

# SEQUENCE LISTING

<110> Fate Therapeutics, Inc.  
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 Bjordahl, Ryan  
 Tong Lee, Tom

<120> Immunotherapies Using Enhanced iPSC Derived Effector Cells

<130> 056932-516001W0

<150> 62/774,278  
 <151> 2018-12-02

<160> 17

<170> PatentIn version 3.5

<210> 1  
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 <213> Artificial sequence

<220>  
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<220>  
 <221> misc\_feature  
 <223> 340 a.a. CD64 domain-based construction, CD16TM, CD16ICD

<400> 1

Met Trp Phe Leu Thr Thr Leu Leu Leu Trp Val Pro Val Asp Gly Gln  
 1 5 10 15

Val Asp Thr Thr Lys Ala Val Ile Thr Leu Gln Pro Pro Trp Val Ser  
 20 25 30

Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu  
 35 40 45

Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln  
 50 55 60

Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser  
 65 70 75 80

Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile  
85 90 95

Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg  
100 105 110

Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys  
115 120 125

Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe  
130 135 140

Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile  
145 150 155 160

Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr  
165 170 175

Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro  
180 185 190

Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val  
195 200 205

Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln  
210 215 220

Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn  
225 230 235 240

Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly  
245 250 255

Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg  
260 265 270

Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Leu Gln Leu Pro Thr Pro  
275 280 285

Val Trp Phe His Tyr Gln Val Ser Phe Cys Leu Val Met Val Leu Leu

290

295

300

Phe Ala Val Asp Thr Gly Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg  
 305 310 315 320

Ser Ser Thr Arg Asp Trp Lys Asp His Lys Phe Lys Trp Arg Lys Asp  
 325 330 335

Pro Gln Asp Lys  
 340

<210> 2

<211> 336

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic polypeptide

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<221> misc\_feature

<223> 336 a.a. CD64 exon-based construction, CD16TM, CD16ICD

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Val Asp Thr Thr Lys Ala Val Ile Thr Leu Gln Pro Pro Trp Val Ser  
 20 25 30

Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu  
 35 40 45

Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln  
 50 55 60

Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser  
 65 70 75 80

Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile  
 85 90 95

Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg  
100 105 110

Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys  
115 120 125

Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe  
130 135 140

Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile  
145 150 155 160

Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr  
165 170 175

Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro  
180 185 190

Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val  
195 200 205

Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln  
210 215 220

Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn  
225 230 235 240

Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly  
245 250 255

Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg  
260 265 270

Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Leu Phe Phe Pro Pro Gly  
275 280 285

Tyr Gln Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp  
290 295 300

Thr Gly Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg  
 305 310 315 320

Asp Trp Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys  
 325 330 335

<210> 3  
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 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Synthetic polypeptide

<220>  
 <221> misc\_feature  
 <223> 335 a.a. CD64 exon-based construction, CD16TM, CD16ICD

<400> 3

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 1 5 10 15

Val Asp Thr Thr Lys Ala Val Ile Thr Leu Gln Pro Pro Trp Val Ser  
 20 25 30

Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu  
 35 40 45

Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln  
 50 55 60

Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser  
 65 70 75 80

Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile  
 85 90 95

Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg  
 100 105 110

Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys  
 115 120 125

Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe  
130 135 140

Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile  
145 150 155 160

Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr  
165 170 175

Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro  
180 185 190

Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val  
195 200 205

Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln  
210 215 220

Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn  
225 230 235 240

Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly  
245 250 255

Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg  
260 265 270

Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Phe Phe Pro Pro Gly Tyr  
275 280 285

Gln Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr  
290 295 300

Gly Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp  
305 310 315 320

Trp Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys  
325 330 335

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 <211> 1032  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic polynucleotide

<400> 4  
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 gtggacacca caaaggcagt gatcactttg cagcctccat gggtcagcgt gttccaagag 120  
 gaaaccgtaa ccttgcattg tgaggtgctc catctgcctg ggagcagctc tacacagtgg 180  
 tttctcaatg gcacagccac tcagacctcg acccccagct acagaatcac ctctgccagt 240  
 gtcaatgaca gtggtgaata caggtgccag agaggtctct cagggcgaag tgaccccata 300  
 cagctggaaa tccacagagg ctggctacta ctgcaggtct ccagcagagt cttcacggaa 360  
 ggagaacctc tggccttgag gtgtcatgcg tggaaggata agctggtgta caatgtgctt 420  
 tactatcgaa atggcaaagc ctttaagttt ttccactgga attctaacct caccattctg 480  
 aaaaccaaca taagtcacaa tggcacctac cattgctcag gcatgggaaa gcatcgctac 540  
 acatcagcag gaatatctgt cactgtgaaa gagctatttc cagctccagt gctgaatgca 600  
 tctgtgacat cccactcct ggaggggaat ctggtcaccc tgagctgtga aacaaagttg 660  
 ctcttgacaga ggcctggttt gcagctttac ttctccttct acatgggcag caagaccctg 720  
 cgaggcagga acacatcctc tgaataccaa atactaactg ctagaagaga agactctggg 780  
 ttatactggg gcgaggctgc cacagaggat ggaaatgtcc ttaagcgag ccctgagttg 840  
 gagcttcaag tgcttggcct ccagttacca actcctgtct ggtttcatta ccaagtctct 900  
 ttctgcttgg tgatgggtact cttttttgca gtggacacag gactatattt ctctgtgaag 960  
 acaaacattc gaagctcaac aagagactgg aaggaccata aatttaaag gagaaaggac 1020  
 cctcaagaca aa 1032

<210> 5  
 <211> 1020  
 <212> DNA  
 <213> Artificial sequence

<220>

<223> Synthetic polynucleotide

<400> 5

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| gtggacacca caaaggcagt gatcactttg cagcctccat gggtcagcgt gttccaagag  | 120  |
| gaaaccgtaa ccttgcatthg tgaggtgctc catctgcctg ggagcagctc tacacagtgg | 180  |
| tttctcaatg gcacagccac tcagacctcg acccccagct acagaatcac ctctgccagt  | 240  |
| gtcaatgaca gtgggtgaata caggtgccag agaggtctct cagggcgaag tgaccccata | 300  |
| cagctggaaa tccacagagg ctggctacta ctgcaggtct ccagcagagt cttcacggaa  | 360  |
| ggagaacctc tggccttgag gtgtcatgctg tggaaggata agctgggtga caatgtgctt | 420  |
| tactatcgaa atggcaaagc ctttaagttt ttccactgga attctaact caccattctg   | 480  |
| aaaaccaaca taagtcacaa tggcacctac cattgctcag gcatgggaaa gcatcgctac  | 540  |
| acatcagcag gaatatctgt cactgtgaaa gagctatttc cagctccagt gctgaatgca  | 600  |
| tctgtgacat cccactcct ggaggggaat ctggtcaccc tgagctgtga aacaaagttg   | 660  |
| ctcttgacga ggcctggttt gcagctttac ttctccttct acatgggcag caagaccctg  | 720  |
| cgaggcagga acacatcctc tgaataccaa atactaactg ctagaagaga agactctggg  | 780  |
| ttatactggg gcgaggctgc cacagaggat ggaaatgtcc ttaagcgag ccctgagttg   | 840  |
| gagcttcaag tgcttggttt gttctttcca cctgggtacc aagtctcttt ctgcttggtg  | 900  |
| atgggtactcc tttttgcagt ggacacagga ctatatttct ctgtgaagac aaacattcga | 960  |
| agctcaacaa gagactggaa ggaccataaa tttaaattga gaaaggaccc tcaagacaaa  | 1020 |

<210> 6

<211> 1005

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic polynucleotide

<400> 6

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| atgtggttct tgacaactct gctcctttgg gttccagttg atgggcaagt ggacaccaca | 60  |
| aaggcagtga tcactttgca gcctccatgg gtcagcgtgt tccaagagga aaccgtaacc | 120 |
| ttgcactgtg aggtgctcca tctgcctggg agcagctcta cacagtgggt tctcaatggc | 180 |

acagccactc agacctcgac ccccagctac agaatcacct ctgccagtgt caatgacagt 240  
 ggtgaataca ggtgccagag aggtctctca gggcgaagtg accccataca gctggaaatc 300  
 cacagaggct ggctactact gcagggtctcc agcagagtct tcacggaagg agaacctctg 360  
 gccttgaggt gtcatgcgtg gaaggataag ctggtgtaca atgtgcttta ctatcgaaat 420  
 ggcaaagcct ttaagttttt ccactggaac tctaacctca ccattctgaa aaccaacata 480  
 agtcacaatg gcacctacca ttgctcaggc atgggaaagc atcgctacac atcagcagga 540  
 atatctgtca ctgtgaaaga gctattttcca gctccagtgc tgaatgcatc tgtgacatcc 600  
 ccactcctgg aggggaatct ggtcaccttg agctgtgaaa caaagttgct cttgcagagg 660  
 cctggtttgc agctttactt ctccttctac atgggcagca agaccctgcg aggcaggaac 720  
 acatcctctg aataccaaat actaactgct agaagagaag actctgggtt atactggtgc 780  
 gaggctgcca cagaggatgg aaatgtcctt aagcgcagcc ctgagttgga gcttcaagtg 840  
 cttggcttct ttccacctgg gtaccaagtc tctttctgct tggatgatgg actccttttt 900  
 gcagtggaca caggactata tttctctgtg aagacaaaca ttcgaagctc aacaagagac 960  
 tggaaggacc ataaatttaa atggagaaaag gaccctcaag acaaa 1005

<210> 7  
 <211> 153  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Synthetic polypeptide

<220>  
 <221> misc\_feature  
 <223> 153 a.a. CD28 co-stim plus CD3-zeta-ITAM

<400> 7

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr  
 1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro  
 20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser

35

40

45

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu  
 50 55 60

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg  
 65 70 75 80

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln  
 85 90 95

Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Phe  
 100 105 110

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp  
 115 120 125

Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe Asp Ala  
 130 135 140

Leu His Met Gln Ala Leu Pro Pro Arg  
 145 150

<210> 8  
 <211> 219  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Synthetic polypeptide

<220>  
 <221> misc\_feature  
 <223> 219 a.a. CD28 hinge plus CD28 TM plus CD28 co-stim plus  
 CD3-zeta-ITAM

<400> 8

Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn  
 1 5 10 15

Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu  
 20 25 30

Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly  
35 40 45

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe  
50 55 60

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn  
65 70 75 80

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr  
85 90 95

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser  
100 105 110

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr  
115 120 125

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys  
130 135 140

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn  
145 150 155 160

Pro Gln Glu Gly Leu Phe Asn Glu Leu Gln Lys Asp Lys Met Ala Glu  
165 170 175

Ala Phe Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly  
180 185 190

His Asp Gly Leu Phe Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Phe  
195 200 205

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg  
210 215

<210> 9  
<211> 263  
<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic polypeptide

<220>

<221> misc\_feature

<223> 263 a.a NKG2D TM plus 2B4 plus CD3-zeta

<400> 9

Ser Asn Leu Phe Val Ala Ser Trp Ile Ala Val Met Ile Ile Phe Arg  
1 5 10 15

Ile Gly Met Ala Val Ala Ile Phe Cys Cys Phe Phe Phe Pro Ser Trp  
20 25 30

Arg Arg Lys Arg Lys Glu Lys Gln Ser Glu Thr Ser Pro Lys Glu Phe  
35 40 45

Leu Thr Ile Tyr Glu Asp Val Lys Asp Leu Lys Thr Arg Arg Asn His  
50 55 60

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

Ile Gln Ser Gln Ser Ser Ala Pro Thr Ser Gln Glu Pro Ala Tyr Thr  
85 90 95

Leu Tyr Ser Leu Ile Gln Pro Ser Arg Lys Ser Gly Ser Arg Lys Arg  
100 105 110

Asn His Ser Pro Ser Phe Asn Ser Thr Ile Tyr Glu Val Ile Gly Lys  
115 120 125

Ser Gln Pro Lys Ala Gln Asn Pro Ala Arg Leu Ser Arg Lys Glu Leu  
130 135 140

Glu Asn Phe Asp Val Tyr Ser Arg Val Lys Phe Ser Arg Ser Ala Asp  
145 150 155 160

Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn

165

170

175

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg  
 180 185 190

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly  
 195 200 205

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu  
 210 215 220

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu  
 225 230 235 240

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His  
 245 250 255

Met Gln Ala Leu Pro Pro Arg  
 260

<210> 10  
 <211> 308  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Synthetic polypeptide

<220>  
 <221> misc\_feature  
 <223> 308 a.a CD8 hinge plus NKG2D TM plus 2B4 plus CD3-zeta

<400> 10

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 Ser Asn Leu  
 35 40 45

Phe Val Ala Ser Trp Ile Ala Val Met Ile Ile Phe Arg Ile Gly Met  
50 55 60

Ala Val Ala Ile Phe Cys Cys Phe Phe Phe Pro Ser Trp Arg Arg Lys  
65 70 75 80

Arg Lys Glu Lys Gln Ser Glu Thr Ser Pro Lys Glu Phe Leu Thr Ile  
85 90 95

Tyr Glu Asp Val Lys Asp Leu Lys Thr Arg Arg Asn His Glu Gln Glu  
100 105 110

Gln Thr Phe Pro Gly Gly Gly Ser Thr Ile Tyr Ser Met Ile Gln Ser  
115 120 125

Gln Ser Ser Ala Pro Thr Ser Gln Glu Pro Ala Tyr Thr Leu Tyr Ser  
130 135 140

Leu Ile Gln Pro Ser Arg Lys Ser Gly Ser Arg Lys Arg Asn His Ser  
145 150 155 160

Pro Ser Phe Asn Ser Thr Ile Tyr Glu Val Ile Gly Lys Ser Gln Pro  
165 170 175

Lys Ala Gln Asn Pro Ala Arg Leu Ser Arg Lys Glu Leu Glu Asn Phe  
180 185 190

Asp Val Tyr Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala  
195 200 205

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg  
210 215 220

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu  
225 230 235 240

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn  
245 250 255

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met  
260 265 270

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly  
275 280 285

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala  
290 295 300

Leu Pro Pro Arg  
305

<210> 11  
<211> 414  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Synthetic polypeptide

<400> 11

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val  
1 5 10 15

His Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu  
20 25 30

Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys  
35 40 45

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr  
50 55 60

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe  
65 70 75 80

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile  
85 90 95

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser  
100 105 110

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu  
115 120 125

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val  
130 135 140

Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly  
145 150 155 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu  
165 170 175

Gln Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp  
180 185 190

Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser  
195 200 205

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu  
210 215 220

Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys  
225 230 235 240

Ile Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr  
245 250 255

Val Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser  
260 265 270

Gly Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala  
275 280 285

Thr Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser  
290 295 300

Pro Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly  
305 310 315 320

Thr Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala  
325 330 335

Ser His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr  
340 345 350

Val Ala Ile Ser Thr Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val  
355 360 365

Ser Leu Leu Ala Cys Tyr Leu Lys Ser Arg Gln Thr Pro Pro Leu Ala  
370 375 380

Ser Val Glu Met Glu Ala Met Glu Ala Leu Pro Val Thr Trp Gly Thr  
385 390 395 400

Ser Ser Arg Asp Glu Asp Leu Glu Asn Cys Ser His His Leu  
405 410

<210> 12  
<211> 1242  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic polynucleotide

<400> 12  
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aatgtcatca gtgacctcaa gaaaatagaa gaccttatac aaagcatgca cattgatgct 180  
actctctaca ctgagtcaga tgtacatccc tcatgcaaag tgacggccat gaaatgtttc 240  
ctcctcgaac ttcaagtcac atctctggaa agtggcgacg cgtccatcca cgacacggtc 300  
gaaaacctga taatactcgc taataatagt ctctcttcaa atggtaacgt aaccgagtca 360  
ggttgcaaag agtgcgaaga gttggaagaa aaaaacataa aggagttcct gcaaagtttc 420  
gtgcacattg tgcagatgtt cattaatacc tctagcggcg gaggatcagg tggcgggtgga 480  
agcggagggtg gaggctccgg tggaggagggt agtggcggag gttctcttca aataacttgt 540  
cctccaccga tgtccgtaga acatgcggat atttgggtaa aatcctatag cttgtacagc 600

cgagagcgggt atatctgcaa cagcggcttc aagcgggaagg ccggcacaag cagcctgacc 660  
 gaggcgtgc tgaacaaggc caccaacgtg gccactgga ccaccctag cctgaagtgc 720  
 atcagagatc ccgccctggt gcatcagcgg cctgcccctc caagcacagt gacaacagct 780  
 ggcgtgaccc cccagcctga gagcctgagc ctttctggaa aagagcctgc cgccagcagc 840  
 cccagcagca acaatactgc cgccaccaca gccgccatcg tgcctggatc tcagctgatg 900  
 cccagcaaga gccctagcac cggcaccacc gagatcagca gccacgagtc tagccacggc 960  
 accccatctc agaccaccgc caagaactgg gagctgacag ccagcgcctc tcaccagcct 1020  
 ccaggcgtgt accctcaggg ccacagcgat accacagtgg ccatcagcac ctccaccgtg 1080  
 ctgctgtgtg gactgagcgc cgtgtcactg ctggcctgct acctgaagtc cagacagacc 1140  
 cctccactgg ccagcgtgga aatggaagcc atggaagcac tgcccgtgac ctggggcacc 1200  
 agctccagag atgaggatct ggaaaactgc tcccaccacc tg 1242

<210> 13  
 <211> 379  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Synthetic polypeptide

<400> 13

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val  
 1 5 10 15

His Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu  
 20 25 30

Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys  
 35 40 45

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr  
 50 55 60

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe  
 65 70 75 80

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile  
85 90 95

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser  
100 105 110

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu  
115 120 125

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val  
130 135 140

Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly  
145 150 155 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu  
165 170 175

Gln Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp  
180 185 190

Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser  
195 200 205

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu  
210 215 220

Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys  
225 230 235 240

Ile Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr  
245 250 255

Val Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser  
260 265 270

Gly Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala  
275 280 285

Thr Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser

290

295

300

Pro Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly  
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Thr Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala  
325 330 335

Ser His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr  
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Val Ala Ile Ser Thr Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val  
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Ser Leu Leu Ala Cys Tyr Leu Lys Ser Arg Gln  
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Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys  
35 40 45

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr  
50 55 60

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe  
65 70 75 80

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile  
85 90 95

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser

100

105

110

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu  
 115 120 125

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val  
 130 135 140

Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly  
 145 150 155 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu  
 165 170 175

Gln Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp  
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Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser  
 195 200 205

Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu  
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Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys  
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Ile Arg

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cgagagcggg atatctgcaa cagcggcttc aagcgggaagg ccggcacaag cagcctgacc 660  
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Gly Thr Glu Gln Glu Ile Phe Gln Val Glu Leu Asn Leu Gln Asn Pro  
35 40 45

Ser Leu Asn His Gln Gly Ile Asp Lys Ile Tyr Asp Cys Gln Gly Leu  
50 55 60

Leu Pro Pro Pro Glu Lys Leu Thr Ala Glu Val Leu Gly Ile Ile Cys  
65 70 75 80

Ile Val Leu Met Ala Thr Val Leu Lys Thr Ile Val Leu Ile Pro Phe  
85 90 95

Leu Glu Gln Asn Asn Phe Ser Pro Asn Thr Arg Thr Gln Lys Ala Arg  
100 105 110

His Cys Gly His Cys Pro Glu Glu Trp Ile Thr Tyr Ser Asn Ser Cys  
115 120 125

Tyr Tyr Ile Gly Lys Glu Arg Arg Thr Trp Glu Glu Ser Leu Leu Ala  
130 135 140

Cys Thr Ser Lys Asn Ser Ser Leu Leu Ser Ile Asp Asn Glu Glu Glu  
145 150 155 160

Met Lys Phe Leu Ala Ser Ile Leu Pro Ser Ser Trp Ile Gly Val Phe  
165 170 175

Arg Asn Ser Ser His His Pro Trp Val Thr Ile Asn Gly Leu Ala Phe  
180 185 190

Lys His Lys Ile Lys Asp Ser Asp Asn Ala Glu Leu Asn Cys Ala Val  
195 200 205

Leu Gln Val Asn Arg Leu Lys Ser Ala Gln Cys Gly Ser Ser Met Ile  
210 215 220

Tyr His Cys Lys His Lys Leu Gly Ser Gly Ala Thr Asn Phe Ser Leu  
225 230 235 240

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Val  
245 250 255

Phe Lys Thr Thr Leu Trp Arg Leu Ile Ser Gly Thr Leu Gly Ile Ile  
260 265 270

Cys Leu Ser Leu Met Ser Thr Leu Gly Ile Leu Leu Lys Asn Ser Phe

275

280

285

Thr Lys Leu Ser Ile Glu Pro Ala Phe Thr Pro Gly Pro Asn Ile Glu  
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Leu Gln Lys Asp Ser Asp Cys Cys Ser Cys Gln Glu Lys Trp Val Gly  
 305 310 315 320

Tyr Arg Cys Asn Cys Tyr Phe Ile Ser Ser Glu Gln Lys Thr Trp Asn  
 325 330 335

Glu Ser Arg His Leu Cys Ala Ser Gln Lys Ser Ser Leu Leu Gln Leu  
 340 345 350

Gln Asn Thr Asp Glu Leu Asp Phe Met Ser Ser Ser Gln Gln Phe Tyr  
 355 360 365

Trp Ile Gly Leu Ser Tyr Ser Glu Glu His Thr Ala Trp Leu Trp Glu  
 370 375 380

Asn Gly Ser Ala Leu Ser Gln Tyr Leu Phe Pro Ser Phe Glu Thr Phe  
 385 390 395 400

Asn Thr Lys Asn Cys Ile Ala Tyr Asn Pro Asn Gly Asn Ala Leu Asp  
 405 410 415

Glu Ser Cys Glu Asp Lys Asn Arg Tyr Ile Cys Lys Gln Gln Leu Ile  
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Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu  
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Glu Asn Pro Gly Pro Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu  
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Leu Leu Pro Leu Leu Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala  
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Gln Ala Gln Ser Asp Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu  
 485 490 495

Ala Gly Ile Val Met Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu  
500 505 510

Ala Val Tyr Phe Leu Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala  
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Glu Ala Ala Thr Arg Lys Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr  
530 535 540

Gln Glu Leu Gln Gly Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr  
545 550 555 560

Gln Arg Pro Tyr Tyr Lys  
565