SEQUENCE LISTING

<110> SAVILE, Christopher
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DEVINE, Paul N.
JANEY, Jacob M.

<120> TRANSAMINASE BIOCATALYSTS

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<150> 61/155,902
<151> 2009-02-26

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Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu His Ser Asp
    50                  55                  60

Val Thr Tyr Thr Val Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Phe Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Gly Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Val Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Ala Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Ser Gly
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210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
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Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Thr Thr Ala Gly Gly Val Trp
275 280 285

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

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu His Ser Asp
50 55 60

Val Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Val Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Gly Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg

165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Val Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Ala Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Thr Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
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Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

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Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu His Ser Asp
50 55 60

Ala Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr

115 120 125

Arg Gly Tyr Ser Ser Thr Pro Gly Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Val Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Ala Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Thr Thr Ala Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
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Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
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Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

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Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu His Ser Asp
50 55 60

Val Thr Tyr Thr Val Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu

65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Leu Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Gly Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Val Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Ala Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Thr Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
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Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
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Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

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        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu His Ser Asp
    50                  55                  60

Val Thr Tyr Thr Val Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Gly Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Val Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Ala Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
            260                 265                 270
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Leu Asp Ala Asp Glu Val Leu Gly Cys Thr Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

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            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu His Ser Asp
    50                  55                  60

Val Thr Tyr Thr Val Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Leu Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Gly Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ala Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Val Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Ala Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
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Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Thr Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

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gacgaccaca tcgaacgtct gttctctaac gctgaatcta tgcgtatcat cccgccgctg 300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccaggtga acgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcagttcag 600

gaaacccacg accgtggttt cgaggctccg ctgctgctgg acggtgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgcactaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 14
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 14

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu His Ser Asp
50 55 60

Ala Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Gly Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

```
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Val Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Ala Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
            260                 265                 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Thr Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 15
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 15

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atggctttct ctgctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat      60

atcacctact ctgaccacga actggacccg gctaacccgc tggctggtgg tgctgcttgg     120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac     180

ctgacttctg acgctaccta caccgggttc cacgtttgga acggtaacgc tttccgtctg     240

gacgaccaca tcgaacgtct gttctctaac gctgaatcta tgcgtatcat cccgccgctg     300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa     360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccaggtga acgtgacatc     420
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accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg ttctccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcatggcag 600

gaaacccacg accgtggttt cgaggctccg ctgctgctgg acggtgacgg tctgctggct 660

gaaggtccgg gttacaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 16
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 16

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
115 120 125

```
Arg Gly Tyr Ser Ser Thr Pro Gly Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Trp Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Ala Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Tyr Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
            260                 265                 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 17
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 17
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atcacctact ctgaccacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgttctctg acgctaccta caccgggttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gctgaatcta tgcgtatcat cccgccgctg 300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcagtagttt ctgtttctat cacccgtggt tactcttcta ccccatatga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg acggtgacgg tctgctggct 660

gaaggtccgg gttacaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 18
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 18

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Phe Ser Asp
50 55 60

Ala Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

```
Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Val Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Tyr Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
            260                 265                 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 19
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 19
atggctttct ctgctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgaccacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgacctctg acgctaccta caccgggttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gctgaatcta tgcgtatcat cccgccgctg 300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcagtagttt ctgtttctat cacccgtggt tactcttcta ccccatatac tcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg acggtgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgatga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 20
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 20

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
20 25 30

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Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Val Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Thr Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
            260                 265                 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285
```

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 21
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 21
atggctttct ctgctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgaccacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgacctctg acgctaccta caccgggttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gctgaatcta tgcgtatcat cccgccgctg 300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccatatat tcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg acggtgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 22
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of ATA117

<400> 22

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Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Ile Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
```

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 23
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 23
atggctttct ctgctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgaccacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgacctctg acgctaccta caccgggttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gctgaatcta tgcgtatcat cccgccgctg 300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccatatac tcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg acggtgacgg tctgctggct 660

gaaggtccgg gttacaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

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tcttcttctc tgctgacccc ggtacagtac 990

<210> 24
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 24

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Thr Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
210 215 220

Tyr Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 25
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 25
atggctttct ctgctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgaccacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgcactctg acgctaccta caccgggttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gctgaatcta tgcgtatcat cccgccgctg 300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcagtagttt ctgtttctat cacccgtggt tactcttcta ccccatatat tcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagg ccgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg acggtgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttgtc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgcactaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 26
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 26

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu His Ser Asp
50 55 60

Ala Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Val Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Ile Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ala Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Val Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Thr Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 27
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 27
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atcacctact ctgaccacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgacctctg acgctaccta caccgggttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gctgaatcta tgcgtatcat cccgccgctg 300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcacatgttt ctgtttctat cacccgtggt tactcttcta ccccatatat tcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg acggtgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 28
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 28

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala His Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Ile Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
            260                 265                 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 29
<211> 990

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 29
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atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgacctctg acgctaccta caccacgttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gctgaatcta tgcgtatcat cccgccgctg 300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccatatat tcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg acggtgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 30
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 30

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

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Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Thr Ser Asp
     50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Ile Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
            260                 265                 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
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Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 31
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 31
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atcacctact ctgaccacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgacctctg acgctaccta cacctgtttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gctgaatcta tgcgtatcat cccgccgctg 300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccatatat tcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg acggtgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

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ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 32
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 32

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Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Cys Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Ile Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
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Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 33
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 33
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atcacctact ctgaccacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgacctctg acgctaccta caccgctttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gctgaatcta tgcgtatcat cccgccgctg 300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccatatat tcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

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gaaacccacg accgtggttt cgagctgccg ctgctgctgg acggtgacgg tctgctggct 660

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gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 34
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 34

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Ala Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Ile Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 35
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 35
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atcacctact ctgaccacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

tatacctctg acgctaccta caccgggttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gctgaatcta tgcgtatcat cccgccgctg 300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccatatat tcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

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gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

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tcttcttctc tgctgacccc ggtacagtac 990

<210> 36
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 36

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Ile Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 37
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 37
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atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgtattctg acgctaccta caccgggttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gctgaatcta tgcgtatcat cccgccgctg 300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccatatat tcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg acggtgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

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ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 38
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 38

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Tyr Ser Asp
50 55 60

Ala Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
85 90 95

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

```
Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Ile Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
            260                 265                 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 39
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 39
atggctttct ctgctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgaccacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgacctctg acgctaccta caccgggttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gctgaatcta tgcgtatcat cccgccgctg 300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccatttat tcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg acggtgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ctggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 40
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 40

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Thr Ser Asp
50 55 60

```
Ala Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Ile Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
            260                 265                 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
```

305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 41
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 41
atggcattct atgctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgaccacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgacctctg acgctaccta caccgggttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gcggaatcta tccgtatcat cccgccgctg 300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccgtatac gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgatgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 42
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 42

Met Ala Phe Tyr Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp His Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Thr Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu

260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 43
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 43
atggcattct ctgctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctatt cggactacga actggatccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgacctctg acgctaccta caccgggttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gcggaatcta tccgtattat cccgccgctg 300

acccaggacg aagttaaaga aatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccatatat tcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctaatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgatgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 44
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 44

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Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Ile
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Ile Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
```

210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 45
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 45
atggctttct cagctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctatt cggactacga actggatccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgacctctg acgctaccta caccgggttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gcggaatcta tccgtattat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccgtatac gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgatgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 46
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 46

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Gly Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Thr Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg

165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 47
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 47
atggctttct cagctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgacctctg acgctaccta cacctgtttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gcggaatcta tccgtatcat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccatatac gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 48
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 48

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Cys Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr

115 120 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Thr Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 49
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 49
atggctttct cagctgacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

ctgacctctg acgctaccta cacctgtttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gcggaatcta tccgtatcat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccatatac gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttccatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 50
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 50

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Cys Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu

65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Thr Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 51
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 51
atggctttct cagctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

tatacttctg acgctaccta cacctccttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gcggaatcta tccgtatcat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccattcac acgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctattccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 52
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 52

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn

20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Ser Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Thr Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Ile Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 53
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 53
atggctttct cagctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

tatacttctg acgctaccta cacctgtttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gcggaatcta tccgtatcat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcagtggttt ctgtttctat cacccgtggt tactcttcta ccccattcac acgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 54
<211> 330
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 54

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Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Cys Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Ile
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Val Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Thr Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
```

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 55
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 55
atggctttct cagctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gcggaatcta tccgtatcat cccgccgctg 300

actcaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcagtggttt ctgtttctat cacccgtggt tactcttcta ccccattcac acgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 56
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 56

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Val Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Thr Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

```
Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
            260                 265                 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 57
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 57

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atggctttct cagctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat      60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg     120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac     180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg     240

gacgaccaca tcgaacgtct gttctctaac gcggaatcta tccgtatcat cccgccgctg     300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa     360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc     420
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accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 58
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 58

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Ile
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 59
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 59
atggctttct cagctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gcggaatcta tccgtatcat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcacatgttt ctgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 60
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 60

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

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Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Ile
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala His Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
            260                 265                 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 61
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 61
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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

tatacctctg acgctaccta cacctgtttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gcggaatcta tccgtatcat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccatatac gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgtta 480

gaccgcatcc gtgacggtgt tcacttaatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggtaac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 62
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 62

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

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Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Cys Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Ile
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Thr Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Leu
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285
```

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 63
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 63
atggctttct cagctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

tatacctctg acgctaccta cacctgtttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gcggaatctc tgcgtatcat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccatatac gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacttaatg gttgctcagt ctgttcgtcg tacgccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccttggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccgttaac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 64
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of ATA117

<400> 64

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Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Cys Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Leu Arg Ile
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Tyr Thr Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
```

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Leu Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 65
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 65
atggctttct cagctgacac ctctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

tatacttctg acgctaccta cacctgtttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gcggaatcta tccgtatcat cccgccgctg 300

accctggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgttc gctattccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 66
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 66

Met Ala Phe Ser Ala Asp Thr Ser Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Cys Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Ile
85 90 95

Ile Pro Pro Leu Thr Leu Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Phe Ala Ile Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

```
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
            260                 265                 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 67
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 67

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atggctttct cagctgacac cccggaaatc gtttacaccc acgacaccgg tctggactat       60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg      120

atcgaaggtg ctttcgttcc ggcgtctgaa gctcgtatct ctatcttcga ccagggttac      180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg      240

ggggaccaca tcgaacgtct gttctctaac gcggaatcta ttcgtttgat cccgccgctg      300

accaaagacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa      360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc      420

accaaacatc gtccgcaggt ttacatgtat gctgttccgt accagtggat cgtaccgttt      480

gaccgcgtcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt      540
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agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg attctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gtttttgaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgtatg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 68
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 68

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Ala
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

Ile Pro Pro Leu Thr Lys Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Val Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Ile Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Phe Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 69
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 69
atggctttct cagctgacac cccggaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc ggcgtctgaa gctcgtatct ctatcttcga ccagggttac 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaac gcggaatcta ttcgtattat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtat gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt ctgttcgtcg tactccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 70
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 70

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Ala
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Ile
85 90 95

```
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 71
<211> 990

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 71
atggctttct cagctgacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

gacgaccaca tcgaacgtct gttctctaac gcggaatcta tccgtatcat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtac gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg tactccgcgt 540

tcttctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccctggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaaccc gatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

tcttcttctc tgctgacccc ggtacagtac 990

<210> 72
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 72

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

```
Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Ile
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
            260                 265                 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
```

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 73
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 73
atggctttct cagctgacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggttac 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaac gcggaatctt tgcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtat gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg ttccccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 74
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 74

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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Leu Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
```

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 75
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 75
atggctttct cagctgacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaac gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtat gctctgccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacgctatg gttgctcagt ctgttcgtcg ttccccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gtttttgaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 76
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 76

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Leu Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

```
Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Phe Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 77
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 77

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atggctttct cagctgacac ccctgaaatc gtttacaccc acgacaccgg tctggactat      60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg     120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt     180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg     240

ggggaccaca tcgaacgtct gttctctaac gcggaatctt tgcgtttgat cccgccgctg     300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa     360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc     420

accaaacatc gtccgcaggt ttacatgtat gctgttccgt accagtggat cgtaccgttt     480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt ctgttcgtcg ttccccgcgt     540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag     600
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gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgctgg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gttactgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 78
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 78

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Leu Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Thr Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 79
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 79
atggctttct cagctgacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatcgttt ctgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtat gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 80
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 80

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

```
Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 81
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 81
atggctttct cagctgacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaac gcggaatctt tgcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcaatcgttt ctgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtat gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt ctgttcgtcg ttccccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacgg tctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 82
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 82

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Leu Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

Arg Ser Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Gly Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu

305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 83
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 83
atggctttct cagctgacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatcgtta ctgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtat gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 84
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 84

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Thr Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu

260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 85
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 85
atggctttct cagctgacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatcgttc atgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtat gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 86
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 86

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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val His Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
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210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 87
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 87
atggctttct cagctgacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatcgtta atgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtat gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 88
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 88

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Asn Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg

165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 89
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 89
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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatcgttt ctgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgcat gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 90
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 90

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Ser Val Ser Ile Thr

115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met His Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 91
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 91
atggctttct cagctgacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

ataacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggttc atgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgcac gctagcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 92
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 92

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu

65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val His Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met His Ala Ser Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 93
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 93
atggctttct cagctgacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgattgtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagt gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 94
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 94

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn

20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val Thr Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 95
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 95
atggctttct cagctgacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta acgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtat gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 96
<211> 330
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 96

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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Asn Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
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Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 97
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 97
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatcgttc atgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtat gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagctgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 98
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 98

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Ile Val His Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 99
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 99
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta acgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtat gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 100
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 100

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Asn Val Ser Ile Thr
115 120 125

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Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 101
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 101
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta acgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgtat gctgttccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacactac 990

<210> 102
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 102

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

```
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Asn Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val His Tyr
                325                 330
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<210> 103
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 103
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 104
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 104

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

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Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285
```

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 105
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 105
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gaaagacatc 420

accaaacatc gtccgcaagt ttacatgagc gctggcccgt acatgtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt ctgttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcaa 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 106
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of ATA117

<400> 106

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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Lys Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Gly Pro Tyr Met Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
```

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 107
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 107
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttcgat cacccgtggt tactcttcta ccccattcga gcctgacatc 420

accaaacatc gtccgcgcgt ttacatgagc gcttccccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcaa 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 108
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 108

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Pro Asp Ile Thr Lys His Arg
130 135 140

Pro Arg Val Tyr Met Ser Ala Ser Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

```
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 109
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 109

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat       60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg      120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt      180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg      240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg      300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa      360

gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc      420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt      480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt      540
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agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 110
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 110

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

```
Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 111
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 111

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat       60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg      120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt      180
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tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgccatc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 112
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 112

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

```
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg His Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 113
<211> 990

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 113
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt tgctatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 114
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 114

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

```
Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Ala Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
```

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 115
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 115
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagcagat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 116
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 116

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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Gln Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
```

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 117
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 117
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcg tggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 118
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 118

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Val Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

```
Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 119
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 119

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat       60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg      120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt      180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg      240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg      300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa      360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc      420

accaaacatc gtccgcaggt ttttatgagc gcttgcccgt accagtggat cgtaccgttt      480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt      540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag      600
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gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 120
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 120

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Phe Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

```
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 121
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 121

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat      60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg     120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt     180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg     240
```

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgttat 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 122
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 122

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

```
Val Ala Lys Thr Glu Leu Arg Tyr Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 123
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 123
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt acgtgtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 124
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 124

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

```
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Val Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
```

305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 125
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 125
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc ctgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 126
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 126

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

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Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Pro Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
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260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 127
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 127
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atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt acacttggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 128
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 128

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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Thr Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
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210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 129
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 129
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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctctg gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 130
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 130

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Leu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg

165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 131
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 131
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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 132
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 132

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Ile Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr

115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 133
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 133
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atcacctact ctcagtacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

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ccttcttctc tgctgacccc ggtacagtac 990

<210> 134
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 134

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

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

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu

65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 135
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 135
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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcggtggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

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gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

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ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 136
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 136

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn

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            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270
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Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 137
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 137
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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc ggattctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 138
<211> 330
<212> PRT

<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 138

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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Asp
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220
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Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 139
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 139
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggaccag gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 140
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 140

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Gln Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 141
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 141
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga acctgacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 142
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 142

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Pro Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
115 120 125

```
Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 143
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 143
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

catgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 144
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 144

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp His Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

```
Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 145
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 145
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atcacctact ctgactacga actggacatg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 146
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 146

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Met Ala Asn
20 25 30

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Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285
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Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 147
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 147
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatcc atatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 148
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of ATA117

<400> 148

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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile His Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
```

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 149
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 149
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg ttgtgactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctgtcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 150
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 150

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Cys Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Val Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

```
Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 151
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 151

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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg      120

atcgaaggtg ctttcgttcc gggttctgaa gctcgtatct ctatcttcga ccagggtttt      180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg      240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg      300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa      360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc      420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt      480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt      540
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agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 152
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 152

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Gly
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
210 215 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 153
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 153
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc ggtttctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 154
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 154

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Val
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

```
Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
            100                 105                 110

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 155
<211> 990

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 155
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

tctgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 156
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 156

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ser Glu Gly Ala Phe Val Pro Pro
35 40 45

```
Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300
```

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 157
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 157
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacac tctggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 158
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 158

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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1               5                  10                  15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Thr Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
    50                  55                  60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255
```

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
260 265 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 159
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 159
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatcc ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 160
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 160

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

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

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

```
Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 161
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 161

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat       60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg      120

atcgaaggtg ctttcgttcc gcagtctgaa gctcgtatct ctatcttcga ccagggtttt      180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg      240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg      300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa      360

gcgatggtta ccgtttctat cacccgtggt tactcttcta ccccattcga gcgtgacatc      420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt      480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt      540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag      600
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gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 162
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 162

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Gln
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

```
Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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<210> 163
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 163

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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg      120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt      180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg      240
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ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 164
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 164

Met Ala Phe Ser Lys Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
85 90 95

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

```
Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Cys Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
```

<210> 165
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 165
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgacggaa gctcgtatct ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccgg cctgcgtgaa 360

gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gctagcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgccccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 166
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 166

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Thr Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Phe Tyr Thr Ser Asp
50 55 60

```
Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Gly Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Ser Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Asp Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Ala Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
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305 310 315 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 167
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 167
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatcc ctatcttcga ccagggtttt 180

tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240

ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300

acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360

gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgagc gctagcccgt accagtggat cgtaccgttt 480

gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg ctcgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gcttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840

tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900

ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960

ccttcttctc tgctgacccc ggtacagtac 990

<210> 168
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of ATA117

<400> 168

Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
1 5 10 15

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Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
            20                  25                  30

Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
        35                  40                  45

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

Ala Thr Tyr Thr Thr Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65                  70                  75                  80

Gly Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Ile Arg Leu
                85                  90                  95

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

Val Ala Lys Thr Glu Leu Arg Glu Ala Met Val Thr Val Thr Ile Thr
        115                 120                 125

Arg Gly Tyr Ser Ser Thr Pro Phe Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140

Pro Gln Val Tyr Met Ser Ala Ser Pro Tyr Gln Trp Ile Val Pro Phe
145                 150                 155                 160

Asp Arg Ile Arg Asp Gly Val His Leu Met Val Ala Gln Ser Val Arg
                165                 170                 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
            180                 185                 190

Gly Asp Leu Ile Arg Ala Ile Gln Glu Thr His Ala Arg Gly Phe Glu
        195                 200                 205

Leu Pro Leu Leu Leu Asp Cys Asp Asn Leu Leu Ala Glu Gly Pro Gly
    210                 215                 220

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
                245                 250                 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Pro Ala Glu Leu
```

```
            260                 265                 270

Tyr Asp Ala Asp Glu Val Leu Gly Cys Ser Thr Gly Gly Gly Val Trp
        275                 280                 285

Pro Phe Val Ser Val Asp Gly Asn Ser Ile Ser Asp Gly Val Pro Gly
    290                 295                 300

Pro Val Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
305                 310                 315                 320

Pro Ser Ser Leu Leu Thr Pro Val Gln Tyr
                325                 330
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