

<110> CJ CheilJedang Corporation

<120> NOVEL O-SUCCINYL HOMOSERINE TRANSFERASE VARIANT AND METHOD OF PRODUCING O-SUCCINYL HOMOSERINE USING THE SAME

<130> OPA18185

<150> KR 10-2017-0083438

<151> 2017-06-30

<160> 94

<170> KoPatentIn 3.0

<210> 1

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<220>

<221> PEPTIDE

<222> (1)..(377)

<223> metX

<400>

1

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          20          25          30
Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
          35          40          45
Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50          55          60
Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65          70          75          80
Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
          85          90          95
Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
          100          105          110
Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
          115          120          125
Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
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Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
          145          150          155          160
Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
          165          170          175
Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
          180          185          190
Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
          195          200          205
Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
          210          215          220

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Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
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 370 375

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> gene
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 <223> metX

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 tccggctgca acccagccac cggactcggc gccgcccgc gcatcgcca cctcacctac 660
 cgtggcgaa tagaaatcga cgaacgctt cggcacc aaag cccaaaagaa cgaaaacca 720
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<212> PRT
<213> Pseudomonas aeruginosa

<220>
<221> PEPTIDE
<222> (1)..(379)
<223> metX1

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Ala Glu Tyr Asp Leu Val Ile Glu Thr Tyr Gly Glu Leu Asn Ala Thr
35 40 45
Gln Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His
50 55 60
Ala Ala Gly Tyr His Ser Val Asp Glu Arg Lys Pro Gly Trp Trp Asp
65 70 75 80
Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Arg Lys Phe Phe Val
85 90 95
Val Ala Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Ser Gly Pro Ala
100 105 110
Ser Ile Asn Pro Ala Thr Gly Lys Val Tyr Gly Ala Asp Phe Pro Met
115 120 125
Val Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg
130 135 140
Leu Gly Ile Arg Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly
145 150 155 160
Met Gln Ala Leu Gln Trp Thr Ile Ser Tyr Pro Glu Arg Val Arg His
165 170 175
Cys Leu Cys Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala
180 185 190
Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Ser Asp Pro Glu Phe Leu
195 200 205
Gly Gly Tyr Phe Gln Glu Gln Gly Val Ile Pro Lys Arg Gly Leu Lys
210 215 220

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Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ala Met
 225 230 235 240
 Gly Ala Lys Phe Gly Arg Val Leu Lys Thr Glu Lys Leu Asn Tyr Asp
 245 250 255
 Leu His Ser Val Glu Phe Gln Val Glu Ser Tyr Leu Arg Tyr Gln Gly
 260 265 270
 Glu Glu Phe Ser Thr Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr
 275 280 285
 Lys Ala Leu Asp Tyr Phe Asp Pro Ala Ala Ala His Gly Asp Asp Leu
 290 295 300
 Val Arg Thr Leu Glu Gly Val Glu Ala Asp Phe Cys Leu Met Ser Phe
 305 310 315 320
 Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Ile Val Asp
 325 330 335
 Ala Leu Ile Ala Ala Lys Lys Asn Val Ser Tyr Leu Glu Ile Asp Ala
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 Pro Gln Gly His Asp Ala Phe Leu Met Pro Ile Pro Arg Tyr Leu Gln
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 Ala Phe Ser Gly Tyr Met Asn Arg Ile Ser Val
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 <211> 1140
 <212> DNA
 <213> Pseudomonas aeruginosa

 <220>
 <221> gene
 <222> (1)..(1140)
 <223> metX1

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ggcgacgacc tgggtgcgcac cctggagggc gtcgaggcgg acttctgcct gatgtccttc	960
accaccgact ggcgtttctc gccggcccg tcgcgggaaa tcgtcgacgc cctgatcgcg	1020
gcgaaaaaga acgtcagcta cctggagatc gacgccccgc aaggccacga cgccttcctc	1080
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	1140

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<220>
 <223> primer 1

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer 2

<400> 6	
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<210> 7
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer 5

<400> 7	
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<210> 8
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer 6

<400> 8	
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<210> 9
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer 7

<400> 9
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<220>
 <223> primer 8

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer 9

<400> 11
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer 10

<400> 12
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<210> 13
 <211> 24
 <212> DNA
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<220>
 <223> primer 11

<400> 13
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 <211> 43
 <212> DNA

<213> Artificial Sequence

<220>

<223> primer 12

<400> 14

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<210> 15

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> primer 13

<400> 15

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43

<210> 16

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> primer 14

<400> 16

tctagatgga accgttgcaa ccac

24

<210> 17

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<220>

<221> PEPTIDE

<222> (1)..(421)

<223> lysc

<400> 17

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Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

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Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125
 Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
 130 135 140
 Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
 145 150 155 160
 Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
 165 170 175
 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
 180 185 190
 Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
 195 200 205
 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
 210 215 220
 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
 225 230 235 240
 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
 245 250 255
 Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
 260 265 270
 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
 275 280 285
 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
 290 295 300
 Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg
 305 310 315 320
 Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
 325 330 335
 Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
 340 345 350
 Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
 355 360 365
 Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
 370 375 380
 Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
 385 390 395 400
 Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
 405 410 415
 Ala Gly Thr Gly Arg
 420

<210> 18
 <211> 1266
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

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<221> gene
 <222> (1)..(1266)
 <223> lysc

<400> 18
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 tccgcaatgg gagacaccac ggatgaactt ctagaacttg cagcggcagt gaatcccgtt 180
 ccgccagctc gtgaaatgga tatgctcctg actgctgggt agcgtatttc taacgctctc 240
 gtcgccatgg ctattgagtc ccttggcgca gaagcccaat ctttcacggg ctctcagggt 300
 ggtgtgctca ccaccgagcg ccacggaaac gcacgcattg ttgatgtcac tccagggtcgt 360
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 <213> Artificial Sequence

<220>
 <223> primer 15

<400> 19
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<210> 20
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
<223> primer 16

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<210> 21
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<212> DNA
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<220>
<223> primer 17

<400> 21
ggcaggtgaa gatgatgtcg gtg 23

<210> 22
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> primer 18

<400> 22
gactctagag ttcacctcag agacgatta 29

<210> 23
<211> 421
<212> PRT
<213> Corynebacterium glutamicum

<220>
<221> PEPTIDE
<222> (1)..(421)
<223> lysC variant (T311I)

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20 25 30
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35 40 45
Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80
Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95
Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

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Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

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

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
405 410 415

Ala Gly Thr Gly Arg
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<210> 24
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> gene

<222> (1)..(1266)
 <223> lysC variant (T311I)

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 cgctaa 1266

<210> 25
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer for L313F

<400> 25
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<210> 26
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse primer for L313F

<400> 26
 ctggtggtag gggtaaaaa tatcggtatc tac 33

<210> 27
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer for L313S

<400> 27
 gtagataccg atatttctta cccctaccac cag 33

<210> 28
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse primer for L313S

<400> 28
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<210> 29
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer for L313Y

<400> 29
 gtagataccg atatttatta cccctaccac cag 33

<210> 30
 <211> 33
 <212> DNA
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<220>
 <223> Reverse primer for L313Y

<400> 30
 ctggtggtag gggtataaaa tatcggtatc tac 33

<210> 31
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer for L313C

<400> 31
gtagataccg atatttgta cccctaccac cag 33

<210> 32
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer for L313C

<400> 32
ctggtggtag gggtaacaaa tatcggtatc tac 33

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

<220>
<223> Forward primer for L313P

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<210> 34
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer for L313P

<400> 34
ctggtggtag gggtaaggaa tatcggtatc tac 33

<210> 35
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer for L313H

<400> 35
gtagataccg atattcatta cccctaccac cag 33

<210> 36
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
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<400> 36
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 <212> DNA
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<220>
 <223> Forward primer for L313Q

<400> 37
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<210> 38
 <211> 33
 <212> DNA
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<220>
 <223> Reverse primer for L313Q

<400> 38
 ctggtggtag gggatttgaa tatcggtatc tac 33

<210> 39
 <211> 33
 <212> DNA
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<220>
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<400> 39
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<210> 40
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 <212> DNA
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<220>
 <223> Reverse primer for L313I

<400> 40
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<210> 41
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer for L313T

<400> 41
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<210> 42

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

 <220>
 <223> Reverse primer for L313T

 <400> 42
 ctggtggtag gggtaggtaa tatcggtatc tac 33

 <210> 43
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 <212> DNA
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 <220>
 <223> Forward primer for L313N

 <400> 43
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 <210> 44
 <211> 33
 <212> DNA
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 <220>
 <223> Reverse primer for L313N

 <400> 44
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 <210> 45
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 <212> DNA
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 <220>
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 <400> 45
 gtagataccg atattaaata cccctaccac cag 33

 <210> 46
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Reverse primer for L313K

 <400> 46
 ctggtggtag gggatatttaa tatcggtatc tac 33

 <210> 47
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer for L313V

<400> 47
 gtagataccg atattgttta cccctaccac cag 33

<210> 48
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse primer for L313V

<400> 48
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<210> 49
 <211> 33
 <212> DNA
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<220>
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<400> 49
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<210> 50
 <211> 33
 <212> DNA
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<220>
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<400> 50
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<210> 51
 <211> 33
 <212> DNA
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<220>
 <223> Forward primer for L313D

<400> 51
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<210> 52
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<220>
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<400> 52
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<210> 53
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<220>
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<400> 53
gtagataccg atattgaata cccctaccac cag 33

<210> 54
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<220>
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<400> 54
ctggtggtag gggatttcaa tatcggtatc tac 33

<210> 55
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<210> 56
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<223> Reverse primer for L313G

<400> 56
ctggtggtag gggatatcaa tatcggtatc tac 33

<210> 57
<211> 33
<212> DNA
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<220>
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<400> 57

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33

<210> 58
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<213> Artificial Sequence

<220>
<223> Reverse primer for L313W

<400> 58
ctggtggtag gggtacaaa tatcggtatc tac

33

<210> 59
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> metX L313R

<400> 59
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Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
20 25 30
Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
35 40 45
Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
50 55 60
Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
65 70 75 80
Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
85 90 95
Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
100 105 110
Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
115 120 125
Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
130 135 140
Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
145 150 155 160
Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
165 170 175
Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
180 185 190
Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
195 200 205
Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
210 215 220

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Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Arg Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365
 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
 370 375

<210> 60
 <211> 1134
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> metX L313R

<400> 60
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 gtagataaag aaggacgcag caatgtcggt ctcatcgaac acgccctcac tggagattcc 180
 aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt 240
 tactgctga tctgtaccaa cgtcatcggg ggttgcaacg gttccaccgg acctggctcc 300
 atgcatccag atggaaattt ctggggtaat cgcttccccg ccacgtccat tcgtgatcag 360
 gtaaacgccg aaaaacaatt cctcgacgca ctcggcacga ccacggtcgc cgcagtactt 420
 ggtggttcca tgggtggtgc ccgcacccta gagtggggccg caatgtaccc agaaactgtt 480
 ggcgcagctg ctgttcttgc agtttctgca cgcgccagcg cctggcaa at cggcattcaa 540
 tccgccc aaa ttaaggcgat tgaaaacgac caccactggc acgaaggcaa ctactacgaa 600
 tccggctgca acccagccac cggactcggc gccgcccgcac gcacgccc cctcacctac 660
 cgtggcgaac tagaaatcga cgaacgcttc ggcaccaaag cccaaaagaa cgaaaaccca 720
 ctcggtccct accgcaagcc cgaccagcgc ttcgccgtgg aatcctactt ggactaccaa 780
 gcagacaagc tagtacagcg tttcgacgcc ggctcctacg tcttgctcac cgacgccttc 840

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aaccgccacg acattggtcg cgaccgcgga ggcctcaaca aggcactcga atccatcaaa 900
 gttccagtcc ttgtcgcagg cgtagatacc gatattcggt acccctacca ccagcaagaa 960
 cacctctcca gaaacctggg aaatctactg gcaatggcaa aaatcgatc ccctgtcggc 1020
 cacgatgctt tcctcaccga aagccgcaa atggatcgca tcgtgaggaa cttcttcagc 1080
 ctcatctccc cagacgaaga caacccttcg acctacatcg agttctacat ctaa 1134

<210> 61
 <211> 377
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 313F

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 1 5 10 15
 Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30
 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr

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245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Phe Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365
 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
 370 375

<210> 62
 <211> 1134
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 313F

<400> 62
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 gtagataaag aaggacgcag caatgtcgtt ctcatcgaac acgccctcac tggagattcc 180
 aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt 240
 tactgctga tctgtacaa cgtcatcggg ggttgcaacg gttccaccgg acctggctcc 300
 atgcatccag atggaaattt ctggggtaat cgcttccccg ccacgtccat tcgtgatcag 360
 gtaaacgccg aaaaacaatt cctcgacgca ctcggcacat ccacgggtcgc cgcagtactt 420
 ggtggttcca tgggtggtgc ccgcacccta gagtggggccg caatgtaccc agaaactggt 480
 ggcgcagctg ctgttcttgc agtttctgca cgcgccagcg cctggcaa at cggcattcaa 540
 tccgccc aaa ttaaggcgat tgaaaacgac caccactggc acgaaggcaa ctactacgaa 600
 tccggctgca acccagccac cggactcggc gccgcccgc gcatcgcca cctcacctac 660
 cgtggcgaac tagaaatcga cgaacgctt gccaccaaag cccaaaagaa cgaaaacca 720
 ctcggtccct accgcaagcc cgaccagcgc ttcgccgtgg aatcctactt ggactacaa 780
 gcagacaagc tagtacagcg tttcgacgcc ggctcctacg tcttgctcac cgacgccctc 840
 aaccgccag acattggtcg cgaccgcgga ggcctcaaca aggcactcga atccatcaaa 900
 gttccagtcc ttgtcgcagg cgtagatacc gatatttttt acccctacca ccagcaagaa 960

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cacctctcca gaaacctggg aaatctactg gcaatggcaa aaatcgtatc ccctgtcggc 1020
cacgatgctt tcctcaccga aagccgcaa atggatcgca tcgtgaggaa cttcttcagc 1080
ctcatctccc cagacgaaga caacccttcg acctacatcg agttctacat ctaa 1134

<210> 63
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> 313S

<400> 63
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Tyr His Arg₃₅ Trp Gly Glu Tyr Arg₄₀ Val Asp Lys Glu Gly₄₅ Arg Ser Asn
Val Val₅₀ Leu Ile Glu His Ala₅₅ Leu Thr Gly Asp Ser₆₀ Asn Ala Ala Asp
Trp Trp Ala Asp Leu₇₀ Gly Pro Gly Lys Ala₇₅ Ile Asn Thr Asp Ile₈₀
Tyr Cys Val Ile Cys₈₅ Thr Asn Val Ile Gly₉₀ Gly Cys Asn Gly Ser₉₅ Thr
Gly Pro Gly Ser₁₀₀ Met His Pro Asp Gly₁₀₅ Asn Phe Trp Gly Asn₁₁₀ Arg Phe
Pro Ala Thr₁₁₅ Ser Ile Arg Asp Gln Val Asn Ala Glu Lys₁₂₅ Gln Phe Leu
Asp Ala Leu Gly Ile Thr Thr₁₃₅ Val Ala Ala Val Leu₁₄₀ Gly Gly Ser Met
Gly Gly Ala Arg Thr Leu₁₅₀ Glu Trp Ala Ala Met₁₅₅ Tyr Pro Glu Thr Val₁₆₀
Gly Ala Ala Ala Val₁₆₅ Leu Ala Val Ser Ala₁₇₀ Arg Ala Ser Ala Trp₁₇₅ Gln
Ile Gly Ile Gln₁₈₀ Ser Ala Gln Ile Lys₁₈₅ Ala Ile Glu Asn Asp₁₉₀ His His
Trp His Glu₁₉₅ Gly Asn Tyr Tyr Glu₂₀₀ Ser Gly Cys Asn Pro Ala Thr Gly
Leu Gly₂₁₀ Ala Ala Arg Arg Ile₂₁₅ Ala His Leu Thr Tyr₂₂₀ Arg Gly Glu Leu
Glu Ile Asp Glu Arg Phe₂₃₀ Gly Thr Lys Ala Gln₂₃₅ Lys Asn Glu Asn Pro₂₄₀
Leu Gly Pro Tyr Arg₂₄₅ Lys Pro Asp Gln Arg₂₅₀ Phe Ala Val Glu Ser₂₅₅ Tyr
Leu Asp Tyr Gln₂₆₀ Ala Asp Lys Leu Val₂₆₅ Gln Arg Phe Asp Ala₂₇₀ Gly Ser

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Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Ser Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365
 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
 370 375

<210> 64
 <211> 1134
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 313s

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 gtagataaag aaggacgcag caatgtcgtt ctcatcgaac acgccctcac tggagattcc 180
 aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt 240
 tactgctga tctgtaccaa cgtcatcggg ggttgcaacg gttccaccgg acctggctcc 300
 atgcatccag atggaaattt ctggggtaat cgcttccccg ccacgtccat tcgtgatcag 360
 gtaaacgccg aaaaacaatt cctcgacgca ctcggcata ccacggtcgc cgcagtactt 420
 ggtggttcca tgggtggtgc ccgcacccta gagtgggccg caatgtacc agaaactgtt 480
 ggcgcagctg ctgttcttgc agtttctgca cgcgccagcg cctggcaa at cggcattcaa 540
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 ctcggtccct accgcaagcc cgaccagcgc ttcgccgtgg aatcctactt ggactaccaa 780
 gcagacaagc tagtacagcg tttcgacgcc ggctcctacg tcttgctcac cgacgccctc 840
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 cacctctcca gaaacctggg aaatctactg gcaatggcaa aaatcgatc ccctgtcggc 1020
 cacgatgctt tcctcaccga aagccgcaa atggatcgca tcgtgaggaa cttcttcagc 1080

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1134

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 <211> 377
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 313Y

<400> 65
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 Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30
 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285

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Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Tyr Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365
 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
 370 375

<210> 66
 <211> 1134
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 313Y

<400> 66
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 aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt 240
 tactgctga tctgtaccaa cgtcatcggt ggttgcaacg gttccaccgg acctggctcc 300
 atgcatccag atggaaattt ctggggtaat cgcttccccg ccacgtccat tcgtgatcag 360
 gtaaacgccg aaaaacaatt cctcgacgca ctcggcata ccacggtcgc cgcagtactt 420
 ggtggttcca tgggtggtgc ccgcacccta gagtgggccc caatgtaccc agaaactggt 480
 ggcgcagctg ctgttcttgc agtttctgca cgcgccagcg cctggcaa at cggcattcaa 540
 tccgccc aaa ttaaggcgat tgaaaacgac caccactggc acgaaggcaa ctactacgaa 600
 tccggctgca acccagccac cggactcggc gccgccgcgc gcacgcacca cctcacctac 660
 cgtggcgaac tagaaatcga cgaacgcttc ggcaccaaag cccaaaagaa cgaaaaccca 720
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 gcagacaagc tagtacagcg tttcgacgcc ggctcctacg tcttgctcac cgacgccctc 840
 aaccgccacg acattggtcg cgaccgcgga ggcctcaaca aggcactcga atccatcaaa 900
 gttccagtcc ttgtcgcagg cgtagatacc gatatttatt acccctacca ccagcaagaa 960
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 cacgatgctt tcctcaccga aagccgcaa atggatcgca tcgtgaggaa cttcttcagc 1080
 ctcatctccc cagacgaaga caacccttcg acctacatcg agttctacat ctaa 1134

<210> 67
 <211> 377
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 313C

<400> 67
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 1 5 10 15
 Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30
 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Cys Tyr Pro Tyr His Gln Gln Glu
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305		310		315		320
His	Leu	Ser	Arg	Asn 325	Leu	Gly
					Leu 330	Ala
						Met
						Ala
						Lys
						Ile
						Val
Ser	Pro	Val	Gly 340	His	Asp	Ala
						Phe
						Leu
						Thr
						Glu
						Ser
						Arg
						Gln
						Met
						Asp
Arg	Ile	Val 355	Arg	Asn	Phe	Phe
						Ser
						Leu
						Ile
						Ser
						Pro
						Asp
						Glu
						Asp
						Asn
Pro	Ser 370	Thr	Tyr	Ile	Glu	Phe
						Tyr
						Ile

<210> 68
 <211> 1134
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 313C

<400> 68

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gtagataaag aaggacgcag caatgtcggt ctcacgaac acgccctcac tggagattcc	180
aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt	240
tactgctga tctgtacaa cgtcatcggt gggtgcaac gttccaccgg acctggctcc	300
atgcatccag atggaaattt ctggggtaat cgcttccccg ccacgtccat tcgtgatcag	360
gtaaacgccg aaaaacaatt cctcgacgca ctcggcacat ccacggtcgc cgcagtactt	420
gggtggtcca tgggtggtgc ccgcacccta gagtggggcc caatgtaccc agaaactggt	480
ggcgcagctg ctgttcttgc agtttctgca cgcgccagcg cctggcaa at cggcattcaa	540
tccgccc aaa ttaaggcgat tgaaaacgac caccactggc acgaaggcaa ctactacgaa	600
tccggctgca acccagccac cggactcggc gccgcccgc gcacgcacca cctcacctac	660
cgtggcgaac tagaaatcga cgaacgctt ggacacaaag cccaaaagaa cgaaaaccca	720
ctcggtcctt accgcaagcc cgaccagcgc ttcgccgtgg aatcctactt ggactaccaa	780
gcagacaagc tagtacagcg tttcgacgcc ggctcctacg tcttgctcac cgacgccctc	840
aaccgccacg acattggtcg cgaccgcgga ggcctcaaca aggcactcga atccatcaaa	900
gttccagtcc ttgtcgcagg cgtagatacc gatatttggt acccctacca ccagcaagaa	960
cacctctcca gaaacctggg aaatctactg gcaatggcaa aaatcgtatc ccctgtcggc	1020
cacgatgctt tcctaccga aagccgcaa atggatcgca tcgtgaggaa cttcttcagc	1080
ctcatctccc cagacgaaga caacccttcg acctacatcg agttctacat ctaa	1134

<210> 69
 <211> 377
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 313P

<400>

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      69
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      20      25      30
Tyr  His  Arg  Trp  Gly  Glu  Tyr  Arg  Val  Asp  Lys  Glu  Gly  Arg  Ser  Asn
      35      40      45
Val  Val  Leu  Ile  Glu  His  Ala  Leu  Thr  Gly  Asp  Ser  Asn  Ala  Ala  Asp
      50      55      60
Trp  Trp  Ala  Asp  Leu  Leu  Gly  Pro  Gly  Lys  Ala  Ile  Asn  Thr  Asp  Ile
      65      70      75      80
Tyr  Cys  Val  Ile  Cys  Thr  Asn  Val  Ile  Gly  Gly  Cys  Asn  Gly  Ser  Thr
      85      90      95
Gly  Pro  Gly  Ser  Met  His  Pro  Asp  Gly  Asn  Phe  Trp  Gly  Asn  Arg  Phe
      100     105     110
Pro  Ala  Thr  Ser  Ile  Arg  Asp  Gln  Val  Asn  Ala  Glu  Lys  Gln  Phe  Leu
      115     120     125
Asp  Ala  Leu  Gly  Ile  Thr  Thr  Val  Ala  Ala  Val  Leu  Gly  Gly  Ser  Met
      130     135     140
Gly  Gly  Ala  Arg  Thr  Leu  Glu  Trp  Ala  Ala  Met  Tyr  Pro  Glu  Thr  Val
      145     150     155     160
Gly  Ala  Ala  Ala  Val  Leu  Ala  Val  Ser  Ala  Arg  Ala  Ser  Ala  Trp  Gln
      165     170     175
Ile  Gly  Ile  Gln  Ser  Ala  Gln  Ile  Lys  Ala  Ile  Glu  Asn  Asp  His  His
      180     185     190
Trp  His  Glu  Gly  Asn  Tyr  Tyr  Glu  Ser  Gly  Cys  Asn  Pro  Ala  Thr  Gly
      195     200     205
Leu  Gly  Ala  Ala  Arg  Arg  Ile  Ala  His  Leu  Thr  Tyr  Arg  Gly  Glu  Leu
      210     215     220
Glu  Ile  Asp  Glu  Arg  Phe  Gly  Thr  Lys  Ala  Gln  Lys  Asn  Glu  Asn  Pro
      225     230     235     240
Leu  Gly  Pro  Tyr  Arg  Lys  Pro  Asp  Gln  Arg  Phe  Ala  Val  Glu  Ser  Tyr
      245     250     255
Leu  Asp  Tyr  Gln  Ala  Asp  Lys  Leu  Val  Gln  Arg  Phe  Asp  Ala  Gly  Ser
      260     265     270
Tyr  Val  Leu  Leu  Thr  Asp  Ala  Leu  Asn  Arg  His  Asp  Ile  Gly  Arg  Asp
      275     280     285
Arg  Gly  Gly  Leu  Asn  Lys  Ala  Leu  Glu  Ser  Ile  Lys  Val  Pro  Val  Leu
      290     295     300
Val  Ala  Gly  Val  Asp  Thr  Asp  Ile  Pro  Tyr  Pro  Tyr  His  Gln  Gln  Glu
      305     310     315     320
His  Leu  Ser  Arg  Asn  Leu  Gly  Asn  Leu  Leu  Ala  Met  Ala  Lys  Ile  Val
      325     330     335

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Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350

Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365

Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
 370 375

<210> 70
 <211> 1134
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 313P

<400> 70
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 gtagataaag aaggacgcag caatgtcggt ctcacgaac acgccctcac tggagattcc 180
 aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt 240
 tactgctga tctgtacaa cgtcatcggg ggttgcaacg gttccaccgg acctggctcc 300
 atgcatccag atggaaattt ctggggtaat cgcttccccg ccacgtccat tcgtgatcag 360
 gtaaagccg aaaaacaatt cctcgacgca ctcggcatca ccacggtcgc cgcagtactt 420
 ggtggttcca tgggtggtgc ccgcacccta gagtgggccc caatgtaccc agaaactggt 480
 ggcgcagctg ctgttcttgc agtttctgca cgcgccagcg cctggcaaat cggcattcaa 540
 tccgccc aaa ttaaggcgat tgaaaacgac caccactggc acgaaggcaa ctactacgaa 600
 tccggctgca acccagccac cggactcggc gccgcccgc gcacgccc cctcacctac 660
 cgtggcgaac tagaaatcga cgaacgcttc ggcaccaaag cccaaaagaa cgaaaaccca 720
 ctcggtccct accgcaagcc cgaccagcgc ttcgccgtgg aatcctactt ggactacaa 780
 gcagacaagc tagtacagcg tttcgacgcc ggctcctacg tcttgctcac cgacgccctc 840
 aaccgccacg acattggtcg cgaccgcgga ggcctcaaca aggcactcga atccatcaaa 900
 gttccagtcc ttgtcgcagg cgtagatacc gatattcctt acccctacca ccagcaagaa 960
 cacctctcca gaaacctggg aaatctactg gcaatggcaa aaatcgtatc ccctgtcggc 1020
 cacgatgctt tcctcaccga aagccgcaa atggatcgca tcgtgaggaa cttcttcagc 1080
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<210> 71
 <211> 377
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 313H

<400> 71
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 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile His Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350

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Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365

Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
 370 375

<210> 72
 <211> 1134
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 313H

<400> 72
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 gtagataaag aaggacgcag caatgtcggt ctcatcgaac acgccctcac tggagattcc 180
 aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt 240
 tactgctga tctgtaccaa cgtcatcggt ggttgcaacg gttccaccgg acctggctcc 300
 atgcatccag atggaaattt ctggggtaat cgcttccccg ccacgtccat tcgtgatcag 360
 gtaaacgccg aaaaacaatt cctcgacgca ctcggcata ccacggtcgc cgcagtactt 420
 ggtggttcca tgggtggtgc ccgcacccta gagtgggccc caatgtaccc agaaactggt 480
 ggcgcagctg ctgttcttgc agtttctgca cgcgccagcg cctggcaa at cggcattcaa 540
 tccgccc aaa ttaaggcgat tgaaaacgac caccactggc acgaaggcaa ctactacgaa 600
 tccggctgca acccagccac cggactcggc gccgccgac gcatcgcca cctcacctac 660
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 ctcggtccct accgcaagcc cgaccagcgc ttcgccgtgg aatcctactt ggactaccaa 780
 gcagacaagc tagtacagcg tttcgacgcc ggctcctacg tcttgctcac cgacgccctc 840
 aaccgccacg acattggtcg cgaccgcgga ggcctcaaca aggcactcga atccatcaaa 900
 gttccagtcc ttgtcgcagg cgtagatacc gatattcatt acccctacca ccagcaagaa 960
 cacctctcca gaaacctggg aaatctactg gcaatggcaa aaatcgatc ccctgtcggc 1020
 cacgatgctt tcctaccga aagccgcaa atggatcgca tcgtgaggaa cttcttcagc 1080
 ctcatctccc cagacgaaga caacccttcg acctacatcg agttctacat ctaa 1134

<210> 73
 <211> 377
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 313Q

<400> 73
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Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30
 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Gln Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365
 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile

370

375

<210> 74
 <211> 1134
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 313Q

<400> 74
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 aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt 240
 tactgctga tctgtacaa cgtcatcggt gggtgcaacg gttccaccgg acctggctcc 300
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 ggtggttcca tgggtggtgc ccgcacccta gagtggggccg caatgtaccc agaaactggt 480
 ggcgcagctg ctgttcttgc agtttctgca cgcgccagcg cctggcaaat cggcattcaa 540
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 tccggctgca acccagccac cggactcggc gccgcccgc gcacgcacca cctcacctac 660
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 aaccgccacg acattggtcg cgaccgcgga ggcctcaaca aggcactcga atccatcaaa 900
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 cacctctcca gaaacctggg aaatctactg gcaatggcaa aaatcgtatc ccctgtcggc 1020
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 ctcactctcc cagacgaaga caacccttcg acctacatcg agttctacat ctaa 1134

<210> 75
 <211> 377
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 313I

<400> 75
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 Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30

6413067_1

Tyr His Arg₃₅ Trp Gly Glu Tyr Arg₄₀ Val Asp Lys Glu Gly₄₅ Arg Ser Asn
 Val Val₅₀ Leu Ile Glu His Ala₅₅ Leu Thr Gly Asp Ser₆₀ Asn Ala Ala Asp
 Trp₆₅ Trp Ala Asp Leu₇₀ Gly Pro Gly Lys Ala₇₅ Ile Asn Thr Asp Ile₈₀
 Tyr Cys Val Ile Cys₈₅ Thr Asn Val Ile Gly₉₀ Gly Cys Asn Gly Ser₉₅ Thr
 Gly Pro Gly Ser₁₀₀ Met His Pro Asp Gly₁₀₅ Asn Phe Trp Gly Asn₁₁₀ Arg Phe
 Pro Ala Thr₁₁₅ Ser Ile Arg Asp Gln₁₂₀ Val Asn Ala Glu Lys₁₂₅ Gln Phe Leu
 Asp Ala₁₃₀ Leu Gly Ile Thr Thr₁₃₅ Val Ala Ala Val Leu₁₄₀ Gly Gly Ser Met
 Gly₁₄₅ Gly Ala Arg Thr Leu₁₅₀ Glu Trp Ala Ala Met₁₅₅ Tyr Pro Glu Thr Val₁₆₀
 Gly Ala Ala Ala Val₁₆₅ Leu Ala Val Ser Ala₁₇₀ Arg Ala Ser Ala Trp₁₇₅ Gln
 Ile Gly Ile Gln₁₈₀ Ser Ala Gln Ile Lys₁₈₅ Ala Ile Glu Asn Asp₁₉₀ His His
 Trp His Glu₁₉₅ Gly Asn Tyr Tyr Glu₂₀₀ Ser Gly Cys Asn Pro₂₀₅ Ala Thr Gly
 Leu Gly₂₁₀ Ala Ala Arg Arg Ile₂₁₅ Ala His Leu Thr Tyr₂₂₀ Arg Gly Glu Leu
 Glu₂₂₅ Ile Asp Glu Arg Phe₂₃₀ Gly Thr Lys Ala Gln₂₃₅ Lys Asn Glu Asn Pro₂₄₀
 Leu Gly Pro Tyr Arg₂₄₅ Lys Pro Asp Gln Arg₂₅₀ Phe Ala Val Glu Ser₂₅₅ Tyr
 Leu Asp Tyr Gln₂₆₀ Ala Asp Lys Leu Val₂₆₅ Gln Arg Phe Asp Ala₂₇₀ Gly Ser
 Tyr Val Leu₂₇₅ Leu Thr Asp Ala Leu₂₈₀ Asn Arg His Asp Ile₂₈₅ Gly Arg Asp
 Arg Gly₂₉₀ Gly Leu Asn Lys Ala₂₉₅ Leu Glu Ser Ile Lys₃₀₀ Val Pro Val Leu
 Val₃₀₅ Ala Gly Val Asp Thr₃₁₀ Asp Ile Ile Tyr Pro₃₁₅ Tyr His Gln Gln Glu₃₂₀
 His Leu Ser Arg Asn₃₂₅ Leu Gly Asn Leu Leu₃₃₀ Ala Met Ala Lys Ile₃₃₅ Val
 Ser Pro Val Gly₃₄₀ His Asp Ala Phe Leu₃₄₅ Thr Glu Ser Arg Gln₃₅₀ Met Asp
 Arg Ile Val₃₅₅ Arg Asn Phe Phe Ser₃₆₀ Leu Ile Ser Pro Asp₃₆₅ Glu Asp Asn
 Pro Ser₃₇₀ Thr Tyr Ile Glu Phe₃₇₅ Tyr Ile

<210> 76

<211> 1134
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 313I

<400> 76
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 aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt 240
 tactgctgta tctgtaccaa cgtcatcggg ggttgcaacg gttccaccgg acctgggtcc 300
 atgcatccag atggaaattt ctggggtaat cgcttccccg ccacgtccat tcgtgatcag 360
 gtaaacgccg aaaaacaatt cctcgacgca ctcggcacga ccacggctgc cgcagtactt 420
 ggtggttcca tgggtggtgc ccgcacccta gagtggggccg caatgtaccc agaaactggt 480
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 tccgccc aaa ttaaggcgat tga aaacgac caccactggc acgaaggcaa ctactacgaa 600
 tccggctgca acccagccac cggactcggc gccgcccgc gcatcgcca cctcacctac 660
 cgtggcgaac tagaaatcga cgaacgctt gccaccaaag cccaaaagaa cgaaaaccca 720
 ctcggtccct accgcaagcc cgaccagcgc ttcgccgtgg aatcctactt ggactaccaa 780
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 aaccgccacg acattggtcg cgaccgcgga ggcctcaaca aggcactcga atccatcaaa 900
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 cacctctcca gaaacctggg aaatctactg gcaatggcaa aaatcgtatc ccctgtcggc 1020
 cacgatgctt tcctcaccga aagccgcaa atggatcgca tcgtgaggaa cttcttcagc 1080
 ctcatctccc cagacgaaga caacccttcg acctacatcg agttctacat ctaa 1134

<210> 77
 <211> 377
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 313T

<400> 77
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 Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30
 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp

6413067_1 60

50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
130 135 140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
145 150 155 160

Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
165 170 175

Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
180 185 190

Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
195 200 205

Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
210 215 220

Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
225 230 235 240

Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
245 250 255

Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
260 265 270

Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
275 280 285

Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
290 295 300

Val Ala Gly Val Asp Thr Asp Ile Thr Tyr Pro Tyr His Gln Gln Glu
305 310 315 320

His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
325 330 335

Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
340 345 350

Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
355 360 365

Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
370 375

<210> 78
<211> 1134
<212> DNA
<213> Artificial Sequence

<220>

<223> 313T

<400>

78

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aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt      240
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atgcatccag atggaaatct ctggggtaat cgcttccccg ccacgtccat tcgtgatcag      360
gtaaacgccg aaaaacaatt cctcgacgca ctcggcata caacggctgc cgcagtactt      420
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tccgccc aaa ttaaggcgat tgaaaacgac caccactggc acgaaggcaa ctactacgaa      600
tccggctgca acccagccac cggactcggc gccgccgac gcacgccc cctcacctac      660
cgtggcgaac tagaaatcga cgaacgcttc ggcaccaaag ccaaaaagaa cgaaaaccca      720
ctcggtcctt accgcaagcc cgaccagcgc ttccgctggg aatcctactt ggactaccaa      780
gcagacaagc tagtacagcg tttcgacgcc ggctcctacg tcttgctcac cgacgccctc      840
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cacctctcca gaaacctggg aaatctactg gcaatggcaa aaatcgatc ccctgtcggc     1020
cacgatgctt tcctcaccga aagccgcaa atggatcgca tcgtgaggaa cttcttcagc     1080
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<210>

79

<211>

377

<212>

PRT

<213>

Artificial Sequence

<220>

<223> 313N

<400>

79

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          20          25          30
Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
          35          40          45
Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
          50          55          60
Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
          65          70          75          80

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Tyr Cys Val Ile Cys₈₅ Thr Asn Val Ile Gly₉₀ Gly Cys Asn Gly Ser₉₅ Thr
 Gly Pro Gly Ser₁₀₀ Met His Pro Asp Gly₁₀₅ Asn Phe Trp Gly Asn₁₁₀ Arg Phe
 Pro Ala Thr₁₁₅ Ser Ile Arg Asp Gln₁₂₀ Val Asn Ala Glu Lys₁₂₅ Gln Phe Leu
 Asp Ala₁₃₀ Leu Gly Ile Thr Thr₁₃₅ Val Ala Ala Val Leu₁₄₀ Gly Gly Ser Met
 Gly₁₄₅ Gly Ala Arg Thr Leu₁₅₀ Glu Trp Ala Ala Met₁₅₅ Tyr Pro Glu Thr Val₁₆₀
 Gly Ala Ala Ala Val₁₆₅ Leu Ala Val Ser Ala₁₇₀ Arg Ala Ser Ala Trp₁₇₅ Gln
 Ile Gly Ile Gln₁₈₀ Ser Ala Gln Ile Lys₁₈₅ Ala Ile Glu Asn Asp₁₉₀ His His
 Trp His Glu₁₉₅ Gly Asn Tyr Tyr Glu₂₀₀ Ser Gly Cys Asn Pro₂₀₅ Ala Thr Gly
 Leu Gly₂₁₀ Ala Ala Arg Arg Ile₂₁₅ Ala His Leu Thr Tyr₂₂₀ Arg Gly Glu Leu
 Glu₂₂₅ Ile Asp Glu Arg Phe₂₃₀ Gly Thr Lys Ala Gln₂₃₅ Lys Asn Glu Asn Pro₂₄₀
 Leu Gly Pro Tyr Arg₂₄₅ Lys Pro Asp Gln Arg₂₅₀ Phe Ala Val Glu Ser₂₅₅ Tyr
 Leu Asp Tyr Gln₂₆₀ Ala Asp Lys Leu Val₂₆₅ Gln Arg Phe Asp Ala₂₇₀ Gly Ser
 Tyr Val Leu₂₇₅ Leu Thr Asp Ala Leu₂₈₀ Asn Arg His Asp Ile₂₈₅ Gly Arg Asp
 Arg Gly₂₉₀ Gly Leu Asn Lys Ala₂₉₅ Leu Glu Ser Ile Lys₃₀₀ Val Pro Val Leu
 Val Ala Gly Val Asp Thr₃₁₀ Asp Ile Asn Tyr Pro Tyr His Gln Gln Glu₃₂₀
 His Leu Ser Arg Asn₃₂₅ Leu Gly Asn Leu Leu₃₃₀ Ala Met Ala Lys Ile₃₃₅ Val
 Ser Pro Val Gly₃₄₀ His Asp Ala Phe Leu₃₄₅ Thr Glu Ser Arg Gln₃₅₀ Met Asp
 Arg Ile Val₃₅₅ Arg Asn Phe Phe Ser₃₆₀ Leu Ile Ser Pro Asp₃₆₅ Glu Asp Asn
 Pro Ser₃₇₀ Thr Tyr Ile Glu Phe Tyr Ile₃₇₅

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 <211> 1134
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 313N

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 aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt 240
 tactgctgta tctgtaccaa cgtcatcggg ggttgcaacg gttccaccgg acctggctcc 300
 atgcatccag atggaaatct ctggggtaat cgcttccccg ccacgtccat tcgtgatcag 360
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 gttccagtcc ttgtcgcagg cgtagatacc gatattaact acccctacca ccagcaagaa 960
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<210> 81
 <211> 377
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 313K

<400> 81
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 20 25 30
 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95

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Gly Pro Gly Ser₁₀₀ Met His Pro Asp Gly₁₀₅ Asn Phe Trp Gly Asn₁₁₀ Arg Phe
 Pro Ala Thr₁₁₅ Ser Ile Arg Asp Gln₁₂₀ Val Asn Ala Glu Lys₁₂₅ Gln Phe Leu
 Asp Ala₁₃₀ Leu Gly Ile Thr Thr₁₃₅ Val Ala Ala Val Leu₁₄₀ Gly Gly Ser Met
 Gly₁₄₅ Gly Ala Arg Thr Leu₁₅₀ Glu Trp Ala Ala Met₁₅₅ Tyr Pro Glu Thr Val₁₆₀
 Gly Ala Ala Ala Val₁₆₅ Leu Ala Val Ser Ala₁₇₀ Arg Ala Ser Ala Trp₁₇₅ Gln
 Ile Gly Ile Gln₁₈₀ Ser Ala Gln Ile Lys₁₈₅ Ala Ile Glu Asn Asp₁₉₀ His His
 Trp His Glu₁₉₅ Gly Asn Tyr Tyr Glu₂₀₀ Ser Gly Cys Asn Pro₂₀₅ Ala Thr Gly
 Leu Gly₂₁₀ Ala Ala Arg Arg Ile₂₁₅ Ala His Leu Thr Tyr₂₂₀ Arg Gly Glu Leu
 Glu₂₂₅ Ile Asp Glu Arg Phe₂₃₀ Gly Thr Lys Ala Gln₂₃₅ Lys Asn Glu Asn Pro₂₄₀
 Leu Gly Pro Tyr Arg₂₄₅ Lys Pro Asp Gln Arg₂₅₀ Phe Ala Val Glu Ser₂₅₅ Tyr
 Leu Asp Tyr Gln₂₆₀ Ala Asp Lys Leu Val₂₆₅ Gln Arg Phe Asp Ala₂₇₀ Gly Ser
 Tyr Val Leu₂₇₅ Leu Thr Asp Ala Leu₂₈₀ Asn Arg His Asp Ile₂₈₅ Gly Arg Asp
 Arg Gly₂₉₀ Gly Leu Asn Lys Ala₂₉₅ Leu Glu Ser Ile Lys₃₀₀ Val Pro Val Leu
 Val Ala Gly Val Asp Thr₃₁₀ Asp Ile Lys Tyr Pro₃₁₅ Tyr His Gln Gln Glu₃₂₀
 His Leu Ser Arg Asn₃₂₅ Leu Gly Asn Leu Leu₃₃₀ Ala Met Ala Lys Ile₃₃₅ Val
 Ser Pro Val Gly₃₄₀ His Asp Ala Phe Leu₃₄₅ Thr Glu Ser Arg Gln₃₅₀ Met Asp
 Arg Ile Val₃₅₅ Arg Asn Phe Phe Ser₃₆₀ Leu Ile Ser Pro Asp₃₆₅ Glu Asp Asn
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 <212> DNA
 <213> Artificial Sequence

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 <223> 313K

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 aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt 240
 tactgctga tctgtaccaa cgtcatcggg ggttgcaacg gttccaccgg acctggctcc 300
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 tccggctgca acccagccac cggactcggc gccgcccgcac gcacgcacca cctcacctac 660
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<210> 83
 <211> 377
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 313V

<400> 83
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 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu

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115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Val Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365
 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
 370 375

<210> 84
 <211> 1134
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 313V

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 aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt 240

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<210> 85
<211> 377
<212> PRT
<213> Artificial Sequence
<220>
<223> 313A

<400> 85
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Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
35 40 45
Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
50 55 60
Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
65 70 75 80
Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
85 90 95
Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
100 105 110
Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
115 120 125
Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
130 135 140

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Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
145 150 155 160
Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
165 170 175
Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
180 185 190
Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
195 200 205
Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
210 215 220
Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
225 230 235 240
Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
245 250 255
Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
260 265 270
Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
275 280 285
Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
290 295 300
Val Ala Gly Val Asp Thr Asp Ile Ala Tyr Pro Tyr His Gln Gln Glu
305 310 315 320
His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
325 330 335
Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
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355 360 365
Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
370 375

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<212> DNA
<213> Artificial Sequence

<220>
<223> 313A

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aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt 240
tactgctga tctgtaccaa cgtcatcggg gtttgcaacg gttccaccgg acctggctcc 300
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 ctcatctccc cagacgaaga caacccttcg acctacatcg agttctacat ctaa 1134

<210> 87
 <211> 377
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 313b

<400> 87
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 Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30
 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160

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Gly Ala Ala Ala Val₁₆₅ Leu Ala Val Ser₁₇₀ Ala Arg Ala Ser Ala Trp₁₇₅ Gln
 Ile Gly Ile Gln₁₈₀ Ser Ala Gln Ile Lys₁₈₅ Ala Ile Glu Asn Asp₁₉₀ His His
 Trp His Glu₁₉₅ Gly Asn Tyr Tyr Glu₂₀₀ Ser Gly Cys Asn Pro₂₀₅ Ala Thr Gly
 Leu Gly₂₁₀ Ala Ala Arg Arg Ile₂₁₅ Ala His Leu Thr Tyr₂₂₀ Arg Gly Glu Leu
 Glu₂₂₅ Ile Asp Glu Arg Phe₂₃₀ Gly Thr Lys Ala Gln₂₃₅ Lys Asn Glu Asn Pro₂₄₀
 Leu Gly Pro Tyr Arg₂₄₅ Lys Pro Asp Gln Arg₂₅₀ Phe Ala Val Glu Ser₂₅₅ Tyr
 Leu Asp Tyr Gln₂₆₀ Ala Asp Lys Leu Val₂₆₅ Gln Arg Phe Asp Ala₂₇₀ Gly Ser
 Tyr Val₂₇₅ Leu Leu Thr Asp Ala Leu₂₈₀ Asn Arg His Asp Ile₂₈₅ Gly Arg Asp
 Arg Gly₂₉₀ Gly Leu Asn Lys Ala₂₉₅ Leu Glu Ser Ile Lys₃₀₀ Val Pro Val Leu
 Val₃₀₅ Ala Gly Val Asp Thr₃₁₀ Asp Ile Asp Tyr Pro₃₁₅ Tyr His Gln Gln Glu₃₂₀
 His Leu Ser Arg Asn₃₂₅ Leu Gly Asn Leu Leu₃₃₀ Ala Met Ala Lys Ile₃₃₅ Val
 Ser Pro Val Gly₃₄₀ His Asp Ala Phe Leu₃₄₅ Thr Glu Ser Arg Gln₃₅₀ Met Asp
 Arg Ile Val₃₅₅ Arg Asn Phe Phe Ser₃₆₀ Leu Ile Ser Pro Asp₃₆₅ Glu Asp Asn
 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile₃₇₀ ₃₇₅

<210> 88
 <211> 1134
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 313b

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 gtagataaag aaggacgcag caatgtcggt ctcatcgaac acgccctcac tggagattcc 180
 aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt 240
 tactgctga tctgtaccaa cgtcatcggt gggtgcaacg gttccaccgg acctggctcc 300
 atgcatccag atggaaattt ctggggtaat cgcttccccg ccacgtccat tcgtgatcag 360
 gtaaacgccg aaaaacaatt cctcgacgca ctcggcatca ccacggtcgc cgcagtactt 420
 ggtggttcca tgggtggtgc ccgcacccta gagtgggccg caatgtaccc agaaactgtt 480

6413067_1

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ggcgcagctg ctgttcttgc agtttctgca cgcgccagcg cctggcaaat cggcattcaa      540
tccgccccaaa ttaaggcgat tgaaaacgac caccactggc acgaaggcaa ctactacgaa      600
tccgggtgca acccagccac cggactcggc gccgcccgcg gcatcgccca cctcacctac      660
cgtggcgaac tagaaatcga cgaacgcttc ggcaccaaag cccaaaagaa cgaaaaccca      720
ctcgggtccct accgcaagcc cgaccagcgc ttcgccgtgg aatcctactt ggactaccaa      780
gcagacaagc tagtacagcg tttcgacgcc ggctcctacg tcttgctcac cgacgccttc      840
aaccgccacg acattggtcg cgaccgcgga ggcctcaaca aggcactcga atccatcaaa      900
gttccagtcc ttgtcgcagg cgtagatacc gatattgact acccctacca ccagcaagaa      960
cacctctcca gaaacctggg aaatctactg gcaatggcaa aaatcgtatc ccctgtcggc     1020
cacgatgctt tcctcaccga aagccgcaa atggatcgca tcgtgaggaa cttcttcagc     1080
ctcatctccc cagacgaaga caacccttcg acctacatcg agttctacat ctaa         1134

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<210>      89
<211>      377
<212>      PRT
<213>      Artificial Sequence

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<220>
<223>      313E

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<400>      89
Met Pro Thr Leu Ala5 Pro Ser Gly Gln Leu10 Glu Ile Gln Ala Ile15 Gly
1
Asp Val Ser Thr20 Glu Ala Gly Ala Ile25 Ile Thr Asn Ala Glu30 Ile Ala
Tyr His Arg35 Trp Gly Glu Tyr Arg40 Val Asp Lys Glu Gly45 Arg Ser Asn
Val Val50 Leu Ile Glu His Ala55 Leu Thr Gly Asp Ser60 Asn Ala Ala Asp
Trp65 Trp Ala Asp Leu Leu70 Gly Pro Gly Lys Ala75 Ile Asn Thr Asp Ile80
Tyr Cys Val Ile Cys85 Thr Asn Val Ile Gly90 Gly Cys Asn Gly Ser95 Thr
Gly Pro Gly Ser100 Met His Pro Asp Gly105 Asn Phe Trp Gly Asn Arg Phe
Pro Ala Thr115 Ser Ile Arg Asp Gln Val Asn Ala Glu Lys125 Gln Phe Leu
Asp Ala130 Leu Gly Ile Thr Thr135 Val Ala Ala Val Leu140 Gly Gly Ser Met
Gly Gly Ala Arg Thr Leu150 Glu Trp Ala Ala Met155 Tyr Pro Glu Thr Val160
Gly Ala Ala Ala Val165 Leu Ala Val Ser Ala170 Arg Ala Ser Ala Trp175 Gln
Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His

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190

Trp	His	Glu 195	Gly	Asn	Tyr	Tyr	Glu 200	Ser	Gly	Cys	Asn	Pro 205	Ala	Thr	Gly
Leu	Gly 210	Ala	Ala	Arg	Arg	Ile 215	Ala	His	Leu	Thr	Tyr 220	Arg	Gly	Glu	Leu
Glu 225	Ile	Asp	Glu	Arg	Phe 230	Gly	Thr	Lys	Ala	Gln 235	Lys	Asn	Glu	Asn	Pro 240
Leu	Gly	Pro	Tyr	Arg 245	Lys	Pro	Asp	Gln	Arg 250	Phe	Ala	Val	Glu	Ser 255	Tyr
Leu	Asp	Tyr	Gln 260	Ala	Asp	Lys	Leu	Val 265	Gln	Arg	Phe	Asp	Ala 270	Gly	Ser
Tyr	Val	Leu 275	Leu	Thr	Asp	Ala	Leu 280	Asn	Arg	His	Asp	Ile 285	Gly	Arg	Asp
Arg	Gly 290	Gly	Leu	Asn	Lys	Ala 295	Leu	Glu	Ser	Ile	Lys 300	Val	Pro	Val	Leu
Val 305	Ala	Gly	Val	Asp	Thr 310	Asp	Ile	Glu	Tyr	Pro 315	Tyr	His	Gln	Gln	Glu 320
His	Leu	Ser	Arg	Asn 325	Leu	Gly	Asn	Leu	Leu 330	Ala	Met	Ala	Lys	Ile 335	Val
Ser	Pro	Val	Gly 340	His	Asp	Ala	Phe	Leu 345	Thr	Glu	Ser	Arg	Gln 350	Met	Asp
Arg	Ile	Val 355	Arg	Asn	Phe	Phe	Ser 360	Leu	Ile	Ser	Pro	Asp 365	Glu	Asp	Asn
Pro	Ser 370	Thr	Tyr	Ile	Glu	Phe 375	Tyr	Ile							

<210>	90
<211>	1134
<212>	DNA
<213>	Artificial Sequence

<220>
<223> 313E

<400>	90						
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gtagataaaag	aaggacgcag	caatgtcgtt	ctcatcgaac	acgccctcac	tggagattcc		180
aacgcagccg	attggtgggc	tgacttgctc	gggtcccggca	aagccatcaa	cactgatatt		240
tactgctgta	tctgtaccaa	cgtcatcggg	ggttgcaacg	gttccaccgg	acctgggtcc		300
atgcatccag	atggaaattt	ctggggtaat	cgcttccccg	ccacgtccat	tcgtgatcag		360
gtaaacgccg	aaaaacaatt	cctcgacgca	ctcggcatca	ccacggtcgc	cgcagtactt		420
ggtggttcca	tgggtggtgc	ccgcacccta	gagtggggccg	caatgtaccc	agaaactggt		480
ggcgagctg	ctgttcttgc	agtttctgca	cgcgccagcg	cctggcaa	at		540
tccgccaaa	ttaaggcgat	tgaaaacgac	caccactggc	acgaaggcaa	ctactacgaa		600

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tccggctgca acccagccac cggactcggc gccgcccgc gcatcgccca cctcacctac      660
cgtggcgaac tagaaatcga cgaacgcttc ggcaccaaag cccaaaagaa cgaaaaccca      720
ctcgggtccct accgcaagcc cgaccagcgc ttcgccgtgg aatcctactt ggactaccaa      780
gcagacaagc tagtacagcg tttcgacgcc ggctcctacg tcttgctcac cgacgccctc      840
aaccgccacg acattggtcg cgaccgcgga ggcctcaaca aggcactcga atccatcaaa      900
gttccagtcc ttgtcgcagg cgtagatacc gatattgaat acccctacca ccagcaagaa      960
cacctctcca gaaacctggg aaatctactg gcaatggcaa aaatcgtatc ccctgtcggc     1020
cacgatgctt tcctcaccga aagccgcaa atggatcgca tcgtgaggaa cttcttcagc     1080
ctcatctccc cagacgaaga caacccttcg acctacatcg agttctacat ctaa          1134

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<210>      91
<211>      377
<212>      PRT
<213>      Artificial Sequence

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<220>
<223>      313G

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<400>      91
Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
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Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
          20          25          30
Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
          35          40          45
Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
          50          55          60
Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
          65          70          75          80
Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
          85          90          95
Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
          100          105          110
Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
          115          120          125
Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
          130          135          140
Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
          145          150          155          160
Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
          165          170          175
Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
          180          185          190
Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
          195          200          205

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Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Gly Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365
 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
 370 375

<210> 92
 <211> 1134
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 313G

<400> 92
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 gtagataaag aaggacgcag caatgtcggt ctcacgaac acgccctcac tggagattcc 180
 aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt 240
 tactgctga tctgtaccaa cgtcatcggt gggtgcaacg gttccaccgg acctggctcc 300
 atgcatccag atggaaattt ctggggtaat cgcttccccg ccacgtccat tcgtgatcag 360
 gtaaagccg aaaaacaatt cctcgacgca ctcggcatca ccacggtcgc cgcagtactt 420
 ggtggttcca tgggtggtgc ccgcacccta gagtgggccc caatgtaccc agaaactggt 480
 ggcgcagctg ctgttcttgc agtttctgca cgcgccagcg cctggcaaact cggcattcaa 540
 tccgccc aaa ttaaggcgat tgaaaacgac caccactggc acgaaggcaa ctactacgaa 600
 tccggctgca acccagccac cggactcggc gccgcccgc gcatcgcca cctcacctac 660
 cgtggcgaac tagaaatcga cgaacgcttc ggcaccaaag ccaaaaagaa cgaaaaccca 720

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ctcggtcctt accgcaagcc cgaccagcgc ttgccgtgg aatcctactt ggactaccaa 780
gcagacaagc tagtacagcg tttcgacgcc ggctcctacg tcttgctcac cgacgccctc 840
aaccgccacg acattggtcg cgaccgcgga ggcctcaaca aggcactcga atccatcaaa 900
gttccagtcc ttgtcgcagg cgtagatacc gatattggat acccctacca ccagcaagaa 960
cacctctcca gaaacctggg aaatctactg gcaatggcaa aaatcgtatc ccctgtcggc 1020
cacgatgctt tcctcaccga aagccgcaa atggatcgca tcgtgaggaa cttcttcagc 1080
ctcatctccc cagacgaaga caacccttcg acctacatcg agttctacat ctaa 1134

<210> 93
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> 313w

<400> 93
Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
1 5 10 15
Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
20 25 30
Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
35 40 45
Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
50 55 60
Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
65 70 75 80
Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
85 90 95
Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
100 105 110
Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
115 120 125
Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
130 135 140
Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
145 150 155 160
Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
165 170 175
Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
180 185 190
Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
195 200 205
Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
210 215 220

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Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Trp Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
 355 360 365
 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
 370 375

<210> 94
 <211> 1134
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> 313W

<400> 94
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 gaagccggag caatcattac aaacgctgaa atcgctatc accgctgggg tgaataccgc 120
 gtagataaag aaggacgcag caatgtcggt ctcatcgaac acgccctcac tggagattcc 180
 aacgcagccg attggtgggc tgacttgctc ggtcccggca aagccatcaa cactgatatt 240
 tactgcgtga tctgtaccaa cgtcatcggt ggttgcaacg gttccaccgg acctggctcc 300
 atgcatccag atggaaattt ctggggtaat cgcttccccg ccacgtccat tcgtgatcag 360
 gtaaacgccg aaaaacaatt cctcgacgca ctcggcata ccacggtcgc cgcagtactt 420
 ggtggttcca tgggtggtgc ccgcacccta gagtggggccg caatgtaccc agaaactggt 480
 ggcgcagctg ctgttcttgc agtttctgca cgcgccagcg cctggcaa at cggcattcaa 540
 tccgccc aaa ttaaggcgat tgaaaacgac caccactggc acgaaggcaa ctactacgaa 600
 tccggctgca acccagccac cggactcggc gccgcccgc gcatcgcca cctcacctac 660
 cgtggcgaac tagaaatcga cgaacgctt ggcaccaaag cccaaaagaa cgaaaaccca 720
 ctcggtccct accgcaagcc cgaccagcgc ttcgccgtgg aatcctactt ggactaccaa 780
 gcagacaagc tagtacagcg tttcgacgcc ggctcctacg tcttgctcac cgacgcctc 840

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aaccgccacg acattggtcg cgaccgcgga ggcctcaaca aggcactcga atccatcaaa	900
gttccagtcc ttgtcgcagg cgtagatacc gatatttggt acccctacca ccagcaagaa	960
cacctctcca gaaacctggg aaatctactg gcaatggcaa aaatcgtatc ccctgtcggc	1020
cacgatgctt tcctcaccga aagccgcaa atggatcgca tcgtgaggaa cttcttcagc	1080
ctcatctccc cagacgaaga caacccttcg acctacatcg agttctacat ctaa	1134