

SEQUENCE LISTING

<110> National University of Singapore

<120> CHIMERIC ANTIGEN RECEPTORS AND GENE EDITING OF CD2 FOR
IMMUNOTHERAPY OF T-CELL MALIGNANCIES

<130> 119419-5005-WO

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<141> 2019-05-23

<150> 62/675,525

<151> 2018-05-23

<160> 53

<170> PatentIn version 3.5

<210> 1

<211> 289

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic polypeptide

<400> 1

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro
 50 55 60

Arg Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn
 85 90 95

Ser Val Glu Pro Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His
 100 105 110

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

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

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

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

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

Arg Ile Asp Pro Tyr Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Thr
195 200 205

Asp Lys Ala Ile Ser Thr Ile Asp Thr Ser Ser Asn Thr Ala Tyr Met
210 215 220

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

Arg Ser Pro Arg Asp Ser Ser Thr Asn Leu Ala Asp Trp Gly Gln Gly
245 250 255

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
260 265 270

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Lys Asp Glu
275 280 285

Leu

<210> 2

<211> 348

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic polypeptide

<400> 2

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

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

Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro
 50 55 60

Arg Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn
 85 90 95

Ser Val Glu Pro Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His
 100 105 110

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

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

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

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

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

Arg Ile Asp Pro Tyr Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Thr
 195 200 205

Asp Lys Ala Ile Ser Thr Ile Asp Thr Ser Ser Asn Thr Ala Tyr Met
210 215 220

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

Arg Ser Pro Arg Asp Ser Ser Thr Asn Leu Ala Asp Trp Gly Gln Gly
245 250 255

Thr Leu Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro Arg
260 265 270

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
275 280 285

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
290 295 300

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
305 310 315 320

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Lys Tyr Lys
325 330 335

Ser Arg Arg Ser Phe Ile Glu Glu Lys Lys Met Pro
340 345

<210> 3

<211> 291

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic polypeptide

<400> 3

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu
20 25 30

Ala Val Ser Ala Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln
35 40 45

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

Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr
65 70 75 80

Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
85 90 95

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

Tyr Tyr Cys His Gln Tyr Leu Ser Ser His Thr Phe Gly Gly Gly Thr
115 120 125

Lys Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

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

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

Glu Trp Ile Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn
195 200 205

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

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

Tyr Tyr Cys Ala Thr Glu Asp Leu Tyr Tyr Ala Met Glu Tyr Trp Gly
245 250 255

Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
260 265 270

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Lys
275 280 285

Asp Glu Leu
290

<210> 4
<211> 350
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic polypeptide

<400> 4

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu
20 25 30

Ala Val Ser Ala Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln
35 40 45

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

Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr
65 70 75 80

Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
85 90 95

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

Tyr Tyr Cys His Gln Tyr Leu Ser Ser His Thr Phe Gly Gly Gly Thr
115 120 125

Lys Leu Glu Ile Lys Arg Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

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

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

Glu Trp Ile Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn
195 200 205

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

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

Tyr Tyr Cys Ala Thr Glu Asp Leu Tyr Tyr Ala Met Glu Tyr Trp Gly
245 250 255

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

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Lys
325 330 335

Tyr Lys Ser Arg Arg Ser Phe Ile Glu Glu Lys Lys Met Pro
340 345 350

<210> 5

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic polypeptide

<400> 5

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu
20 25 30

Ala Val Ser Ala Gly Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln
35 40 45

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

Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr
65 70 75 80

Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr
85 90 95

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

Tyr Tyr Cys His Gln Tyr Leu Ser Ser His Thr Phe Gly Gly Gly Thr
115 120 125

Lys Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
130 135 140

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

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

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

Glu Trp Ile Gly Asn Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn
195 200 205

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

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

Tyr Tyr Cys Ala Thr Glu Asp Leu Tyr Tyr Ala Met Glu Tyr Trp Gly
245 250 255

Gln Gly Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg
260 265 270

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
275 280 285

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
290 295 300

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
305 310 315 320

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg
325 330 335

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
340 345 350

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
355 360 365

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
370 375 380

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
385 390 395 400

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
405 410 415

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
420 425 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
435 440 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
450 455 460

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
465 470 475 480

His Met Gln Ala Leu Pro Pro Arg
485

<210> 6

<211> 892

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic polynucleotide

<400> 6

gaattcggct tccaccatgg ctctgccctg gaccgccctg ctgctgcctc tggctctgct 60

gctgcacgct gccgcccaa tcgtgatgac ccagagccca gccaccctgt ccgtgacacc 120

tggcgaccgg gtgtctctga gctgcagagc ctccagtct atcagcgatt acctgcactg 180

gtatcagcag aagtcacacg agtctccccg gctgctgac aagtagccta gccagtctat 240

cagcggcatc ctagccgggt tctccggatc tggaagcgga tccgacttta ccctgagcat 300

caactccgtg gagccagagg atgtgggcgt gtactattgc cagaatggcc actccttccc 360

cctgaccttt ggcgccggca caaagctgga gctgcggaga ggcgggcgcg gctctggagg 420

aggaggaagc ggaggaggag gctcccaggt gcagctgcag cagccaggaa cagagctggt 480

gcggcccggc agctccgtga agctgtcctg taaggcctct ggctacacct tcacaagcta 540

ttgggtgaac tgggtgaagc agaggcctga ccagggcctg gaggatcg gaagatcga 600

cccatacgat tctgagacac actataacca gaagtttaca gacaaggcca tcagcaccat 660
 cgatacatct agcaataaccg cctatatgca gctgtccacc ctgacatctg atgccagcgc 720
 cgtgtactat tgttctagga gccctcgca ctctctaca aatctggcag attggggaca 780
 gggcaccctg gtgacagtga gctccggtgg tggcggcagt ggtggcggtg gctcaggcgg 840
 tggcggctcc ggtggcggtg gctctgcaga aaaagatgag ttgtaactcg ag 892

<210> 7
 <211> 1069
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic polynucleotide

<400> 7
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 tggcgaccgg gtgtctctga gctgcagagc ctccagctct atcagcgatt acctgcactg 180
 gtatcagcag aagtcaccag agtctccccg gctgctgac aagtacgcta gccagtctat 240
 cagcggcatc ctagccggt tctccgcatc tggaagcgga tccgacttta cctgagcat 300
 caactccgtg gagccagagg atgtgggcgt gtactattgc cagaatggcc actccttccc 360
 cctgaccttt ggcgccggca caaagctgga gctgcggaga ggcgggcg gctctggagg 420
 aggaggaagc ggaggaggag gctcccaggt gcagctgcag cagccaggaa cagagctggt 480
 gcggcccggc agctccgtga agctgtctg taaggcctct ggctacacct tcacaagcta 540
 ttgggtgaac tgggtgaagc agaggcctga ccagggcctg gaggatcg gaaggatcga 600
 cccatacgat tctgagacac actataacca gaagtttaca gacaaggcca tcagcaccat 660
 cgatacatct agcaataaccg cctatatgca gctgtccacc ctgacatctg atgccagcgc 720
 cgtgtactat tgttctagga gccctcgca ctctctaca aatctggcag attggggaca 780
 gggcaccctg gtgacagtga gctccaagcc aaccacaacc cctgcaccaa ggccacctac 840
 accagcacct accatcgcaa gccagccact gtccctgagg ccagaggcat gtaggcctgc 900
 agcaggaggc gccgtgcaca cacgcggcct ggactttgcc tgcgatatct acatctgggc 960
 accactggca ggaacctgtg gcgtgtgct gctgagcctg gtgattacc tgtataagta 1020
 caagtcaga cgctcattca ttaggaaaa gaaaatgcct taactcgag 1069

<210> 8
<211> 898
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic polynucleotide

<400> 8
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gctgcacgct gcccgcccaa acatcatgat gaccagtc ccagctccc tggccgtgtc 120
tgccggagag aaggtgacca tgacatgcaa gtctagccag tccgtgctgt actcctctaa 180
ccagaagaat tacctggcct ggtatcagca gaagcccggc cagagcccta agctgctgat 240
ctattgggca agcaccggg agtccggagt gccagacaga ttcaccggaa gcggatccgg 300
aacagacttc accctgacaa tcagctccgt gcagcctgag gacctggccg tgtactattg 360
ccaccagtac ctgtctagcc acaccttcgg cggcggcaca aagctggaga tcaagagggg 420
aggaggagga tccggaggag gaggtcttgg cggcggcggc agccagctgc agcagccagg 480
agcagagctg gtgaggcccg gctcctctgt gaagctgtct tgtaaggcca gcggctacac 540
cttcacaagg tattggatcc actgggtgaa gcagcgcct atccagggcc tggagtggat 600
cggcaacatc gaccatctg atagcgagac aactacaat cagaagtta aggacaaggc 660
caccctgaca gtggataaga gctccggcac cgctatatg cagctgtcta gcctgacatc 720
cgaggactct gccgtgtact attgtgccac agaggatctg tactatgcca tggagtactg 780
gggccagggc acctccgtga cagtgtcctc tgggtgtggc ggagtggtg gcggtggctc 840
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<210> 9
<211> 1075
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic polynucleotide

<400> 9
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gctgcacgct gcccgcccaa acatcatgat gaccagtc ccagctccc tggccgtgtc 120

tgccggagag aaggtgacca tgacatgcaa gtctagccag tccgtgctgt actcctctaa 180
 ccagaagaat tacctggcct ggtatcagca gaagcccggc cagagcccta agctgctgat 240
 ctattgggca agcaccggg agtccggagt gccagacaga ttcaccggaa gcggatccgg 300
 aacagacttc accctgacaa tcagctccgt gcagcctgag gacctggccg tgtactattg 360
 ccaccagtac ctgtctagcc acaccttcgg cggcggcaca aagctggaga tcaagagggg 420
 aggaggagga tccggaggag gaggtcttgg cggcggcggc agccagctgc agcagccagg 480
 agcagagctg gtgaggcccg gctcctctgt gaagctgtct tgtaaggcca gcggctacac 540
 cttcacaagg tattggatcc actgggtgaa gcagcgcct atccagggcc tggagtggat 600
 cggcaacatc gacctatctg atagcgagac aactacaat cagaagtta aggacaaggc 660
 caccctgaca gtggataaga gctccggcac cgcctatatg cagctgtcta gcctgacatc 720
 cgaggactct gccgtgtact attgtgccac agaggatctg tactatgcca tggagtactg 780
 gggccagggc acctccgtga cagtgtctc taagccaacc acaaccctg caccaaggcc 840
 acctacacca gcacctacca tcgaagcca gccactgtcc ctgaggccag aggcatgtag 900
 gcctgcagca ggaggcgccg tgcacacacg cggcctggac ttgcctgcg atatctacat 960
 ctgggcacca ctggcaggaa cctgtggcgt gctgctgctg agcctgggta ttaccctgta 1020
 taagtacaag tccagacgct cattcattga ggaaaagaaa atgccttaac tcgag 1075

<210> 10

<211> 1549

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic polynucleotide

<400> 10

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 tgccggagag aaggtgacca tgacatgcaa gtctagccag tccgtgctgt actcctctaa 180
 ccagaagaat tacctggcct ggtatcagca gaagcccggc cagagcccta agctgctgat 240
 ctattgggca agcaccggg agtccggagt gccagacaga ttcaccggaa gcggatccgg 300
 aacagacttc accctgacaa tcagctccgt gcagcctgag gacctggccg tgtactattg 360
 ccaccagtac ctgtctagcc acaccttcgg cggcggcaca aagctggaga tcaagagggg 420

aggaggagga tccggaggag gaggtcttgg cggcggcggc agccagctgc agcagccagg 480
 agcagagctg gtgaggcccc gctcctctgt gaagctgtct tgtaaggcca gcggctacac 540
 cttcacaagg tattggatcc actgggtgaa gcagcgcct atccagggcc tggagtggat 600
 cggcaacatc gacctatctg atagcgagac aactacaat cagaagtta aggacaaggc 660
 caccctgaca gtggataaga gtcctggcac cgcctatatg cagctgtcta gcctgacatc 720
 cgaggactct gccgtgtact attgtgccac agaggatctg tactatgcca tggagtactg 780
 gggccagggc acctccgtga cagtgtctc taccactaca cctgcacaa ggctccac 840
 acccgctccc actatcgtt cccagccact gtccctgagg cccgaggcct gcaggccagc 900
 agctggcgga gccgtcata ctagggggct ggacttcgct tgcgacatct acatctgggc 960
 cccactggca gggacatgcg gagtctgtct gctgtccctg gtcacacac tgtactgaa 1020
 gcgggggcgc aaaaaactgc tgtatatctt taagcagcct tcatgagac cagtgcagac 1080
 aaccaggag gaagatgggt gctcatgccg gtttcccag gaggaggaag gcggctgcga 1140
 gctgagggtg aagttttccc gtcagcaga tgctctgcc taccagcagg gccagaacca 1200
 gctgtataat gagctgaacc tgggcagacg cgaagagtat gatgtgctgg aaaaaggcg 1260
 gggaagagac ccgaaatgg gagggaagcc aaggcggaaa aacccccagg agggcctgta 1320
 caatgagctg cagaaggaca aaatggcaga ggcttacagt gagattggga tgaagggaga 1380
 gagacggagg ggaaaaggc acgatggcct gtaccagggg ctgagcacag caaccaaaga 1440
 tacttatgac gcactgcaca tgcaggcact gccaccaga tgacagccag gggatttcac 1500
 cactcaaagg ccagacctgc agacgccag attatgagac aactcgag 1549

<210> 11

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic polypeptide

<400> 11

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

1 5 10 15

His Ala Ala Arg Pro

<210> 12
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic polypeptide

<400> 12

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

<210> 13
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic polypeptide

<400> 13

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

Gly Gly Gly Ser Ala Glu Lys Asp Glu Leu
 20 25

<210> 14
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic polypeptide

<400> 14

Leu Tyr Lys Tyr Lys Ser Arg Arg Ser Phe Ile Glu Glu Lys Lys Met
 1 5 10 15

Pro

<210> 15
 <211> 67

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic polypeptide

<400> 15

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
35 40 45

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Ile
50 55 60

Thr Leu Tyr
65

<210> 16
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic polypeptide

<400> 16

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
35 40

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

<220>

<223> synthetic polypeptide

<400> 17

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 18

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic polypeptide

<400> 18

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

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

Trp Val Asn Trp Val Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asp Pro Tyr Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
50 55 60

Thr Asp Lys Ala Ile Ser Thr Ile Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

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

Ser Arg Ser Pro Arg Asp Ser Ser Thr Asn Leu Ala Asp Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 19

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic polypeptide

<400> 19

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

Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu
20 25 30

His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile Lys
35 40 45

Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser
50 55 60

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

Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His Ser Phe Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Arg Arg

100

105

<210> 20

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic polypeptide

<400> 20

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

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

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

Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys Asp
50 55 60

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

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

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

Thr Val Ser Ser
115

<210> 21

<211> 113

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<400> 21

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

Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

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

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Pro Glu Asp Leu Ala Val Tyr Tyr Cys His Gln
85 90 95

Tyr Leu Ser Ser His Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg

<210> 22

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<400> 22

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

Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu
20 25 30

His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile Lys
35 40 45

Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser

50 55 60

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

Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His Ser Phe Pro Leu Thr
85 90 95

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

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

Pro Gly Thr Glu Leu Val Arg Pro Gly Ser Ser Val Lys Leu Ser Cys
130 135 140

Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Val Asn Trp Val Lys
145 150 155 160

Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Tyr
165 170 175

Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Thr Asp Lys Ala Ile Ser
180 185 190

Thr Ile Asp Thr Ser Ser Asn Thr Ala Tyr Met Gln Leu Ser Thr Leu
195 200 205

Thr Ser Asp Ala Ser Ala Val Tyr Tyr Cys Ser Arg Ser Pro Arg Asp
210 215 220

Ser Ser Thr Asn Leu Ala Asp Trp Gly Gln Gly Thr Leu Val Thr Val
225 230 235 240

Ser Ser

<210> 23

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<400> 23

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

Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

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

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Pro Glu Asp Leu Ala Val Tyr Tyr Cys His Gln
85 90 95

Tyr Leu Ser Ser His Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

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

Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Trp Ile
145 150 155 160

His Trp Val Lys Gln Arg Pro Ile Gln Gly Leu Glu Trp Ile Gly Asn
165 170 175

Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys Asp
180 185 190

Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Gly Thr Ala Tyr Met Gln

195

200

205

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

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

Thr Val Ser Ser

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<400> 24

Lys Asp Glu Leu

1

<210> 25

<211> 4

<212> PRT

<213> Artificial Sequence

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Lys Lys Asp Glu

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<223> Xaa can be any naturally occurring amino acid

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Lys Lys Xaa Xaa
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<210> 27

<211> 4

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<400> 27

Lys Lys Met Pro
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<210> 28

<211> 4

<212> PRT

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<400> 28

Tyr Gln Arg Leu
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<210> 29

<211> 6

<212> PRT

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<223> synthetic polypeptide

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Ala Glu Lys Asp Glu Leu
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<210> 30

<211> 26

<212> PRT

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

Gly Gly Gly Ser Ala Glu Lys Asp Glu Leu
20 25

<210> 31

<211> 17

<212> PRT

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<400> 31

Leu Tyr Lys Tyr Lys Ser Arg Arg Ser Phe Ile Glu Glu Lys Lys Met
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Pro

<210> 32

<211> 4

<212> PRT

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<221> MOD_RES

<222> (1)..(4)

<223> wherein n is 1-10

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Gly Gly Gly Ser
1

<210> 33

<211> 4

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Gly Gly Ser Gly
1

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Gly Gly Ser Gly Gly
1 5

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Gly Gly Gly Gly Ser
1 5

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Gly Gly Gly Gly Ser
1 5

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<400> 37

Gly Gly Gly Gly Ser
1 5

<210> 38
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<400> 38

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

<210> 39
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<400> 39

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

Gly Gly Gly Ser
20

<210> 40
<211> 4
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<400> 40

Tyr Gly Arg Leu
1

<210> 41
<211> 4
<212> PRT
<213> Artificial Sequence

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<400> 41

Tyr Gln Arg Leu
1

<210> 42
<211> 4
<212> PRT
<213> Artificial Sequence

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<400> 42

Tyr Lys Gly Leu
1

<210> 43
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<223> Xaa can be any naturally occurring amino acid

<400> 43

Tyr Xaa Xaa Leu
1

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caaagagatt acgaatgcct 20

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<400> 45
cttgtagata tcctgatcat 20

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<400> 46
cacgcacctg gacagctgac 20

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<400> 47

ggttggttg atacaagtcc

20

<210> 48

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agcttgaac agactcacgg

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aatgggcgga ggagagtagt

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gcagaatcca ggtggcaaca

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agggaactgt gggatgactg 20

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<400> 53
gaacacctga gccttgagc 20