser Glu
20 25 30

Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser
35 40 45

Phe Thr Gly Tyr Asn Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser
50 55 60

Leu Glu Trp Ile Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr
65 70 75 80

Asn Arg Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
85 90 95

Ser Thr Ala Tyr Met Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala
100 105 110

Val Tyr Tyr Cys Ala Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ser Glu Ile
145 150 155 160

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
165 170 175

Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn Val Tyr Ser Tyr Leu Ala
180 185 190

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe
195 200 205

Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly
210 215 220

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp
225 230 235 240

Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe
245 250 255

Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Ser Ser Glu Pro Lys Ser
260 265 270

Ser Asp Lys Thr His Thr Ser Pro Pro Cys Pro Ala Pro Glu Leu Leu
275 280 285

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
290 295 300

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
305 310 315 320

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
325 330 335

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
340 345 350

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
355 360 365

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
370 375 380

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
385 390 395 400

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
405 410 415

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
420 425 430

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

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
450 455 460

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465 470 475 480

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
485 490 495

Ser Pro Gly Lys
500

<210> 25
<211> 1488
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 25
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agaggagtcg aaattgtgtt gacacagtct ccagccaccc tgtctttgtc tccaggcgaa 120

agagccaccc tctcctgccg aacaagtgaa aatgtttaca gctacttagc ctggtaccaa 180

cagaaacctg gccaggctcc taggctcctc atctattttg caaaaacctt agcagaagga 240

attccagcca ggttcagtgg cagtggatcc gggacagact tcactctcac catcagcagc 300

ctagagcctg aagattttgc agtttattac tgtcaacatc attccgataa tccgtggaca 360

ttcggccaag ggaccaaggt ggaaatcaaa ggtggcggtg gctcgggcgg tggtggatct 420

ggaggaggtg gagctagcgc ggtccagctg cagcagtctg gacctgagtc ggaaaagcct 480

ggcgcttcag tgaagatttc ctgcaaggct tctggttact cattcactgg ctacaatatg 540

aactgggtga agcagaataa tggaaagagc cttgagtgga ttggaaatat tgatccttat 600

tatggtggta ctacctacaa ccggaagttc aagggcaagg ccacattgac tgtagacaaa 660

tcctccagca cagcctacat gcagctcaag agtctgacat ctgaggactc tgcagtctat 720

tactgtgcaa gatcggtcgg ccctatggac tactggggtc aaggaacctc agtcaccgtc 780

tcctcgagcg agcccaaatc ttctgacaaa actcacacat ctccaccgtg cccagcacct 840

gaactcctgg gtggaccgtc 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 gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc 1140

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1200

ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1260

tatccaagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1320

accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1380

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1440

cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatga 1488

<210> 26
<211> 495
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 26

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1               5                  10                  15

Val Ile Ile Ala Arg Gly Val Glu Ile Val Leu Thr Gln Ser Pro Ala
            20                  25                  30

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr
        35                  40                  45

Ser Glu Asn Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
    50                  55                  60

Gln Ala Pro Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly
65                  70                  75                  80

Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
                85                  90                  95

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
            100                 105                 110

His His Ser Asp Asn Pro Trp Thr Phe Gly Gln 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

Ala Ser Ala Val Gln Leu Gln Gln Ser Gly Pro Glu Ser Glu Lys Pro
145                 150                 155                 160

Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr
                165                 170                 175

Gly Tyr Asn Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu
            180                 185                 190

Trp Ile Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg
        195                 200                 205

Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr
    210                 215                 220

Ala Tyr Met Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
225                 230                 235                 240

Tyr Cys Ala Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr
                245                 250                 255
```

Ser Val Thr Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His
260 265 270

Thr Ser Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
275 280 285

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
290 295 300

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
305 310 315 320

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
325 330 335

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
355 360 365

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

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

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

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

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

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

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
465 470 475 480

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

<210> 27
<211> 1503
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 27
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gcggtccagc tgcagcagtc tggacctgag tcggaaaagc ctggcgcttc agtgaagatt 120

tcctgcaagg cttctggtta ctcattcact ggctacaata tgaactgggt gaagcagaat 180

aatggaaaga gccttgagtg gattggaaat attgatcctt attatggtgg tactacctac 240

aaccggaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac 300

atgcagctca agagtctgac atctgaggac tctgcagtct attactgtgc aagatcggtc 360

ggccctatgg actactgggg tcaaggaacc tcagtcaccg tctcttctgg tggcggtggc 420

tcgggcggtg gtgggtcggg tggcggcgga tcaggaggag gcgggagtgc tagcgaaatt 480

gtgttgacac agtctccagc caccctgtct ttgtctccag gcgaaagagc caccctctcc 540

tgccgaacaa gtgaaaatgt ttacagctac ttagcctggt accaacagaa acctggccag 600

gctcctaggc tcctcatcta ttttgcaaaa accttagcag aaggaattcc agccaggttc 660

agtggcagtg gatccgggac agacttcact ctcaccatca gcagcctaga gcctgaagat 720

tttgcagttt attactgtca acatcattcc gataatccgt ggacattcgg ccaagggacc 780

aaggtggaaa tcaaaggctc gagcgagccc aaatcttctg acaaaactca cacatgccca 840

ccgtgcccag cacctgaact cctgggtgga ccgtcagtct tcctcttccc cccaaaaccc 900

aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 960

cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 1020

aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 1080

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 1140

ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1200

gtgtacaccc tgccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 1260

ctggtcaaag gcttctatcc aagcgacatc gccgtggagt gggagagcaa tgggcagccg 1320

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1380

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 1440

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tga 1503

<210> 28
<211> 500
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 28

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
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Asp Thr Thr Gly Ala Val Gln Leu Gln Gln Ser Gly Pro Glu Ser Glu
20 25 30

```
Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser
        35                  40                  45

Phe Thr Gly Tyr Asn Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser
    50                  55                  60

Leu Glu Trp Ile Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr
65                  70                  75                  80

Asn Arg Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
                85                  90                  95

Ser Thr Ala Tyr Met Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala
            100                 105                 110

Val Tyr Tyr Cys Ala Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln
        115                 120                 125

Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
    130                 135                 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ser Glu Ile
145                 150                 155                 160

Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg
                165                 170                 175

Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn Val Tyr Ser Tyr Leu Ala
            180                 185                 190

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Phe
        195                 200                 205

Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly
    210                 215                 220

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp
225                 230                 235                 240

Phe Ala Val Tyr Tyr Cys Gln His His Ser Asp Asn Pro Trp Thr Phe
                245                 250                 255

Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Ser Ser Glu Pro Lys Ser
            260                 265                 270

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
        275                 280                 285

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
    290                 295                 300

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
305                 310                 315                 320
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His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
                325                 330                 335

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
            340                 345                 350

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
        355                 360                 365

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
    370                 375                 380

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
385                 390                 395                 400

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
                405                 410                 415

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
            420                 425                 430

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

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
    450                 455                 460

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465                 470                 475                 480

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
                485                 490                 495

Ser Pro Gly Lys
            500
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<210> 29
<211> 1479
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 29
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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

ggagctagcg cggtccagct gcagcagtct ggacctgagt cggaaaagcc tggcgcttca 480

gtgaagattt cctgcaaggc ttctggttac tcattcactg gctacaatat gaactgggtg 540

aagcagaata atggaaagag ccttgagtgg attggaaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggcaag gccacattga ctgtagacaa atcctccagc 660

acagcctaca tgcagctcaa gagtctgaca tctgaggact ctgcagtcta ttactgtgca 720

agatcggtcg gccctatgga ctactggggt caaggaacct cagtcaccgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tctccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaatga 1479

<210> 30
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 30

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Ala
    130                 135                 140

Val Gln Leu Gln Gln Ser Gly Pro Glu Ser Glu Lys Pro Gly Ala Ser
145                 150                 155                 160

Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
    210                 215                 220

Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
                245                 250                 255

Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro
            260                 265                 270

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        275                 280                 285

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305                 310                 315                 320

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                325                 330                 335

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

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        355                 360                 365
```

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
435 440 445

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
465 470 475 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 31
<211> 1479
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 31
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

ggagctagcg cggtccagct gcagcagtct ggacctgagt cggaaaagcc tggcgcttca 480

gtgaagattt cctgcaaggc ttctggttac tcattcactg gctacaatat gaactgggtg 540

aagcagaata atggaaagag ccttgagtgg attggaaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggcaag gccacattga ctgtagacaa atcctccagc 660

acagcctaca tgcagctcaa gagtctgaca tctgaggact ctgcagtcta ttactgtgca 720

agatcggtcg gccctatgga ctactggggt caaggaacct cagtcaccgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaatga 1479

<210> 32
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 32

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Ala
130 135 140

Val Gln Leu Gln Gln Ser Gly Pro Glu Ser Glu Lys Pro Gly Ala Ser
145 150 155 160

Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175

Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
210 215 220

Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
245 250 255

Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
260 265 270

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305 310 315 320

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
325 330 335

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

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
355 360 365

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
435 440 445

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
465 470 475 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 33
<211> 1479
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 33
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ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180
ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240
aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300
gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360
gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420
ggagctagcc aggtgcagct ggtggagtct ggtggaggcg tggtccagcc tgggaggtcc 480
ctgagactct cctgtgcagc ctctggattc accttcagtg gctacaatat gaactgggtc 540
cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600
actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660
accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720
cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 840
ggtggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 900
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

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tacacgcaga agagcctctc cctgtctccg ggtaaatga 1479

<210> 34
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 34

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
130 135 140

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
145 150 155 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
260 265 270

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305 310 315 320

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
325 330 335

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

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
355 360 365

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
435 440 445

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
465 470 475 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 35
<211> 1479
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 35
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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

ggagctagcc aggtgcagct ggtggagtct ggtggaggcg tggtccagcc tgggaggtcc 480

ctgagactct cctgtgcagc ctctggattc accttcagtg gctacaatat gaactgggtc 540

cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttccccccа aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccca cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

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cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaatga 1479

<210> 36
<211> 492
<212> PRT
<213> Artificial sequence

<220>

<223> Humanized TRU-016

<400> 36

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Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1               5                  10                  15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
        35                  40                  45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Gln
    130                 135                 140

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
145                 150                 155                 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro
            260                 265                 270
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Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305 310 315 320

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
325 330 335

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

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
355 360 365

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
435 440 445

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
465 470 475 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 37
<211> 1476
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 37
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

ggggctagcg aggtgcagct ggtggagtct ggtggaggct tggtccagcc tggagggtcc 480

ctgagactct cctgtgcagc ctctggattc accttcagtg gctacaatat gaactgggtc 540

cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tctccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaa 1476

<210> 38
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 38

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

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Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
    130                 135                 140

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
145                 150                 155                 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro
            260                 265                 270

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        275                 280                 285

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305                 310                 315                 320
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Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
325 330 335

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

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
355 360 365

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
435 440 445

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
465 470 475 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 39
<211> 1476
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 39
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

ggggctagcg aggtgcagct ggtggagtct ggtggaggct tggtccagcc tggagggtcc 480

ctgagactct cctgtgcagc ctctggattc accttcagtg gctacaatat gaactgggtc 540

cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaa 1476

<210> 40
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 40

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
    130                 135                 140

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
145                 150                 155                 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
            260                 265                 270

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        275                 280                 285

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305                 310                 315                 320

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                325                 330                 335

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

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        355                 360                 365

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    370                 375                 380
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Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
385 390 395 400

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
435 440 445

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
465 470 475 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 41
<211> 1476
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 41
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

ggggctagcg aggtgcagct ggtggagtct ggtggaggct ctgtccagcc tggagggtcc 480

ctgagactct cctgtgcagc ctctggattc accttcagtg gctacaatat gaactgggtc 540

cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tctccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaa 1476

<210> 42
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 42

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
130 135 140

Val Gln Leu Val Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Gly Ser
145 150 155 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro
260 265 270

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305 310 315 320

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
325 330 335

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

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
355 360 365

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
435 440 445

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
465 470 475 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 43
<211> 1476
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 43
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gaacaagtga aaatgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

ggggctagcg aggtgcagct ggtggagtct ggtggaggct ctgtccagcc tggagggtcc 480

ctgagactct cctgtgcagc ctctggattc accttcagtg gctacaatat gaactgggtc 540

cgccagatgc ccgggaaagg cctggagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctcgagc 780

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 840

ggtggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1200

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaa 1476

<210> 44
<211> 492
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 44

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
130 135 140

Val Gln Leu Val Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Gly Ser
145 150 155 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

Val Ser Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
260 265 270

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305 310 315 320

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
325 330 335

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

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
355 360 365

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

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

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

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
435 440 445

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

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
465 470 475 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 45

<211> 1482
<212> DNA

<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 45
atggaagccc cagctcagct tctcttcctc ctgctactct ggctcccaga taccaccgga 60

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccaggcga aagagccacc 120

ctctcctgcc gagcaagtca aagtgtttac agctacttag cctggtacca acagaaacct 180

ggccaggctc ctaggctcct catctatttt gcaaaaacct tagcagaagg aattccagcc 240

aggttcagtg gcagtggatc cgggacagac ttcactctca ccatcagcag cctagagcct 300

gaagattttg cagtttatta ctgtcaacat cattccgata atccgtggac attcggccaa 360

gggaccaagg tggaaatcaa aggtggcggt ggctcgggcg gtggtggatc tggaggaggt 420

gggaccggtg aggtgcagct ggtgcagtct ggagcagagg tgaaaaagcc cggagagtct 480

ctgaagattt cctgtaaggg atccggttac tcattcactg gctacaatat gaactgggtg 540

cgccagatgc ccgggaaagg cctcgagtgg atgggcaata ttgatcctta ttatggtggt 600

actacctaca accggaagtt caagggccag gtcactatct ccgccgacaa gtccatcagc 660

accgcctacc tgcaatggag cagcctgaag gcctcggaca ccgccatgta ttactgtgca 720

cgctcagtcg gccctatgga ctactggggc cgcggcaccc tggtcactgt ctcctctgat 780

caggagccca aatcttctga caaaactcac acatctccac cgtgcccagc acctgaactc 840

ctgggtggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 900

cggaccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 960

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1020

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1080

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1140

accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatcc 1200

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatcca 1260

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1320

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 1380

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1440

cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 1482

<210> 46
<211> 493
<212> PRT
<213> Artificial sequence

<220>

<223> Humanized TRU-016

<400> 46

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Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1               5                  10                  15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
    130                 135                 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145                 150                 155                 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
            260                 265                 270
```

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
275 280 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
290 295 300

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
305 310 315 320

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
325 330 335

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

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

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

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

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

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
435 440 445

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

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

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

<210> 47
<211> 1500
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 47
aagcttgccg ccatggaagc cccagcgcag cttctcttcc tcctgctact ctggctccca 60

gataccaccg gagaaattgt gttgacacag tctccagcca ccctgtcttt gtctccaggc 120

gaaagagcca ccctctcctg ccgagcaagt gaaaatgttt acagctactt agcctggtac 180

caacagaaac ctggccaggc tcctaggctc ctcatctatt ttgcaaaaac cttagcagaa 240

ggaattccag ccaggttcag tggcagtgga tccgggacag acttcactct caccatcagc 300

agcctagagc ctgaagattt tgcagtttat tactgtcaac atcattccga taatccgtgg 360

acattcggcc aagggaccaa ggtggaaatc aaaggtggcg gcggctcggg cggtggtgga 420

tctggaggag gtgggaccgg tgaggtgcag ctggtgcagt ctggagcaga ggtgaaaaag 480

cccggagagt ctctgaagat ttcctgtaag ggatccggtt actcattcac tggctacaat 540

atgaactggg tgcgccagat gcccgggaaa ggcctcgagt ggatgggcaa tattgatcct 600

tattatggtg gtactaccta caaccggaag ttcaagggcc aggtcactat ctccgccgac 660

aagtccatca gcaccgccta cctgcaatgg agcagcctga aggcctcgga caccgccatg 720

tattactgtg cacgctcagt cggccctttc gactactggg gccagggcac cctggtcact 780

gtctcctctg atcaggagcc caaatcttct gacaaaactc acacatctcc accgtgccca 840

gcacctgaac tcctgggtgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 960

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1140

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atgatctaga 1500

<210> 48
<211> 493
<212> PRT

<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 48

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
35 40 45

```
Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
    130                 135                 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145                 150                 155                 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
                245                 250                 255

Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
            260                 265                 270

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        275                 280                 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    290                 295                 300

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
305                 310                 315                 320

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                325                 330                 335
```

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

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

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

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

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

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        435                 440                 445

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

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

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                485                 490
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<210> 49
<211> 356
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 49
gctagcgagg tgcagctggt gcagtctgga gcagaggtga aaaagcccgg agagtctctg 60

aagatttcct gtaagggatc cggttactca ttcactggct acaatatgaa ctgggtgcgc 120

cagatgcccg ggaaaggcct ggagtggatg ggcaatattg atccttatta tggtggtact 180

acctacaacc ggaagttcaa gggccaggtc actatctccg ccgacaagtc catcagcacc 240

gcctacctgc aatggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgcgc 300

tcagtcggcc ctatggacgt ctggggccaa ggcaccactg tcactgtctc ctcgag 356

<210> 50
<211> 143
<212> PRT
<213> Artificial sequence

<220>

<223> Humanized TRU-016

<400> 50

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly
130 135 140

<210> 51
<211> 1381
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 51
aagcttgccg ccatggaagc cccagcgcag cttctcttcc tcctgctact ctggctccca 60

gataccaccg gagaaattgt gttgacacag tctccagcca ccctgtcttt gtctccaggc 120

gaaagagcca ccctctcctg ccgagcaagt gaaaatgttt acagctactt agcctggtac 180

caacagaaac ctggccaggc tcctaggctc ctcatctatt ttgcaaaaac cttagcagaa 240

ggaattccag ccaggttcag tggcagtgga tccgggacag acttcactct caccatcagc 300

agcctagagc ctgaagattt tgcagtttat tactgtcaac atcattccga taatccgtgg 360

acattcggcc aagggaccaa ggtggaaatc aaaggtggcg gtggctcggg cggtggtgga 420

tctggaggag gtgggaccgg tgaggtgcag ctggtgcagt ctggagcaga ggtgaaaaag 480

cccggagagt ctctgaagat ttcctgtaag ggatccggtt actcattcac tggctacaat 540

atgaactggg tgcgccagat gcccgggaaa ggcctcgagt ggatgggcaa tattgatcct 600

tattatggtg gtactaccta caaccggaag ttcaagggcc aggtcactat ctccgccgac 660

aagtccatca gcaccgccta cctgcaatgg agcagcctga aggcctcgga caccgccatg 720

tattactgtg cacgctcagt cggccctttc gactcctggg gccagggcac cctggtcact 780

gtctcctctg atcaggagcc caaatcttct gacaaaactc acacatctcc accgtgccca 840

gcacctgaac tcctgggtgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 960

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1140

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

a 1381

<210> 52
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 52

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

```
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
    130                 135                 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145                 150                 155                 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
                165                 170                 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
            180                 185                 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
        195                 200                 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Phe Asp Ser Trp Gly Gln Gly Thr Leu Val Thr
                245                 250                 255

Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
            260                 265                 270

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        275                 280                 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    290                 295                 300

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
305                 310                 315                 320

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                325                 330                 335

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

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

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

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

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

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        435                 440                 445

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

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

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                485                 490
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<210> 53
<211> 356
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 53
gctagcgagg tgcagctggt gcagtctgga gcagaggtga aaaagcccgg agagtctctg 60

aagatttcct gtaagggatc cggttactca ttcactggct acaatatgaa ctgggtgcgc 120

cagatgcccg ggaaaggcct ggagtggatg ggcaatattg atccttatta tggtggtact 180

acctacaacc ggaagttcaa gggccaggtc actatctccg ccgacaagtc catcagcacc 240

gcctacctgc aatggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgcgc 300

tcagtcggcc cttttgaccc ctggggccaa ggcaccctgg tcactgtctc ctcgag 356

<210> 54
<211> 143
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 54

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Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1               5                   10                  15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
        35                  40                  45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60
```

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly
130 135 140

<210> 55
<211> 356
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 55
gctagcgagg tgcagctggt gcagtctgga gcagaggtga aaaagcccgg agagtctctg 60

aagatttcct gtaagggatc cggttactca ttcactggct acaatatgaa ctgggtgcgc 120

cagatgcccg ggaaaggcct ggagtggatg ggcaatattg atccttatta tggtggtact 180

acctacaacc ggaagttcaa gggccaggtc actatctccg ccgacaagtc catcagcacc 240

gcctacctgc aatggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgcgc 300

tcagtcggcc cttttcagca ctggggccaa ggcaccctcg tcactgtctc ctcgag 356

<210> 56
<211> 143
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 56

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly
130 135 140

<210> 57
<211> 356
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 57
gctagcgagg tgcagctggt gcagtctgga gcagaggtga aaaagcccgg agagtctctg 60

aagatttcct gtaagggatc cggttactca ttcactggct acaatatgaa ctgggtgcgc 120

cagatgcccg ggaaaggcct ggagtggatg ggcaatattg atccttatta tggtggtact 180

acctacaacc ggaagttcaa gggccaggtc actatctccg ccgacaagtc catcagcacc 240

gcctacctgc aatggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgcgc 300

tcagtcggcc cttttgacgt ctggggccaa ggcaccatgg tcactgtctc ctcgag 356

<210> 58
<211> 143
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 58

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
            100                 105                 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly
    130                 135                 140
```

<210> 59
<211> 356
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 59

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gctagcgagg tgcagctggt gcagtctgga gcagaggtga aaaagcccgg agagtctctg     60

aagatttcct gtaagggatc cggttactca ttcactggct acaatatgaa ctgggtgcgc    120

cagatgcccg ggaaaggcct ggagtggatg ggcaatattg atccttatta tggtggtact    180

acctacaacc ggaagttcaa gggccaggtc actatctccg ccgacaagtc catcagcacc    240

gcctacctgc aatggagcag cctgaaggcc tcggacaccg ccatgtatta ctgtgcgcgc    300

tcagtcggcc cttttgacat ctggggccaa ggcaccatgg tcactgtctc ctcgag        356
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<210> 60
<211> 143
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 60

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Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1               5                  10                  15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
        35                  40                  45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50                  55                  60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
65                  70                  75                  80

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

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly
130 135 140

<210> 61
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 61

Arg Ala Ser Glu Asn Val Tyr Ser Tyr Leu Ala
1 5 10

<210> 62
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 62

Arg Thr Ser Glu Asn Val Tyr Ser Tyr Leu Ala
1 5 10

<210> 63
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 63

Gly Tyr Asn Met Asn
1 5

<210> 64
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 64

Phe Ala Lys Thr Leu Ala Glu
1 5

<210> 65
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 65

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

Gly

<210> 66
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 66

Gln His His Ser Asp Asn Pro Trp Thr
1 5

<210> 67
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 67

Ser Val Gly Pro Phe Asp Tyr
1 5

<210> 68
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 68

Ser Val Gly Pro Phe Asp Ser
1 5

<210> 69
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 69

Ser Val Gly Pro Met Asp Tyr
1 5

<210> 70
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 70

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

Glu Arg Ala Thr Leu Ser Cys
20

<210> 71
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 71

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
20 25 30

<210> 72
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 72

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 73
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 73

Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
1 5 10

<210> 74
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 74

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

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

<210> 75
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 75

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

Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
20 25 30

<210> 76
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 76

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 77
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 77

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 78
<211> 11
<212> PRT
<213> Artificial sequence

<220>

<223> Humanized TRU-016

<400> 78

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 79
<211> 1500
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 79
aagcttgccg ccatggaagc cccagcgcag cttctcttcc tcctgctact ctggctccca 60

gataccaccg gagaaattgt gttgacacag tctccagcca ccctgtcttt gtctccaggc 120

gaaagagcca ccctctcctg ccgagcaagt gaaaatgttt acagctactt agcctggtac 180

caacagaaac ctggccaggc tcctaggctc ctcatctatt ttgcaaaaac cttagcagaa 240

ggaattccag ccaggttcag tggcagtgga tccgggacag acttcactct caccatcagc 300

agcctagagc ctgaagattt tgcagtttat tactgtcaac atcattccga taatccgtgg 360

acattcggcc aagggaccaa ggtggaaatc aaaggtggcg gtggctcggg cggtggtgga 420

tctggaggag gtgggaccgg tgaggtgcag ctggtgcagt ctggagcaga ggtgaaaaag 480

cccggagagt ctctgaagat ttcctgtaag ggatccggtt actcattcac tggctacaat 540

atgaactggg tgcgccagat gcccgggaaa ggcctcgagt ggatgggcaa tattgatcct 600

tattatggtg gtactaccta caaccggaag ttcaagggcc aggtcactat ctccgccgac 660

aagtccatca gcaccgccta cctgcaatgg agcagcctga aggcctcgga caccgccatg 720

tattactgtg cacgctcagt cggccctttc gacctctggg gcagaggcac cctggtcact 780

gtctcctctg atcaggagcc caaatcttct gacaaaactc acacatctcc accgtgccca 840

gcacctgaac tcctgggtgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 960

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1140

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

ctgccccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atgatctaga 1500

<210> 80
<211> 493

<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 80

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

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Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
            260                 265                 270

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        275                 280                 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    290                 295                 300

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
305                 310                 315                 320

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                325                 330                 335

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

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

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

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

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

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        435                 440                 445

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

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

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                485                 490
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<210> 81
<211> 1494
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 81
aagcttgccg ccatggaagc cccagctcag cttctcttcc tcctgctact ctggctccca 60
gataccaccg gagaaattgt gttgacacag tctccagcca ccctgtcttt gtctccaggc 120
gaaagagcca ccctctcctg ccgagcaagt gaaaatgttt acagctactt agcctggtac 180
caacagaaac ctggccaggc tcctaggctc ctcatctatt ttgcaaaaac cttagcagaa 240
ggaattccag ccaggttcag tggcagtgga tccgggacag acttcactct caccatcagc 300
agcctagagc ctgaagattt tgcagtttat tactgtcaac atcattccga taatccgtgg 360
acattcggcc aagggaccaa ggtggaaatc aaaggtggcg gtggctcggg cggtggtgga 420
tctggaggag gtggggctag cgaggtgcag ctggtgcagt ctggagcaga ggtgaaaaag 480
cccggagagt ctctgaagat ttcctgtaag ggatccggtt actcattcac tagctacaat 540
atgaactggg tgcgccagat gcccgggaaa ggcctggagt ggatgggcaa tattgatcct 600
tattatggtg gtactaacta cgcccagaag ttccagggcc aggtcactat ctccgccgac 660
aagtccatca gcaccgccta cctgcaatgg agcagcctga aggcctcgga caccgccatg 720
tattactgtg cacgctcagt cggccctatg gactactggg gccgcggcac cctggtcact 780
gtctcctctg atcaggagcc caaatcttct gacaaaactc acacatctcc accgtgccca 840
gcacctgaac tcctgggtgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900
ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 960
cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080
caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1140
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200
ctgccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260
ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380
accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atga 1494

<210> 82
<211> 493
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 82

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
260 265 270

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
275 280 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
290 295 300

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Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
305                 310                 315                 320

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                325                 330                 335

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

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

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

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

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

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        435                 440                 445

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

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

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                485                 490
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<210> 83
<211> 1476
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 83

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aagcttgccg ccatggaagc cccagcgcag cttctcttcc tcctgctact ctggctccca     60

gataccaccg gagaaattgt gttgacacag tctccagcca ccctgtcttt gtctccaggc    120

gaaagagcca ccctctcctg ccgagcaagt gagaatgttt acagctactt agcctggtac    180

caacagaaac ctggccaggc tcctaggctc ctcatctatt ttgcaaaaac cttagcagaa    240

gggattccag ccagattcag tggcagtggt tccgggacag acttcactct caccatcagc    300

agcctagagc ctgaagattt tgcagtttat tactgtcaac atcattccga taatccgtgg    360
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acattcggcc aagggaccaa ggtggaaatc aaaggtggcg gtggctcggg cggtggtgga 420

tctggaggag gtgggagcgg aggaggagct agcgaggtgc agctggtgca gtctggagca 480

gaggtgaaaa agcccggaga gtctctgaag atttcctgta agggatccgg ttactcattc 540

actggctaca atatgaactg ggtgcgccag atgcccggga aaggcctcga atggatgggc 600

aatattgatc cttattatgg tggtactacc tacaaccgga agttcaaggg ccaggtcact 660

atctccgccg acaagtccat cagcaccgcc tacctgcaag gagcagcctg aaggcctcgg 720

acaccgccat gtattactgt gcacgctcag tcggcccttt cgactcctgg ggccagggca 780

ccctggtcac tgtctcgagt tgtccaccgt gcccagcacc tgaactcctg ggtggaccgt 840

cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg acccctgagg 900

tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc aactggtacg 960

tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag tacaacagca 1020

cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat ggcaaggagt 1080

acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc atctccaaag 1140

ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg gatgagctga 1200

ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc gacatcgccg 1260

tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct cccgtgctgg 1320

actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc aggtggcagc 1380

aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac tacacgcaga 1440

agagcctctc cctgtctccg ggtaaatgac tctaga 1476

<210> 84
<211> 485
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 84

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Ala Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
145 150 155 160

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
165 170 175

Thr Gly Tyr Asn Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu
180 185 190

Glu Trp Met Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn
195 200 205

Arg Lys Phe Lys Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser
210 215 220

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met
225 230 235 240

Tyr Tyr Cys Ala Arg Ser Val Gly Pro Phe Asp Ser Trp Gly Gln Gly
245 250 255

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

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
275 280 285

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

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
340 345 350

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
355 360 365

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

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

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
405 410 415

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
435 440 445

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
450 455 460

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
465 470 475 480

Leu Ser Pro Gly Lys
485

<210> 85
<211> 1494
<212> DNA
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 85
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gataccaccg gagaaattgt gttgacacag tctccagcca ccctgtcttt gtctccaggc 120

gaaagagcca ccctctcctg ccgaacaagt gaaaatgttt acagctactt agcctggtac 180

caacagaaac ctggccaggc tcctaggctc ctcatctatt ttgcaaaaac cttagcagaa 240

ggaattccag ccaggttcag tggcagtgga tccgggacag acttcactct caccatcagc 300

agcctagagc ctgaagattt tgcagtttat tactgtcaac atcattccga taatccgtgg 360

acattcggcc aagggaccaa ggtggaaatc aaaggtggcg gtggctcggg cggtggtgga 420

tctggaggag gtgggaccgg tgaggtgcag ctggtgcagt ctggagcaga ggtgaaaaag 480

cccggagagt ctctgaagat ttcctgtaag ggatccggtt actcattcac tggctacaat 540

atgaactggg tgcgccagat gcccgggaaa ggcctggagt ggatgggcaa tattgatcct 600

tattatggtg gtactaccta caaccggaag ttcaagggcc aggtcactat ctccgccgac 660

aagtccatca gcaccgccta cctgcaatgg agcagcctga aggcctcgga caccgccatg 720

tattactgtg cacgctcagt cggccctatg gactactggg gccgcggcac cctggtcact 780

gtctcctctg atcaggagcc caaatcttct gacaaaactc acacatctcc accgtgccca 840

gcacctgaac tcctgggtgg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 900

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 960

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1080

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1140

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

ctgcccccat cccgggatga gctgaccaag aaccaggtca gcctgacctg cctggtcaaa 1260

ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atga 1494

<210> 86
<211> 493
<212> PRT
<213> Artificial sequence

<220>
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<400> 86

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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
210 215 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
245 250 255

Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
260 265 270

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
275 280 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
290 295 300

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
305 310 315 320

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
325 330 335

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

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

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

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

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

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
435 440 445

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

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

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

<210> 87
<211> 1494
<212> DNA
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gaaagagcca ccctctcctg ccgaacaagt gaaaatgttt acagctactt agcctggtac 180

caacagaaac ctggccaggc tcctaggctc ctcatctatt ttgcaaaaac cttagcagaa 240

ggaattccag ccaggttcag tggcagtgga tccgggacag acttcactct caccatcagc 300

agcctagagc ctgaagattt tgcagtttat tactgtcaac atcattccga taatccgtgg 360

acattcggcc aagggaccaa ggtggaaatc aaaggtggcg gtggctcggg cggtggtgga 420

tctggaggag gtggggctag cgaggtgcag ctggtgcagt ctggagcaga ggtgaaaaag 480

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tattactgtg cacgctcagt cggccctatg gactactggg gccgcggcac cctggtcact 780

gtctcctctg atcaggagcc caaatcttct gacaaaactc acacatctcc accgtgccca 840

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cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1020

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caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1140

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1200

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ggcttctatc caagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1320

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 1380

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1440

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atga 1494

<210> 88
<211> 493
<212> PRT
<213> Artificial sequence

<220>
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<400> 88

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Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Thr Ser Glu Asn
35 40 45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Phe Ala Lys Thr Leu Ala Glu Gly Ile Pro Ala
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 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His His Ser
100 105 110

Asp Asn Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Ser Glu
130 135 140

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser
145 150 155 160

Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
180 185 190

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205

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Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu
    210                 215                 220

Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala
225                 230                 235                 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Arg Gly Thr Leu Val Thr
                245                 250                 255

Val Ser Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser
            260                 265                 270

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
        275                 280                 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    290                 295                 300

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
305                 310                 315                 320

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                325                 330                 335

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

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

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

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

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

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

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        435                 440                 445

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

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
465                 470                 475                 480
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His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<210> 89
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<212> DNA

<213> Artificial sequence

<220>
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<210> 90
<211> 15
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<400> 90

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
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<210> 91
<211> 45
<212> DNA
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<220>
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<400> 92

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

<210> 93
<211> 45
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<210> 94

<211> 15

<212> PRT
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<400> 94

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

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<210> 96
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<400> 96

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<400> 98

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
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<400> 100

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<400> 102

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro
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<400> 103
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<400> 104

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<400> 106

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

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<400> 107
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<220>
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<400> 108

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

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<400> 109
gagcccaaat cttgtgacaa aactcacaca tctccaccga gccca 45

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<400> 110

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<210> 112
<211> 15
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<400> 112

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

<210> 113
<211> 45
<212> DNA
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<400> 113
gagcccaaat cttgtgacaa aactcacaca tgtccaccga gctca 45

<210> 114
<211> 15
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<220>
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<400> 114

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

<210> 115
<211> 19
<212> PRT
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<220>
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<400> 115

Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro
1 5 10 15

Ser Pro Ser

<210> 116
<211> 6
<212> PRT
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<220>
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<400> 116

Val Pro Pro Pro Pro Pro
1 5

<210> 117
<211> 186
<212> DNA
<213> Artificial sequence

<220>
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<400> 117
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tcctgcgata cgcctccgcc atgtccacgg tgcccagagc ccaaatcatg cgatacgccc 120

ccaccgtgtc cccgctgtcc tgaaccaaag tcatgcgata ccccaccacc atgtccaaga 180

tgccca 186

<210> 118
<211> 62
<212> PRT
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<400> 118

Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys
1 5 10 15

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
20 25 30

Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu
35 40 45

Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
50 55 60

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<212> DNA
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1 5 10 15

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<400> 122

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

<210> 123
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<400> 124

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

<210> 125
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<220>
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gagcccaaat cttgtgacac acctcccccа tccccacggt gccca 45

<210> 126
<211> 15
<212> PRT
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<220>
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<400> 126

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

<210> 127
<211> 58
<212> PRT
<213> Artificial sequence

<220>
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<400> 127

Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala Gln Pro Gln
1 5 10 15

Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro Ala Thr Thr Arg
20 25 30

Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Lys Glu Lys Glu Lys Glu
35 40 45

Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro
50 55

<210> 128
<211> 11
<212> PRT
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<220>
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<400> 128

Arg Thr Ser Gln Asn Val Tyr Ser Tyr Leu Ala
1 5 10

<210> 129
<211> 11
<212> PRT
<213> Artificial sequence

<220>
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<400> 129

Arg Thr Ser Glu Ser Val Tyr Ser Tyr Leu Ala
1 5 10

<210> 130
<211> 11
<212> PRT
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<220>
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<400> 130

Arg Ala Ser Gln Ser Val Tyr Ser Tyr Leu Ala
1 5 10

<210> 131
<211> 11
<212> PRT
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<220>
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<400> 131

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 132
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<212> PRT
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<220>
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<400> 132

Arg Ala Ser Gln Ser Val Ser Tyr Tyr Leu Ala
1 5 10

<210> 133
<211> 5
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<400> 133

Ser Tyr Met Asn Met
1 5

<210> 134
<211> 5
<212> PRT
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<220>
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<400> 134

Ser Tyr Trp Ile Gly
1 5

<210> 135
<211> 7
<212> PRT
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<400> 135

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 136
<211> 7
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<400> 136

Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 137
<211> 7
<212> PRT
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<220>
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<400> 137

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 138
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 138

Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

Gly

<210> 139
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 139

Arg Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Ser Pro Ser Phe Gln
1 5 10 15

Gly

<210> 140
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 140

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

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

<210> 141
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 141

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser
20 25 30

<210> 142
<400> 142
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<210> 143
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<212> PRT
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<220>
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<400> 143

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

Thr Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr
20 25 30

<210> 144
<211> 30
<212> PRT
<213> Artificial sequence

<220>
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<400> 144

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
20 25 30

<210> 145
<211> 30
<212> PRT
<213> Artificial sequence

<220>
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<400> 145

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

Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr
20 25 30

<210> 146
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Humanized TRU-016

<400> 146

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

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

<210> 147
<211> 14
<212> PRT
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<220>
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<400> 147

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
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<210> 148
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<210> 149
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<210> 150
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<212> PRT
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<220>
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<400> 150

Trp Val Gln Gln Ala Pro Gly Lys Gly Leu Glu Trp Met Gly
1 5 10

<210> 151
<211> 14
<212> PRT
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<220>
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<400> 151

Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
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<210> 152
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<210> 153
<211> 14
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<220>
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<400> 153

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 154
<211> 32
<212> PRT
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<220>
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<400> 154

Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 155
<211> 32
<212> PRT
<213> Artificial sequence

<220>
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<400> 155

Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 156
<211> 32
<212> PRT
<213> Artificial sequence

<220>
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<400> 156

Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

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Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Asp Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Thr
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<400> 158

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

Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
20 25 30

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His Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln
1 5 10 15

Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
20 25 30

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Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln
1 5 10 15

Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
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Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
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Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
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Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
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<400> 169

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
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<400> 170

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
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Glu Arg Ala Thr Leu Ser Cys
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<400> 171

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

Glu Arg Ala Thr Leu Ser Cys
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<400> 172

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

Asp Arg Val Thr Ile Thr Cys
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Asn Ile Gln Met Thr Gln Ser Pro Ser Ala Met Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys
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<400> 177

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

Asp Arg Val Thr Ile Thr Cys
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<400> 178

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

Asp Arg Val Thr Ile Thr Cys
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<400> 179

Ala Ile Arg Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
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<400> 180

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

Asp Arg Val Thr Ile Thr Cys
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<400> 181

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys
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<400> 182

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

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Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

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Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr
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Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr
1 5 10 15

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<400> 187

Trp Phe Gln Gln Lys Pro Gly Lys Val Pro Lys His Leu Ile Tyr
1 5 10 15

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<400> 188

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

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

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

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Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
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<400> 203

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

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

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Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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<400> 207

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

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<400> 208

Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
1 5 10

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<400> 209

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
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<400> 210

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
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Ser Val Gly Pro Phe Gln His
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Ser Val Gly Pro Phe Asp Val
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Ser Val Gly Pro Phe Asp Ile
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Ser Val Gly Pro Phe Asp Leu
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1 5 10

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

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1 5 10 15

Gly Gly Gly Ser
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Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 226
<211> 30
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<220>
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<400> 226
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 Gly Gly Gly Gly Ser
20 25 30