SEQUENCE LISTING

<110> CODEXIS, INC.
QUINTANAR-AUDELO, Martina
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NAZOR, Jovana
SMITH, Derek
WANG, Cuixia

<120> ENGINEERED TRANSAMINASE POLYPEPTIDES FOR INDUSTRIAL BIOCATALYSIS

<130> CX2-129USP1

<160> 306

<170> PatentIn version 3.5

<210> 1
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

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<210> 2
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 2
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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 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

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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
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<210> 3
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 3

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gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
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gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
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gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660
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<210> 4
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 4

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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
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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
Arg 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> 5
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 5

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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 ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480
gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
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gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
cgggctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
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ccttcttctc tgatgacccc ggtacagtac 990

<210> 6
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 6
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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
Arg 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 Met Thr Pro Val Gln Tyr
325 330

<210> 7
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

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atcgaaggtg ctttcgttcc gccgtctgaa gctcgtatct ctatcttcga ccagggtttt 180

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accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480
gaccgcatcc gtgacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
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gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
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<210> 8
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

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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 Cys 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
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<210> 9
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

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atcgaaggtg ctttcgttcc ggattctgaa gctcgtatct ctatcttcga ccagggtttt 180
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acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgagc gcttgcccgt accagtggat cgtaccgttt 480
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gaaacccacg accgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660
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ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 10
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 10
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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 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 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

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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 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> 11
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 11

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atcgaaggtg ctttcgttcc gacttctgaa 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
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
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<210> 12
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 12

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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 Thr
        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
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    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> 13
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 13

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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
cgggaaggtg 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
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> 14
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 14

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

<220>
<223> Engineered transaminase variant

<400> 15

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aaggaaggtg 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
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 taatgacccc ggtacagtac                                  990
```

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

<220>
<223> Engineered transaminase variant

<400> 16
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 Lys 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 Met Thr Pro Val Gln Tyr
325 330

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

<220>
<223> Engineered transaminase variant

<400> 17
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
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 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> 18
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 18
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 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 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> 19
<211> 990

<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 19
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
atcgaaggtg ctttcgttcc gccgtctgaa aagcgtatct 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
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> 20
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 20
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 Lys 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> 21
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 21
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
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 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> 22
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 22
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 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> 23
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 23

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
atcgaaggtg ctttcgttcc ggagtctgaa 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
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> 24
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 24

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

<220>
<223> Engineered transaminase variant

<400> 25
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tttgaaggtg 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
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
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<210> 26
<211> 330
<212> PRT

<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 26
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 Phe 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> 27
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 27
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
agggaaggtg 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

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 tgatgacccc ggtacagtac 990

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

<220>
<223> Engineered transaminase variant

<400> 28
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 Arg 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 Met Thr Pro Val Gln Tyr
325 330

<210> 29
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 29
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
atcgaaggtg ctttcgttcc gaagtctgaa 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
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> 30
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 30
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 Lys
        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> 31
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 31

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

<220>
<223> Engineered transaminase variant

<400> 32

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

<220>
<223> Engineered transaminase variant

<400> 33

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
atggaaggtg 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
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> 34
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 34

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

<220>
<223> Engineered transaminase variant

<400> 35
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aatgaaggtg 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
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> 36
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Engineered transaminase variant

<400> 36
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 Asn 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> 37
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 37
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgtgaaggtg 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
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 cacccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

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

<220>
<223> Engineered transaminase variant

<400> 38
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 Cys 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> 39
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 39
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
gcgcaggtta 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> 40
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 40
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 Gln 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> 41
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 41
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
gcgtttgtta 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> 42
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 42
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 Phe 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> 43
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 43
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 acatttggat 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> 44
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 44
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

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

<220>
<223> Engineered transaminase variant

<400> 45

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

<220>
<223> Engineered transaminase variant

<400> 46

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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 Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Gln 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> 47
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 47

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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 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
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ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

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

<220>
<223> Engineered transaminase variant

<400> 48
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 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> 49
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 49
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 acaagtggat 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> 50
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

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

<220>
<223> Engineered transaminase variant

<400> 51
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 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> 52
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 52
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 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
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> 53
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 53
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 acgcttggat 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> 54
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 54
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

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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 Ser Ala Cys Pro Tyr Ala 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> 55
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 55

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

<220>
<223> Engineered transaminase variant

<400> 56

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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
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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 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 Thr 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> 57
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 57
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
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg accgtggttt cgagttgccg ctgctgctgg accttgacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgcacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
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<210> 58
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 58
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 Leu 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
His 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> 59
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 59
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
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg accgtggttt cgagttgccg ctgctgctgg accatgacaa 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> 60
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 60
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 His 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> 61

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

<220>
<223> Engineered transaminase variant

<400> 61
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> 62
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 62
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 Gly 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 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
    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> 63
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 63
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttatatgagc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc cggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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 ggtacagtat                                  990


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

<220>
<223> Engineered transaminase variant

<400> 64
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 Gly 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 Thr 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
            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> 65
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 65

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> 66
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 66

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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 Gly 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 Val 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 Phe Ala Ser 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
    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> 67
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 67

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggcggtc agttcgttcc gccgtctgaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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
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<210> 68
<211> 330

<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<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 Gly Gly Gln 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 Val 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 Phe Ala Ser 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
    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> 69
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 69
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacatggat cgtaccgttt 480

gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt gaccccggct gaactgtacg 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> Engineered transaminase variant

<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 Gly 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 Phe Ala Ser 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
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 Val 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> 71
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 71
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt gaccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

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

<220>
<223> Engineered transaminase variant

<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 Gly 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 Val 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 Phe Ala Ser 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
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 Val 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> 73
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 73
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggcggtc agttcgttcc gccgtctgaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt gaccccggct gaactgtacg 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> Engineered transaminase variant

<400> 74
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 Gly Gly Gln 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 Val 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 Phe Ala Ser 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
    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 Val 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> 75
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 75

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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggcggtc agttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> 76
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 76

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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 Gly Gly Gln 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
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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 Phe Ala Ser 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
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> 77
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 77
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> 78
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<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 Gly 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 Phe Ala Ser 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
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> 79
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 79
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attgccggtc agttcgttcc gccgtctgaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt gaccccggct 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> Engineered transaminase variant

<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 Ala Gly Gln 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 Val 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 Phe Ala Ser 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
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 Val 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> 81
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 81
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggcggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatggca gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt gaccccggct 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> Engineered transaminase variant

<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 Gly 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 Ala Ala Ser 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
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 Val 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> Engineered transaminase variant

<400> 83
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggcggtc agttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatggca gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaggacggtg 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> Engineered transaminase variant

<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 Gly Gly Gln 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 Ala Ala Ser 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
    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> 85
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 85

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtagtgc tttccgtctg 240
ggggaccaca tcgaacgcct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttgcaat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgagc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agcactatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg actgcgacaa catgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccgacc gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc gatccagtac                                  990
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<210> 86
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<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 Gly 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 Ser 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 Ala 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 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 Thr 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 Met 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 Thr 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 Ile Gln Tyr
                325                 330
```

<210> 87
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 87
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gcccgtatcc cgttgttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttgcaat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgagc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg actgcgacaa catgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccgacc gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
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<210> 88
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<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 Gly Gly Ala Phe Val Pro Pro
35 40 45
Ser Glu Ala Arg Ile Pro Leu 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 Ala 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 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 Met 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 Thr 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> Engineered transaminase variant

<400> 89
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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agcactatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg actgcgacaa catgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccgacc 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> Engineered transaminase variant

<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 Gly 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 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 Thr 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 Met 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 Thr 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> Engineered transaminase variant

<400> 91
atggcgttct caaaagacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg cttttgttcc gccgaccgaa gctcgtatcc cgatcttcga 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 acacacagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> 92
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 92
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 Gly Gly Ala Phe Val Pro Pro
35 40 45
Thr 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 Thr 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> 93
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 93
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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 acacacagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> 94
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<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 Gly 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 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 Thr 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> 95
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 95
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 acacacagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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
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ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 96
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 96
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 Gly 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

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        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 Thr 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
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<210> 97
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 97

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
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attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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
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ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
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<210> 98
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 98

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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 Gly 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 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 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
    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> 99
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 99

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attggaggtg ctttcgttcc gccgaccgaa gctcgtatcc cgatcttcga 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 acacacagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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
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<210> 100
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<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 Gly Gly Ala Phe Val Pro Pro
35 40 45
Thr 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 Thr 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> 101
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 101
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 gctagcccgt acacaagtat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> 102
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<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 Gly 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 Thr Ser 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> 103
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 103
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttggacaa 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 tactgacccc ggtacagtac 990

<210> 104
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<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
Pro Leu Ala Gly Gly Ala Ala Trp Ile Gly 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 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 Leu 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> Engineered transaminase variant

<400> 105
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> Engineered transaminase variant

<400> 106
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 Gly 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 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 Gly 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> Engineered transaminase variant

<400> 107

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 acatttcgat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> Engineered transaminase variant

<400> 108

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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 Gly 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 Ile Ser 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> Engineered transaminase variant

<400> 109
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 acgtttctat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> Engineered transaminase variant

<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 Gly 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 Val Ser 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> Engineered transaminase variant

<400> 111
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 acctttcgat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> Engineered transaminase variant

<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 Gly 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 Leu Ser 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> 113
<211> 990
<212> DNA

<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 113
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 acaagtcgat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> Engineered transaminase variant

<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 Gly 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 Lys Ser 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> Engineered transaminase variant

<400> 115
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 tactcttcga ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgagc gctagcccgt acacatggat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgtcatc 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> Engineered transaminase variant

<400> 116
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 Gly 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 Thr Trp Ile Val Pro Pro
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> Engineered transaminase variant

<400> 117

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aaaggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacctggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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
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<210> 118
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 118

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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 Lys Gly 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 Phe Ala Ser 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 Gly 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> Engineered transaminase variant

<400> 119
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acatctggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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
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<210> 120
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<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 Cys Gly 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 Phe Ala Ser Pro Tyr Ile 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 Gly 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> Engineered transaminase variant

<400> 121
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt taccccggct 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> Engineered transaminase variant

<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 Gly 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 Phe Ala Ser 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 Gly 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 Val 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> Engineered transaminase variant

<400> 123
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aaaggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> Engineered transaminase variant

<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 Lys Gly 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 Val 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 Phe Ala Ser 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 Gly 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> 125
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 125

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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acaaacagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt taccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
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<210> 126
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 126

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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 Cys Gly 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 Val 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 Phe Ala Ser Pro Tyr Lys 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 Gly 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 Val 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> 127
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 127

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attggaggtg ctttcgttcc gccgacggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccgg cctgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acctgtggat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa 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> Engineered transaminase variant

<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 Gly Gly Ala Phe Val Pro Pro
        35                  40                  45
Thr 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 Val 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 Phe Ala Ser Pro Tyr Leu Trp Ile Val Pro Pro
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 Leu 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> 129
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 129
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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> Engineered transaminase variant

<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 Gly 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 Phe Ala Ser Pro Tyr Leu 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 Gly 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> Engineered transaminase variant

<400> 131
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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgacggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaaacagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780

gaagctatcc tggctgacgt taccccggct 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> Engineered transaminase variant

<400> 132
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 Cys Gly Gly Ala Phe Val Pro Pro
35 40 45
Thr 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 Phe Ala Ser Pro Tyr Lys 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 Gly 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 Val 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> Engineered transaminase variant

<400> 133

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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacccagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa 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> 134
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<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 Asp Tyr Glu Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Cys Gly 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 Phe Ala Ser Pro Tyr Thr 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 Leu 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> Engineered transaminase variant

<400> 135
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attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaaacagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt taccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 136
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<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
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 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 Phe Ala Ser Pro Tyr Lys 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 Val 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> 137
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 137

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aatggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acatctggat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> Engineered transaminase variant

<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 Asn Gly 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 Phe Ala Ser Pro Tyr Ile Trp Ile Val Pro Pro
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> 139
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 139

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aaaggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaaatggat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt taccccggct 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> Engineered transaminase variant

<400> 140

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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
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```
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 Lys Gly 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 Phe Ala Ser Pro Tyr Lys Trp Ile Val Pro Pro
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 Gly 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 Val 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> Engineered transaminase variant

<400> 141

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aatggaggtg ctttcgttcc gccgacggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acctgtggat cgtaccgccg 480
gaccgcatcc ggaacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa 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
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ccttcttctc tgctgacccc ggtacagtac 990

<210> 142
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<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 Leu Asp Pro Ala Asn
20 25 30
Pro Leu Ala Gly Gly Ala Ala Trp Asn Gly Gly Ala Phe Val Pro Pro
35 40 45
Thr 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 Phe Ala Ser Pro Tyr Leu Trp Ile Val Pro Pro
145 150 155 160
Asp Arg Ile Arg Asn 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 Leu 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> 143
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 143
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaaatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> Engineered transaminase variant

<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 Cys Gly 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 Phe Ala Ser Pro Tyr Lys 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 Gly 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> 145
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 145
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aaaggaggtg ctttcgttcc ggagtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaaacagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> Engineered transaminase variant

<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 Pro Ala Asn
            20   25   30
Pro Leu Ala Gly Gly Ala Ala Trp Lys Gly Gly Ala Phe Val Pro Glu
        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 Phe Ala Ser Pro Tyr Lys 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> 147
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 147
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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacccagat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa 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> Engineered transaminase variant

<400> 148
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 Cys Gly 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 Phe Ala Ser Pro Tyr Thr Gln Ile Val Pro Pro
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 Leu 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> 149
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 149

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaaatggat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> Engineered transaminase variant

<400> 150

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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 Cys Gly 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 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 Phe Ala Ser Pro Tyr Lys Trp Ile Val Pro Pro
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> Engineered transaminase variant

<400> 151

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acatccagat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt taccccggct 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> Engineered transaminase variant

<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 Gly 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 Phe Ala Ser Pro Tyr Ile Gln Ile Val Pro Pro
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 Leu 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 Val 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> Engineered transaminase variant

<400> 153
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaaatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa 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> Engineered transaminase variant

<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 Cys Gly 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 Phe Ala Ser Pro Tyr Lys 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 Leu 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> Engineered transaminase variant

<400> 155
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacacagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt 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> Engineered transaminase variant

<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 Ile Gly 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 Phe Ala Ser Pro Tyr Thr 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 Gly 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 Val 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> Engineered transaminase variant

<400> 157
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacctggat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa 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> Engineered transaminase variant

<400> 158
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 Gly 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 Phe Ala Ser Pro Tyr Thr Trp Ile Val Pro Pro
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 Leu 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> 159
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 159

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacctgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acatccagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> Engineered transaminase variant

<400> 160

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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
Leu Leu Ala Gly Gly Ala Ala Trp Ile Gly 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 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 Phe Ala Ser Pro Tyr Ile 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 Gly 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> 161
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 161
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aaaggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaaatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa 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
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<210> 162
<211> 330
<212> PRT

<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<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 Lys Gly 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 Phe Ala Ser Pro Tyr Lys 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 Leu 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> 163
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 163
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> Engineered transaminase variant

<400> 164
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 Gly 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 Val 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 Phe Ala Ser 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
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> Engineered transaminase variant

<400> 165
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acacccagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> 166
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<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 Cys Gly 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 Val 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 Phe Ala Ser Pro Tyr Thr 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 Gly 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> 167
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 167
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacatggat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> 168
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 168
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 Gly 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 Phe Ala Ser Pro Tyr Thr Trp Ile Val Pro Pro
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 Gly 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> 169
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 169

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acctgtggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa 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
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<210> 170
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 170

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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 Cys Gly 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
```

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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 Phe Ala Ser Pro Tyr Leu 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 Leu 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> 171
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 171
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaaacagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt taccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
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<210> 172
<211> 330
<212> PRT
<213> Artificial Sequence

<220>

<223> Engineered transaminase variant

<400> 172
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 Cys Gly 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 Phe Ala Ser Pro Tyr Lys 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 Gly 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 Val 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> 173
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 173
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgacggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acatctggat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720

gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt taccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 174
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 174
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 Cys Gly Gly Ala Phe Val Pro Pro
35 40 45
Thr 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 Phe Ala Ser Pro Tyr Ile Trp Ile Val Pro Pro
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 Gly 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 Val 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> 175
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 175
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acctgtggat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt taccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 176
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 176
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 Cys Gly 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 Phe Ala Ser Pro Tyr Leu Trp Ile Val Pro Pro
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 Gly 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 Val 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> 177
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 177
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggccggtgg tgctgcttgg 120
aaaggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaaacagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> 178
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 178
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 Lys Gly 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 Phe Ala Ser Pro Tyr Lys 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 Gly 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> 179
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 179
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aaaggaggtg ctttcgttcc ggagtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acctgtggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa 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> 180
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 180
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 Lys Gly Gly Ala Phe Val Pro Glu
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

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            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 Phe Ala Ser Pro Tyr Leu 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 Leu 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> 181
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 181

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacctgc tggctggtgg tgctgcttgg 120
aaaggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acatctggat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa 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
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<210> 182
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 182

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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
Leu Leu Ala Gly Gly Ala Ala Trp Lys Gly 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 Phe Ala Ser Pro Tyr Ile Trp Ile Val Pro Pro
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 Leu 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> 183
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 183

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aaaggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acctgtggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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
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ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 184
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 184
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 Lys Gly 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 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 Phe Ala Ser Pro Tyr Leu 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 Gly 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> 185
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 185
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120

aatggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacccagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> 186
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 186
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 Asn Gly 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 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 Phe Ala Ser Pro Tyr Thr 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> 187
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 187
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acgtgcagat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> 188
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 188
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 Gly 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 Val 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 Phe Ala Ser Pro Tyr Val Gln Ile Val Pro Pro
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> 189
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 189
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacccagat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt taccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 190
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 190
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 Gly 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

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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 Phe Ala Ser Pro Tyr Thr Gln Ile Val Pro Pro
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 Leu 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 Val 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> 191
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 191

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacctgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaaatggat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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
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<210> 192
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 192

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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
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            20                  25                  30
Leu Leu Ala Gly Gly Ala Ala Trp Cys Gly 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 Phe Ala Ser Pro Tyr Lys Trp Ile Val Pro Pro
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 Gly 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> 193
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 193

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acatctggat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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
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<210> 194
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 194
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 Gly 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 Phe Ala Ser Pro Tyr Ile Trp Ile Val Pro Pro
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 Gly 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> 195
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 195
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acatctggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa 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> 196
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 196
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 Cys Gly 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 Phe Ala Ser Pro Tyr Ile 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 Leu 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> 197

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

<220>
<223> Engineered transaminase variant

<400> 197
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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgacggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccgg cctgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acaaacagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> 198
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 198
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 Gly Gly Ala Phe Val Pro Pro
        35   40   45
Thr 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 Val 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 Phe Ala Ser Pro Tyr Lys 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 Gly 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

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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> 199
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 199
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaaatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa 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> 200
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 200
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 Cys Gly 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 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 Phe Ala Ser Pro Tyr Lys 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 Leu 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> 201
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 201

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acatccagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa 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> 202
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 202

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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 Gly 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 Phe Ala Ser Pro Tyr Ile 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 Leu 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> 203
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 203
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacacggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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
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<210> 204
<211> 330

<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 204
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 Gly 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 Phe Ala Ser Pro Tyr Thr Arg 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> 205
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 205
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aaaggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccgg cctgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acaaatggat cgtaccgttt 480

gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa 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> 206
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 206
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 Lys Gly 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 Val 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 Phe Ala Ser Pro Tyr Lys 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 Leu 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> 207
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 207
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaaacagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> 208
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 208
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 Gly 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 Phe Ala Ser Pro Tyr Lys 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> 209
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 209
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aaaggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacatggat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> 210
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 210
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 Lys Gly 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 Phe Ala Ser Pro Tyr Thr Trp Ile Val Pro Pro
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> 211
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 211

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aaaggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaaatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acttagacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt taccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
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<210> 212
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 212

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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 Lys Gly 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 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 Phe Ala Ser Pro Tyr Lys 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 Leu 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 Val 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> 213
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 213
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aaaggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> 214
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 214
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 Lys Gly 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 Phe Ala Ser 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
    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> 215
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 215
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
aaaggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660

gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt taccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 216
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 216
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 Lys Gly 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 Phe Ala Ser 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 Gly 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 Val 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> 217
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 217
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
tgcggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acaaatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> 218
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 218
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 Cys Gly 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 Val 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 Phe Ala Ser Pro Tyr Lys 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> 219
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 219
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgacggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccgg cctgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acacccagat cgtaccgccg 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacgt taccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 220
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 220
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 Gly Gly Ala Phe Val Pro Pro
35 40 45
Thr 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 Val 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 Phe Ala Ser Pro Tyr Thr Gln Ile Val Pro Pro
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 Gly 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 Val 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> 221
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 221
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacctgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gggctctgaa gcgcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accatgacaa 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> 222
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 222
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
Leu Leu Ala Gly Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Gly
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

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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 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 Phe Ala Ser 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 His 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> 223
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 223

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggcttgcgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gcgcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaagtggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accatgacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
cgtgctctgc 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
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<210> 224
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 224
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 Cys Gly Ala Ala Trp Ile Gly 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 Phe Ala Ser Pro Tyr Lys 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 His 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
Arg 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> 225
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 225
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggcttgcgg tgctgcttgg 120
attggaggtg ctttcgttcc gaagtctgaa gcgcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accatgacaa 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> 226
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 226
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 Cys Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Lys
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 Phe Ala Ser 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 His 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> 227
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 227
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60

atcacctact ctgactacga actggacccg gctaacccgc tggcttgcgg tgctgcttgg 120
attggaggtg ctttcgttcc gggctctgaa gcgcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acatctggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accatgacaa 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> 228
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 228
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 Cys Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Gly
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 Phe Ala Ser Pro Tyr Ile 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 His 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> 229
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 229
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga ggtggctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acaagtggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accatgacaa 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> 230
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 230
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 Gly 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 Val 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 Phe Ala Ser Pro Tyr Lys 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 His 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> 231
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 231
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gggctctgaa gcgcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt 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> 232
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 232
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 Gly Gly Ala Phe Val Pro Gly
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 Phe Ala Ser 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
    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> 233
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 233

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acctgtggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accatgacaa 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
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<210> 234
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 234

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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 Gly 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 Phe Ala Ser Pro Tyr Leu 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 His 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> 235
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 235

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggcttgcgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gcgcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acatctggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accatgacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
cgtgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaaccg gtggtggtgt ctggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
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<210> 236
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 236
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 Cys Gly Ala Ala Trp Ile Gly 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 Phe Ala Ser Pro Tyr Ile 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 His 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
Arg 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> 237
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 237
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggcttgcgg tgctgcttgg 120
attggaggtg ctttcgttcc gaagtctgaa gcgcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acatctggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accatgacaa 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> 238
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 238
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 Cys Gly Ala Ala Trp Ile Gly Gly Ala Phe Val Pro Lys
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 Phe Ala Ser Pro Tyr Ile 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 His 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> 239
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 239
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gcgcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acatctggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accatgacaa 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> 240
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 240
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 Gly 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 Phe Ala Ser Pro Tyr Ile 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 His 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> 241
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 241
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggcttgcgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtctgaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acacatggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg actgcgacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
cgtgctctgc 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> 242
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 242
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 Cys Gly Ala Ala Trp Ile Gly 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 Phe Ala Ser 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
    210                 215                 220
Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225                 230                 235                 240
Arg 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> 243
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 243

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggcttgcgg tgctgcttgg 120
attggaggtg ctttcgttcc gccatctgaa gcgcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acgtctggat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accatgacaa 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> 244
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 244

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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 Cys Gly Ala Ala Trp Ile Gly 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 Phe Ala Ser 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 His 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> 245
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 245
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacctgc tggctggcgg tgctgcttgg 120
attggaggtg ctttcgttcc gccatcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acaagcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accacgacaa 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> 246

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

<220>
<223> Engineered transaminase variant

<400> 246
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
Leu Leu Ala Gly Gly Ala Ala Trp Ile Gly 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 Phe Ala Ser Pro Tyr Lys 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 His 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> 247
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 247
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggcgg tgctgcttgg 120
attggaggtg ctttcgttcc gggttcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gattgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420

accaaacatc gtccgcaggt ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accacgacaa 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> 248
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 248
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 Gly Gly Ala Phe Val Pro Gly
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 Phe Ala Ser Pro Tyr Leu 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 His 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> 249
<211> 990
<212> DNA

<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 249
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacctgc tggctggcgg tgctgcttgg 120
attggaggtg ctttcgttcc gccatcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt accttcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accacgacaa 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> 250
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 250
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
Leu Leu Ala Gly Gly Ala Ala Trp Ile Gly 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 Phe Ala Ser Pro Tyr Leu 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 His 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> 251
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 251
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacctgc tggctggcgg tgctgcttgg 120
attggaggtg ctttcgttcc gccatcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatttctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acaagcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accacgacaa 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> 252
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 252
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
Leu Leu Ala Gly Gly Ala Ala Trp Ile Gly 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 Ser 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 Phe Ala Ser Pro Tyr Lys 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 His 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> 253
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 253

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacctgc tggctggcgg tgctgcttgg 120
attggaggtg ctttcgttcc gccatcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gattgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt accttcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg accacgacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
agggctctgc 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> 254
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 254

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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
Leu Leu Ala Gly Gly Ala Ala Trp Ile Gly 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 Phe Ala Ser Pro Tyr Leu 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 His 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
Arg 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> 255
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 255
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
ttcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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
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<210> 256
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 256
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 Phe Gly 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 Phe Ala Ser Pro Tyr Leu 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 Gly 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> 257
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 257
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
ttcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgcaggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttatatgttc gctaccccgt acgttcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600

gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gcggctctgc 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> 258
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 258
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 Phe Gly 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 Gln 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 Phe Ala Thr Pro Tyr Val 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 Gly 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> 259
<211> 990
<212> DNA
<213> Artificial Sequence

<220>

<223> Engineered transaminase variant

<400> 259
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
ataggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgcaggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttatatgttc gctaccccgt acgttcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg attgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
cgagctctgc 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> 260
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 260
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 Gly 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 Gln 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 Phe Ala Thr Pro Tyr Val Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Ile 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 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
Arg 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> 261
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 261

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
ttcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acattcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg attgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gcggctctgc 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> 262
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 262

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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 Phe Gly 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 Phe Ala Ser Pro Tyr Ile Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Ile 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 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> 263
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 263

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
ttcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg attgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
cgagctctgc 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> 264
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 264

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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 Phe Gly 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 Phe Ala Ser Pro Tyr Leu Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Ile 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 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
Arg 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> 265
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 265
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atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
ataggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttatatgttc gctagcccgt acattcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg attgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
cgagctctgc 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> 266
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 266
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 Gly 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 Phe Ala Ser Pro Tyr Ile Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Ile 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 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
Arg 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> 267
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 267
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
ttcggaggtg ctttcgttcc gccatcggaa gcacgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acattcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gcggctctgc 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> 268
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 268
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 Phe Gly 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 Phe Ala Ser Pro Tyr Ile 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 Gly 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> 269
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 269

atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacctgc tggctggcgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acattcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> 270
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 270
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
Leu Leu Ala Gly Gly Ala Ala Trp Ile Gly 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 Phe Ala Ser Pro Tyr Ile 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 Gly 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> 271
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 271
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ttcggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg attgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> 272
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 272
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 Phe Gly 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 Phe Ala Ser Pro Tyr Leu Gln Ile Val Pro Phe
145 150 155 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Ile 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 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> 273
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 273

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
ataggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgcaggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttatatgttc gctagcccgt acattcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
cgagctctgc 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> 274
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 274

```
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 Gly 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 Gln 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 Phe Ala Ser Pro Tyr Ile 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 Gly 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
Arg 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> 275
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 275
```
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
ataggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgcaggtta ccgttacgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttatatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg attgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
cgagctctgc 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> 276
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 276
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Met Ala Phe Ser Ala Asp Thr Pro Glu Ile Val Tyr Thr His Asp Thr
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```
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 Gly 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 Gln 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 Phe Ala Ser Pro Tyr Leu Gln Ile Val Pro Phe
145                 150                 155                 160
Asp Arg Ile Arg Asp Gly Val His Leu Met Ile 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 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
Arg 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> 277
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 277

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacctctg acgctaccta caccagcttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttacgat cacccgtggt tactcttcta ccccatttga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> 278
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 278
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 Gly 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 Ser 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 Phe Ala Ser Pro Tyr Leu 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 Gly 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> 279
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 279
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcgagcg gtggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 280
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 280
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 Gly 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 Phe Ala Ser Pro Tyr Leu 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 Gly 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 Ser 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> 281
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 281
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ccccgtttga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgcgttacca ttggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 282
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 282
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 Gly 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 Phe Ala Ser Pro Tyr Leu 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 Gly 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 Val Thr Ile 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> 283
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 283
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ccccgtatga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgcgttaccc ctggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 284
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 284
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 Gly 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 Tyr Glu Arg Asp Ile Thr Lys His Arg

```
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Leu 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 Gly 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 Val Thr Pro 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> 285
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 285

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ccccgtttga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acctgtatat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgcagcaccg gcggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 286
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 286

```
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 Gly 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 Phe Ala Ser Pro Tyr Leu Tyr 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 Gly 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> 287
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 287

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ccccgataga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acctgtatat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgcgttacca ttggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 288
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 288
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 Gly 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 Ile Glu Arg Asp Ile Thr Lys His Arg
130 135 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Leu Tyr 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 Gly 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 Val Thr Ile 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> 289
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 289
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ccccatttga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgctcaacca ttggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac 990

<210> 290
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 290
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 Gly 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 Phe Ala Ser Pro Tyr Leu 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 Gly 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 Ile 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> 291
<211> 990

<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 291
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ccccgataga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> 292
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 292
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 Gly 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 Ile Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Leu 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 Gly 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> 293
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 293
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ccccgataga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccga tcttcaacgt 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> 294
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 294
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 Gly 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 Ile Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Leu 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 Gly Asp Asn Leu Leu Ala Glu Gly Pro Ile
    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> 295
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 295

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ccccgataga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acctgtatat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa cctgctggct 660
gaaggtccgg gtttcaacgt tgttgttatc aaagacggtg ttgttcgttc tccgggtcgt 720
gctgctctgc cgggtatcac ccgtaaaacc gttctggaaa tcgctgaatc tctgggtcac 780
gaagctatcc tggctgacat caccccggct gaactgtacg acgctgacga agttctgggt 840
tgcagcaccc ctggtggtgt ttggccgttc gtttctgttg acggtaactc tatctctgac 900
ggtgttccgg gtccggttac ccagtctatc atccgtcgtt actgggaact gaacgttgaa 960
ccttcttctc tgctgacccc ggtacagtac                                  990
```

<210> 296
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 296

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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 Gly 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 Ile Glu Arg Asp Ile Thr Lys His Arg
    130                 135                 140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Leu Tyr 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 Gly 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 Pro 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> 297
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 297
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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ccatttatga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagttcggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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
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<210> 298
<211> 330
<212> PRT

<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 298
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 Gly 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 Ile Tyr Glu Arg Asp Ile Thr Lys His Arg
    130   135   140
Pro Gln Val Tyr Met Phe Ala Ser Pro Tyr Leu 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 Phe
            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 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> 299
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 299
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta caccaccttc cacgtttgga acggtaacgc tttccgtctg 240
ggggaccaca tcgaacgtct gttctctaat gcggaatcta ttcgtttgat cccgccgctg 300
acccaggacg aagttaaaga gatcgctctg gaactggttg ctaaaaccga actgcgtgaa 360
gcgatggtta ccgttatgat cacccgtggt tactcttcta ccccattcga gcgtgacatc 420
accaaacatc gtccgcaggt ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540

agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> 300
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 300
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 Gly 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 Met 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 Ser Pro Tyr Leu 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 Gly 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> 301
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 301
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga 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 ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggatgg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> 302
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 302
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 Gly 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 Phe Ala Ser Pro Tyr Leu 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
Met 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 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> 303
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 303
atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtttt 180
tatacttctg acgctaccta cgcaaccttc 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 ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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> 304
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 304
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 Gly 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 Ala 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 Phe Ala Ser Pro Tyr Leu 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

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            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 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> 305
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 305

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atggcgttct cagcggacac ccctgaaatc gtttacaccc acgacaccgg tctggactat 60
atcacctact ctgactacga actggacccg gctaacccgc tggctggtgg tgctgcttgg 120
attggaggtg ctttcgttcc gccgtcggaa gctcgtatcc cgatcttcga ccagggtgtt 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 ttacatgttc gctagcccgt acctgcagat cgtaccgttt 480
gaccgcatcc gggacggtgt tcacctgatg gttgctcagt cagttcgtcg tacaccgcgt 540
agctctatcg acccgcaggt taaaaacttc cagtggggtg acctgatccg tgcaattcag 600
gaaacccacg atcgtggttt cgagttgccg ctgctgctgg acggggacaa 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
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<210> 306
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered transaminase variant

<400> 306

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