SEQUENCE LISTING

<110> DHAWAN, Ish
MILLER, Gregory
ZHANG, Xiyun

<120> TRANSAMINASE POLYPEPTIDES

<130> 376247-034WO

<141> 2010-01-08

<150> 61/143,401
<151> 2009-01-08

<160> 198

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<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
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<210> 2
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> transaminase from V. fluvialis

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Met Asn Lys Pro Gln Ser Trp Glu Ala Arg Ala Glu Thr Tyr Ser Leu

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            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val Asn Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Val His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Arg Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Met Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Ser Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Thr Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
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Phe Ala Glu Val Ala
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<210> 3
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 3

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gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttttgg ccgtatgagc gatcagaccg tgatgttgtc tgaaaaactg 300
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accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttgt gcatctgacc 540
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tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
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<210> 4
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 4

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Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val Asn Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Val His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Arg Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
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Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
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Ala Gly Phe Phe Pro Met Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Lys Phe Pro His Gly
305 310 315 320
Phe Thr Ala Ser Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Thr Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
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<210> 5
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

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gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
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accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttgt gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtggcgcgt 600
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<210> 6
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 6

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            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val Asn Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Val His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Arg Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Met Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Ser Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Thr Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
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<210> 7
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

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gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
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<210> 8
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 8
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20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val Asn Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Val His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Arg Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255

Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Met Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Ser Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Thr Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
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<210> 9
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

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atcgtggatg tgaacggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
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<210> 10
<211> 453
<212> PRT
<213> Artificial Sequence

<220>

<223> variant of transaminase from V. fluvialis

<400> 10
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val Asn Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Val His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Arg Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Met Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Ser Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Thr Pro Phe Asp Gly Asn Leu Arg Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Asn Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 11
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 11
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgaacggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttgt gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtggcgcgt 600
ctggcccgtg aactggaaga aaccattcag cgtgaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcga gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa accccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 12
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 12
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val Asn Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Val His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Arg Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240

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Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Ser Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Thr Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 13
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 13

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atgaacaaac cacaaagttg ggaagcgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgaacggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttttgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttgt gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtggcgcgt 600
ctggcccgtg aactggaaga aaccattcag cgtgaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgatttac cccggatgcg 840
attattagca gcaaaaacct gaccgcgggt ttttttccga tgggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcga gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa accccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 14
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 14

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Met Asn Lys Pro Gln Ser Trp Glu Ala Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val Asn Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Val His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Arg Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Met Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Ser Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Thr Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 15
<211> 1362
<212> DNA

<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 15
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
aatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgaacggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttgt gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtggcgcgt 600
ctggcccgtg aactggaaga aatcattcag cgtgaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcga gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa accccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 16
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 16
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asn Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val Asn Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Val His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Ile
195 200 205
Ile Gln Arg Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220

```
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Ser Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Thr Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 17
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 17

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atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 18
<211> 453

<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 18

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 19

<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 19
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttcggg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 20
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

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

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Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 21
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 21

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gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
gactatcatg cgtttcatgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcttgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 22
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 22

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Asp Tyr His Ala Phe His Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 23
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 23
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gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttaatgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 24
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 24
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Asn Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190

```
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 25
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 25

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gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttttgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 26
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 26
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala

450

<210> 27
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 27
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gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgct gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 28
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 28
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Leu Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175

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Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 29
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 29

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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggccatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgtt cggccagagc 1260
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gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 30
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 30
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly His His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Phe Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val

435 440 445
Phe Ala Glu Val Ala
450

<210> 31
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 31
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cggcgtacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaaagaatt gccccatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
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aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 32
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 32
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Ala Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160

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Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Leu Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 33
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 33

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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgcta ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt gggtcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
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ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 34
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 34

Met	Asn	Lys	Pro	Gln	Ser	Trp	Glu	Thr	Arg	Ala	Glu	Thr	Tyr	Ser	Leu
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Tyr	Gly	Phe	Thr	Asp	Met	Pro	Ser	Leu	His	Gln	Arg	Gly	Thr	Val	Val
			20					25					30		
Val	Thr	His	Gly	Glu	Gly	Pro	Tyr	Ile	Val	Asp	Val	His	Gly	Arg	Arg
		35					40					45			
Tyr	Leu	Asp	Ala	Asn	Ser	Gly	Leu	Trp	Asn	Met	Val	Ala	Gly	Phe	Asp
	50					55					60				
His	Lys	Gly	Leu	Ile	Asp	Ala	Ala	Lys	Ala	Gln	Tyr	Glu	Arg	Phe	Pro
65					70					75					80
Gly	Tyr	His	Ala	Phe	Tyr	Gly	Arg	Met	Ser	Asp	Gln	Thr	Val	Met	Leu
				85					90					95	
Ser	Glu	Lys	Leu	Val	Glu	Val	Ser	Pro	Phe	Asp	Ser	Gly	Arg	Val	Phe
			100					105					110		
Tyr	Thr	Asn	Ser	Gly	Ser	Glu	Ala	Asn	Asp	Thr	Met	Val	Lys	Met	Leu
		115					120					125			
Trp	Phe	Leu	His	Ala	Ala	Glu	Gly	Lys	Pro	Gln	Lys	Arg	Lys	Ile	Leu
	130					135					140				
Thr	Arg	Trp	Asn	Ala	Tyr	His	Gly	Ala	Thr	Ala	Val	Ser	Ala	Ser	Met
145					150					155					160
Thr	Gly	Lys	Pro	Tyr	Asn	Ser	Val	Phe	Gly	Leu	Pro	Leu	Pro	Gly	Phe
				165					170					175	
Leu	His	Leu	Thr	Cys	Pro	His	Tyr	Trp	Arg	Tyr	Gly	Glu	Glu	Gly	Glu
			180					185					190		
Thr	Glu	Glu	Gln	Phe	Val	Ala	Arg	Leu	Ala	Arg	Glu	Leu	Glu	Glu	Thr
		195					200					205			
Ile	Gln	Lys	Glu	Gly	Ala	Asp	Thr	Ile	Ala	Gly	Phe	Phe	Ala	Glu	Pro
	210					215					220				
Val	Met	Gly	Ala	Gly	Gly	Val	Ile	Pro	Pro	Ala	Lys	Gly	Tyr	Phe	Gln
225					230					235					240
Ala	Ile	Leu	Pro	Ile	Leu	Arg	Lys	Tyr	Asp	Ile	Pro	Val	Ile	Ser	Asp
				245					250					255	
Glu	Val	Ile	Cys	Gly	Phe	Gly	Arg	Thr	Gly	Asn	Thr	Trp	Gly	Cys	Val
			260					265					270		
Thr	Tyr	Asp	Phe	Thr	Pro	Asp	Ala	Ile	Ile	Ser	Ser	Lys	Asn	Leu	Thr
		275					280					285			
Ala	Gly	Phe	Phe	Pro	Val	Gly	Ala	Val	Ile	Leu	Gly	Pro	Glu	Leu	Ser
	290					295					300				
Lys	Arg	Leu	Glu	Thr	Ala	Ile	Glu	Ala	Ile	Glu	Glu	Leu	Gly	His	Gly
305					310					315					320
Phe	Thr	Ala	Gly	Gly	His	Pro	Val	Gly	Cys	Ala	Ile	Ala	Leu	Lys	Ala
				325					330					335	
Ile	Asp	Val	Val	Met	Asn	Glu	Gly	Leu	Ala	Glu	Asn	Val	Arg	Arg	Leu
			340					345					350		
Ala	Pro	Arg	Phe	Glu	Glu	Arg	Leu	Lys	His	Ile	Ala	Glu	Arg	Pro	Asn
		355					360					365			
Ile	Gly	Glu	Tyr	Arg	Gly	Ile	Gly	Phe	Met	Trp	Ala	Leu	Glu	Ala	Val
	370					375					380				
Lys	Asp	Lys	Ala	Ser	Lys	Ala	Pro	Phe	Asp	Gly	Asn	Leu	Ser	Val	Ser
385					390					395					400
Glu	Arg	Ile	Ala	Asn	Thr	Cys	Thr	Asp	Leu	Gly	Leu	Ile	Cys	Arg	Pro
				405					410					415	
Leu	Gly	Gln	Ser	Val	Val	Leu	Cys	Pro	Pro	Phe	Ile	Leu	Thr	Glu	Ala

420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 35
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 35
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagtctcta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
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aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgcta ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
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<210> 36
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 36
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Ser Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

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Thr Arg Trp Asn Ala Tyr His Gly Ala Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 37
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 37

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gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgtttcata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccagaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
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atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacaccag caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 38
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 38

Met	Asn	Lys	Pro	Gln	Ser	Trp	Glu	Thr	Arg	Ala	Glu	Thr	Tyr	Ser	Leu
1				5				10					15		
Tyr	Gly	Phe	Thr	Asp	Met	Pro	Ser	Leu	His	Gln	Arg	Gly	Thr	Val	Val
			20					25					30		
Val	Thr	His	Gly	Glu	Gly	Pro	Tyr	Ile	Val	Asp	Val	His	Gly	Arg	Arg
		35					40					45			
Tyr	Leu	Asp	Ala	Asn	Ser	Gly	Leu	Trp	Asn	Met	Val	Ala	Gly	Phe	Asp
	50					55					60				
His	Lys	Gly	Leu	Ile	Asp	Ala	Ala	Lys	Ala	Gln	Tyr	Glu	Arg	Phe	Pro
65					70					75					80
Gly	Tyr	His	Ala	Phe	Tyr	Gly	Arg	Met	Ser	Asp	Gln	Thr	Val	Met	Leu
				85					90					95	
Ser	Glu	Lys	Leu	Val	Glu	Val	Ser	Pro	Phe	Asp	Ser	Gly	Arg	Val	Phe
			100					105					110		
His	Thr	Asn	Ser	Gly	Ser	Glu	Ala	Asn	Asp	Thr	Met	Val	Lys	Met	Leu
		115					120					125			
Trp	Phe	Leu	His	Ala	Ala	Glu	Gly	Lys	Pro	Gln	Lys	Arg	Lys	Ile	Leu
	130					135					140				
Thr	Arg	Trp	Asn	Ala	Tyr	His	Gly	Val	Thr	Ala	Val	Ser	Ala	Ser	Met
145					150					155					160
Thr	Gly	Lys	Pro	Tyr	Asn	Ser	Val	Phe	Gly	Leu	Pro	Leu	Pro	Gly	Phe
				165					170					175	
Leu	His	Leu	Thr	Cys	Pro	His	Tyr	Trp	Arg	Tyr	Gly	Glu	Glu	Gly	Glu
			180					185					190		
Thr	Glu	Glu	Gln	Phe	Val	Ala	Arg	Leu	Ala	Arg	Glu	Leu	Glu	Glu	Thr
		195					200					205			
Ile	Gln	Lys	Glu	Gly	Ala	Asp	Thr	Ile	Ala	Gly	Phe	Phe	Ala	Glu	Pro
	210					215					220				
Val	Met	Gly	Ala	Gly	Gly	Val	Ile	Pro	Pro	Ala	Lys	Gly	Tyr	Phe	Gln
225					230					235					240
Ala	Ile	Leu	Pro	Ile	Leu	Arg	Lys	Tyr	Asp	Ile	Pro	Val	Ile	Ser	Asp
				245					250					255	
Glu	Val	Ile	Cys	Gly	Phe	Gly	Arg	Thr	Gly	Asn	Thr	Trp	Gly	Cys	Val
			260					265					270		
Thr	Tyr	Asp	Phe	Thr	Pro	Asp	Ala	Ile	Ile	Ser	Ser	Lys	Asn	Leu	Thr
		275					280					285			
Ala	Gly	Phe	Phe	Pro	Val	Gly	Ala	Val	Ile	Leu	Gly	Pro	Glu	Leu	Ser
	290					295					300				
Lys	Arg	Leu	Glu	Thr	Ala	Ile	Glu	Ala	Ile	Glu	Glu	Phe	Pro	His	Gly
305					310					315					320
Phe	Thr	Ala	Gly	Gly	His	Pro	Val	Gly	Cys	Ala	Ile	Ala	Leu	Lys	Ala
				325					330					335	
Ile	Asp	Val	Val	Met	Asn	Glu	Gly	Leu	Ala	Glu	Asn	Val	Arg	Arg	Leu
			340					345					350		
Ala	Pro	Arg	Phe	Glu	Glu	Arg	Leu	Lys	His	Ile	Ala	Glu	Arg	Pro	Asn
		355					360					365			
Ile	Gly	Glu	Tyr	Arg	Gly	Ile	Gly	Phe	Met	Trp	Ala	Leu	Glu	Ala	Val
	370					375					380				
Lys	Asp	Lys	Ala	Ser	Lys	Ala	Pro	Phe	Asp	Gly	Asn	Leu	Ser	Val	Ser
385					390					395					400
Glu	Arg	Ile	Ala	Asn	Thr	Ser	Thr	Asp	Leu	Gly	Leu	Ile	Cys	Arg	Pro

405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 39
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 39
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cggcgtacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgcta ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataag 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 40
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 40
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Ala Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125

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Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Ala Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 41
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 41
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggccttat taacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900

ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gtctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 42
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 42

Met	Asn	Lys	Pro	Gln	Ser	Trp	Glu	Thr	Arg	Ala	Glu	Thr	Tyr	Ser	Leu
1				5				10					15		
Tyr	Gly	Phe	Thr	Asp	Met	Pro	Ser	Leu	His	Gln	Arg	Gly	Thr	Val	Val
			20					25					30		
Val	Thr	His	Gly	Glu	Gly	Pro	Tyr	Ile	Val	Asp	Val	His	Gly	Arg	Arg
		35					40					45			
Tyr	Leu	Asp	Ala	Asn	Ser	Gly	Leu	Ile	Asn	Met	Val	Ala	Gly	Phe	Asp
	50					55					60				
His	Lys	Gly	Leu	Ile	Asp	Ala	Ala	Lys	Ala	Gln	Tyr	Glu	Arg	Phe	Pro
65					70					75					80
Gly	Tyr	His	Ala	Phe	Tyr	Gly	Arg	Met	Ser	Asp	Gln	Thr	Val	Met	Leu
				85					90					95	
Ser	Glu	Lys	Leu	Val	Glu	Val	Ser	Pro	Phe	Asp	Ser	Gly	Arg	Val	Phe
			100					105					110		
Tyr	Thr	Asn	Ser	Gly	Ser	Glu	Ala	Asn	Asp	Thr	Met	Val	Lys	Met	Leu
		115					120					125			
Trp	Phe	Leu	His	Ala	Ala	Glu	Gly	Lys	Pro	Gln	Lys	Arg	Lys	Ile	Leu
	130					135					140				
Thr	Arg	Trp	Asn	Ala	Tyr	His	Gly	Val	Thr	Ala	Val	Ser	Ala	Ser	Met
145					150					155					160
Thr	Gly	Lys	Pro	Tyr	Asn	Ser	Val	Phe	Gly	Leu	Pro	Leu	Pro	Gly	Phe
				165					170					175	
Leu	His	Leu	Thr	Cys	Pro	His	Tyr	Trp	Arg	Tyr	Gly	Glu	Glu	Gly	Glu
			180					185					190		
Thr	Glu	Glu	Gln	Phe	Val	Ala	Arg	Leu	Ala	Arg	Glu	Leu	Glu	Glu	Thr
		195					200					205			
Ile	Gln	Lys	Glu	Gly	Ala	Asp	Thr	Ile	Ala	Gly	Phe	Phe	Ala	Glu	Pro
	210					215					220				
Val	Met	Gly	Ala	Gly	Gly	Val	Ile	Pro	Pro	Ala	Lys	Gly	Tyr	Phe	Gln
225					230					235					240
Ala	Ile	Leu	Pro	Ile	Leu	Arg	Lys	Tyr	Asp	Ile	Pro	Val	Ile	Ser	Asp
				245					250					255	
Glu	Val	Ile	Cys	Gly	Phe	Gly	Arg	Thr	Gly	Asn	Thr	Trp	Gly	Cys	Val
			260					265					270		
Thr	Tyr	Asp	Phe	Thr	Pro	Asp	Ala	Ile	Ile	Ser	Ser	Lys	Asn	Leu	Thr
		275					280					285			
Ala	Gly	Phe	Phe	Pro	Val	Gly	Ala	Val	Ile	Leu	Gly	Pro	Glu	Leu	Ser
	290					295					300				
Lys	Arg	Leu	Glu	Thr	Ala	Ile	Glu	Ala	Ile	Glu	Glu	Phe	Pro	His	Gly
305					310					315					320
Phe	Thr	Ala	Gly	Gly	His	Pro	Val	Gly	Cys	Ala	Ile	Ala	Leu	Lys	Ala
				325					330					335	
Ile	Asp	Val	Val	Met	Asn	Glu	Gly	Leu	Ala	Glu	Asn	Val	Arg	Arg	Leu
			340					345					350		
Ala	Pro	Arg	Phe	Glu	Glu	Arg	Leu	Lys	His	Ile	Ala	Glu	Arg	Pro	Asn
		355					360					365			
Ile	Gly	Glu	Tyr	Arg	Gly	Ile	Gly	Phe	Met	Trp	Ala	Leu	Glu	Ala	Val
	370					375					380				
Lys	Asp	Lys	Ala	Ser	Lys	Ala	Pro	Phe	Asp	Gly	Asn	Leu	Ser	Val	Ser

385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 43
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 43
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcagta ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 44
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 44
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110

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Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 45
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 45
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctcat taacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcagta ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780

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ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                     1362
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<210> 46
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 46

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Ile Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
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370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 47
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 47
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttctgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcagta ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 48
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 48
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Ser Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95

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Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 49
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 49
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660

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tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tggtcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg cgccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                     1362
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<210> 50
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 50

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Gly His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
```

```
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Ala Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 51
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 51
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gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggccatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa   1362

<210> 52
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 52
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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                   10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
```

Gly His His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 53
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 53
atgaacaaac cgcagagctg ggaaacgcgt gcgggaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540

tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcagg tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 54
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 54

Met	Asn	Lys	Pro	Gln	Ser	Trp	Glu	Thr	Arg	Ala	Gly	Thr	Tyr	Ser	Leu
1				5				10						15	
Tyr	Gly	Phe	Thr	Asp	Met	Pro	Ser	Leu	His	Gln	Arg	Gly	Thr	Val	Val
			20					25					30		
Val	Thr	His	Gly	Glu	Gly	Pro	Tyr	Ile	Val	Asp	Val	His	Gly	Arg	Arg
		35					40					45			
Tyr	Leu	Asp	Ala	Asn	Ser	Gly	Leu	Trp	Asn	Met	Val	Ala	Gly	Phe	Asp
	50					55					60				
His	Lys	Gly	Leu	Ile	Asp	Ala	Ala	Lys	Ala	Gln	Tyr	Glu	Arg	Phe	Pro
65					70					75					80
Gly	Tyr	His	Ala	Phe	Tyr	Gly	Arg	Met	Ser	Asp	Gln	Thr	Val	Met	Leu
				85					90					95	
Ser	Glu	Lys	Leu	Val	Glu	Val	Ser	Pro	Phe	Asp	Ser	Gly	Arg	Val	Phe
			100					105					110		
Tyr	Thr	Asn	Ser	Gly	Ser	Glu	Ala	Asn	Asp	Thr	Met	Val	Lys	Met	Leu
		115					120					125			
Trp	Phe	Leu	His	Ala	Ala	Glu	Gly	Lys	Pro	Gln	Lys	Arg	Lys	Ile	Leu
	130					135					140				
Thr	Arg	Trp	Asn	Ala	Tyr	His	Gly	Val	Thr	Ala	Val	Ser	Ala	Ser	Met
145					150					155					160
Thr	Gly	Lys	Pro	Tyr	Asn	Ser	Val	Phe	Gly	Leu	Pro	Leu	Pro	Gly	Phe
				165					170					175	
Leu	His	Leu	Thr	Cys	Pro	His	Tyr	Trp	Arg	Tyr	Gly	Glu	Glu	Gly	Glu
			180					185					190		
Thr	Glu	Glu	Gln	Phe	Val	Ala	Arg	Leu	Ala	Arg	Glu	Leu	Glu	Glu	Thr
		195					200					205			
Ile	Gln	Lys	Glu	Gly	Ala	Asp	Thr	Ile	Ala	Gly	Phe	Phe	Ala	Glu	Pro
	210					215					220				
Val	Met	Gly	Ala	Gly	Gly	Val	Ile	Pro	Pro	Ala	Lys	Gly	Tyr	Phe	Gln
225					230					235					240
Ala	Ile	Leu	Pro	Ile	Leu	Arg	Lys	Tyr	Asp	Ile	Pro	Val	Ile	Ser	Asp
				245					250					255	
Glu	Val	Ile	Cys	Gly	Phe	Gly	Arg	Thr	Gly	Asn	Thr	Trp	Gly	Cys	Val
			260					265					270		
Thr	Tyr	Asp	Phe	Thr	Pro	Asp	Ala	Ile	Ile	Ser	Ser	Lys	Asn	Leu	Thr
		275					280					285			
Ala	Gly	Phe	Phe	Pro	Val	Gly	Ala	Val	Ile	Leu	Gly	Pro	Glu	Leu	Ser
	290					295					300				
Lys	Arg	Leu	Glu	Thr	Ala	Ile	Glu	Ala	Ile	Glu	Glu	Phe	Pro	His	Gly
305					310					315					320
Phe	Thr	Ala	Gly	Gly	His	Pro	Val	Gly	Cys	Ala	Ile	Ala	Leu	Lys	Ala
				325					330					335	
Ile	Asp	Val	Val	Met	Asn	Glu	Gly	Leu	Ala	Glu	Asn	Val	Arg	Arg	Leu

```
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Val Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 55
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 55
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cggtgtacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 56
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 56
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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                   10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
```

```
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Val Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 57
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 57
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgagctacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420

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cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362


<210> 58
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 58
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Ser Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
```

325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 59
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 59
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgacctacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 60
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 60
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45

```
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Thr Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 61
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 61
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cggcgtacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300

gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 62
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 62

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

```
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 63
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 63

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atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgaactacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
```

<210> 64
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 64

```
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                   10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
```

```
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Asn Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 65
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 65
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180

gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtgctacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 66
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 66
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Cys Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser

```
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 67
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 67

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atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcacca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
```

<210> 68
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 68

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
```

Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Thr Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 69
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 69
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60

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gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcaaca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
```

<210> 70
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 70

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Asn Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
```

```
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 71
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 71

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atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcggca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 72
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 72

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Gly Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 73
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 73
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gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaaat gccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 74
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 74
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val

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            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Met Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 75
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 75
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaata tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 76
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 76
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Tyr Pro His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 77
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>

<223> variant of transaminase from V. fluvialis

<400> 77
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gcagaccggc cggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 78
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 78
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp

245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Ala Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 79
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 79
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcagggt 960
tttaccgcgg gtggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 80
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 80

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro Gln Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 81
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 81
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatgcg 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 82
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 82
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln

225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Ala
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 83
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 83
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgat tggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 84
<211> 453
<212> PRT

<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 84

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Ile Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 85
<211> 1362

<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 85
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgtg cggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 86
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 86
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro

210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Cys Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 87
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 87
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttcatgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgcca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgtg tggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaggcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 88

<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 88

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe His Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Ala Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Cys Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 89
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 89
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttcatgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgcca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
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ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
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ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
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gaacgtattg cgaacacctg caccgatctg ggcctgatct gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
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<210> 90
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

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

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        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 91
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 91

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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttcatgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
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tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
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aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
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gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgtg tggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
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<210> 92
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 92
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe His Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Cys Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 93
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 93
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
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ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
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<210> 94
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 94
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Ala Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu

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            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 95
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 95

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atcgtggatg cgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
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aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtatagcag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
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gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
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ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 96
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 96
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Ala His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Ser Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445

Phe Ala Glu Val Ala
450

<210> 97
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 97
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
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ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
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cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
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<210> 98
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 98
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Ala Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe

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                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
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<210> 99
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 99

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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
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tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
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aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
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gaacgtattg cgaacacctg caccggtctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 100
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 100

Met	Asn	Lys	Pro	Gln	Ser	Trp	Glu	Thr	Arg	Ala	Glu	Thr	Tyr	Ser	Leu
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Tyr	Gly	Phe	Thr	Asp	Met	Pro	Ser	Leu	His	Gln	Arg	Gly	Thr	Val	Val
			20					25					30		
Val	Thr	His	Gly	Glu	Gly	Pro	Tyr	Ile	Val	Asp	Val	His	Gly	Arg	Arg
		35					40					45			
Tyr	Leu	Asp	Ala	Asn	Ser	Gly	Leu	Trp	Asn	Met	Val	Ala	Gly	Phe	Asp
	50					55					60				
His	Lys	Gly	Leu	Ile	Asp	Ala	Ala	Lys	Ala	Gln	Tyr	Glu	Arg	Phe	Pro
65					70					75					80
Gly	Tyr	His	Ala	Phe	Tyr	Gly	Arg	Met	Ser	Asp	Gln	Thr	Val	Met	Leu
				85					90					95	
Ser	Glu	Lys	Leu	Val	Glu	Val	Ser	Pro	Phe	Asp	Ser	Gly	Arg	Val	Phe
			100					105					110		
Tyr	Thr	Asn	Ser	Gly	Ser	Glu	Ala	Asn	Asp	Thr	Met	Val	Lys	Met	Leu
		115					120					125			
Trp	Phe	Leu	His	Ala	Ala	Glu	Gly	Lys	Pro	Gln	Lys	Arg	Lys	Ile	Leu
	130					135					140				
Thr	Arg	Trp	Asn	Ala	Tyr	His	Gly	Val	Thr	Ala	Val	Ser	Ala	Ser	Met
145					150					155					160
Thr	Gly	Lys	Pro	Tyr	Asn	Ser	Val	Phe	Gly	Leu	Pro	Leu	Pro	Gly	Phe
				165					170					175	
Leu	His	Leu	Thr	Cys	Pro	His	Tyr	Trp	Arg	Tyr	Gly	Glu	Glu	Gly	Glu
			180					185					190		
Thr	Glu	Glu	Gln	Phe	Val	Ala	Arg	Leu	Ala	Arg	Glu	Leu	Glu	Glu	Thr
		195					200					205			
Ile	Gln	Lys	Glu	Gly	Ala	Asp	Thr	Ile	Ala	Gly	Phe	Phe	Ala	Glu	Pro
	210					215					220				
Val	Met	Gly	Ala	Gly	Gly	Val	Ile	Pro	Pro	Ala	Lys	Gly	Tyr	Phe	Gln
225					230					235					240
Ala	Ile	Leu	Pro	Ile	Leu	Arg	Lys	Tyr	Asp	Ile	Pro	Val	Ile	Ser	Asp
				245					250					255	
Glu	Val	Ile	Cys	Gly	Phe	Gly	Arg	Thr	Gly	Asn	Thr	Trp	Gly	Cys	Val
			260					265					270		
Thr	Tyr	Asp	Phe	Thr	Pro	Asp	Ala	Ile	Ile	Ser	Ser	Lys	Asn	Leu	Thr
		275					280					285			
Ala	Gly	Phe	Phe	Pro	Val	Gly	Ala	Val	Ile	Leu	Gly	Pro	Glu	Leu	Ser
	290					295					300				
Lys	Arg	Leu	Glu	Thr	Ala	Ile	Glu	Ala	Val	Glu	Glu	Phe	Pro	His	Gly
305					310					315					320
Phe	Thr	Ala	Gly	Gly	His	Pro	Val	Gly	Cys	Ala	Ile	Ala	Leu	Lys	Ala
				325					330					335	
Ile	Asp	Val	Val	Met	Asn	Glu	Gly	Leu	Ala	Glu	Asn	Val	Arg	Arg	Leu
			340					345					350		
Ala	Pro	Arg	Phe	Glu	Glu	Arg	Leu	Lys	His	Ile	Ala	Glu	Arg	Pro	Asn
		355					360					365			
Ile	Gly	Glu	Tyr	Arg	Gly	Ile	Gly	Phe	Met	Trp	Ala	Leu	Glu	Ala	Val
	370					375					380				
Lys	Asp	Lys	Ala	Ser	Lys	Ala	Pro	Phe	Asp	Gly	Asn	Leu	Ser	Val	Ser
385					390					395					400
Glu	Arg	Ile	Ala	Asn	Thr	Cys	Thr	Gly	Leu	Gly	Leu	Ile	Cys	Arg	Pro
				405					410					415	
Leu	Gly	Gln	Ser	Val	Val	Leu	Cys	Pro	Pro	Phe	Ile	Leu	Thr	Glu	Ala
			420					425					430		

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Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 101
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 101
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgcca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattacac cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
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ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgtg tggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 102
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 102
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Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Ala Thr Ala Val Ser Ala Ser Met
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145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Thr Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Cys Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
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<210> 103
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 103
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttatttcgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
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tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
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aaacatattg cggaacgtcc gaacattggc gaatatcgtg gtattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
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<210> 104
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 104

Met	Asn	Lys	Pro	Gln	Ser	Trp	Glu	Thr	Arg	Ala	Glu	Thr	Tyr	Ser	Leu
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Tyr	Gly	Phe	Thr	Asp	Met	Pro	Ser	Leu	His	Gln	Arg	Gly	Thr	Val	Val
			20					25					30		
Val	Thr	His	Gly	Glu	Gly	Pro	Tyr	Ile	Val	Asp	Val	His	Gly	Arg	Arg
		35					40					45			
Tyr	Leu	Asp	Ala	Asn	Ser	Gly	Leu	Trp	Asn	Met	Val	Ala	Gly	Phe	Asp
	50					55					60				
His	Lys	Gly	Leu	Ile	Asp	Ala	Ala	Lys	Ala	Gln	Tyr	Glu	Arg	Phe	Pro
65					70					75					80
Gly	Tyr	His	Ala	Phe	Tyr	Gly	Arg	Met	Ser	Asp	Gln	Thr	Val	Met	Leu
				85					90					95	
Ser	Glu	Lys	Leu	Val	Glu	Val	Ser	Pro	Phe	Asp	Ser	Gly	Arg	Val	Phe
			100					105					110		
Tyr	Thr	Asn	Ser	Gly	Ser	Glu	Ala	Asn	Asp	Thr	Met	Val	Lys	Met	Leu
		115					120					125			
Trp	Phe	Leu	His	Ala	Ala	Glu	Gly	Lys	Pro	Gln	Lys	Arg	Lys	Ile	Leu
	130					135					140				
Thr	Arg	Trp	Asn	Ala	Tyr	His	Gly	Ser	Thr	Ala	Val	Ser	Ala	Ser	Met
145					150					155					160
Thr	Gly	Lys	Pro	Tyr	Asn	Ser	Val	Phe	Gly	Leu	Pro	Leu	Pro	Gly	Phe
				165					170					175	
Leu	His	Leu	Thr	Cys	Pro	His	Tyr	Trp	Arg	Tyr	Gly	Glu	Glu	Gly	Glu
			180					185					190		
Thr	Glu	Glu	Gln	Phe	Val	Ala	Arg	Leu	Ala	Arg	Glu	Leu	Glu	Glu	Thr
		195					200					205			
Ile	Gln	Lys	Glu	Gly	Ala	Asp	Thr	Ile	Ala	Gly	Phe	Phe	Ala	Glu	Pro
	210					215					220				
Val	Met	Gly	Ala	Gly	Gly	Val	Ile	Ser	Pro	Ala	Lys	Gly	Tyr	Phe	Gln
225					230					235					240
Ala	Ile	Leu	Pro	Ile	Leu	Arg	Lys	Tyr	Asp	Ile	Pro	Val	Ile	Ser	Asp
				245					250					255	
Glu	Val	Ile	Cys	Gly	Phe	Gly	Arg	Thr	Gly	Asn	Thr	Trp	Gly	Cys	Val
			260					265					270		
Thr	Tyr	Asp	Phe	Thr	Pro	Asp	Ala	Ile	Ile	Ser	Ser	Lys	Asn	Leu	Thr
		275					280					285			
Ala	Gly	Phe	Phe	Pro	Val	Gly	Ala	Val	Ile	Leu	Gly	Pro	Glu	Leu	Ser
	290					295					300				
Lys	Arg	Leu	Glu	Thr	Ala	Ile	Glu	Ala	Ile	Glu	Glu	Phe	Pro	His	Gly
305					310					315					320
Phe	Thr	Ala	Gly	Gly	His	Pro	Val	Gly	Cys	Ala	Ile	Ala	Leu	Lys	Ala
				325					330					335	
Ile	Asp	Val	Val	Met	Asn	Glu	Gly	Leu	Ala	Glu	Asn	Val	Arg	Arg	Leu
			340					345					350		
Ala	Pro	Arg	Phe	Glu	Glu	Arg	Leu	Lys	His	Ile	Ala	Glu	Arg	Pro	Asn
		355					360					365			
Ile	Gly	Glu	Tyr	Arg	Gly	Ile	Gly	Phe	Met	Trp	Ala	Leu	Glu	Ala	Val
	370					375					380				
Lys	Asp	Lys	Ala	Ser	Lys	Ala	Pro	Phe	Asp	Gly	Asn	Leu	Ser	Val	Ser
385					390					395					400
Glu	Arg	Ile	Ala	Asn	Thr	Cys	Thr	Asp	Leu	Gly	Leu	Ile	Cys	Arg	Pro
				405					410					415	

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Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 105
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 105

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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttcatgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgcca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgggggcggt gttattccac cggcgaaagg ctattttcag 720
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ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
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gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgat cggccagagc 1260
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<210> 106
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 106

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            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe His Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
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    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Ala Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Gly Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Ile Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 107
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 107
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgacgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgcca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960

tttaccgcgg gcggccatcc ggtgggttgt gcgatagcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccatttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgtg tggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 108
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 108

Met	Asn	Lys	Pro	Gln	Ser	Trp	Glu	Thr	Arg	Ala	Glu	Thr	Tyr	Ser	Leu
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			20					25					30		
Val	Thr	His	Gly	Glu	Gly	Pro	Tyr	Ile	Val	Asp	Val	His	Gly	Arg	Arg
		35					40					45			
Tyr	Leu	Asp	Ala	Asn	Ser	Gly	Leu	Trp	Asn	Met	Val	Ala	Gly	Phe	Asp
	50					55					60				
His	Lys	Gly	Leu	Ile	Asp	Ala	Ala	Lys	Ala	Gln	Tyr	Glu	Arg	Phe	Pro
65					70					75					80
Gly	Tyr	His	Ala	Phe	Tyr	Gly	Arg	Met	Ser	Asp	Gln	Thr	Val	Thr	Leu
				85					90					95	
Ser	Glu	Lys	Leu	Val	Glu	Val	Ser	Pro	Phe	Asp	Ser	Gly	Arg	Val	Phe
			100					105					110		
Tyr	Thr	Asn	Ser	Gly	Ser	Glu	Ala	Asn	Asp	Thr	Met	Val	Lys	Met	Leu
		115					120					125			
Trp	Phe	Leu	His	Ala	Ala	Glu	Gly	Lys	Pro	Gln	Lys	Arg	Lys	Ile	Leu
	130					135					140				
Thr	Arg	Trp	Asn	Ala	Tyr	His	Gly	Ala	Thr	Ala	Val	Ser	Ala	Ser	Met
145					150					155					160
Thr	Gly	Lys	Pro	Tyr	Asn	Ser	Val	Phe	Gly	Leu	Pro	Leu	Pro	Gly	Phe
				165					170					175	
Leu	His	Leu	Thr	Cys	Pro	His	Tyr	Trp	Arg	Tyr	Gly	Glu	Glu	Gly	Glu
			180					185					190		
Thr	Glu	Glu	Gln	Phe	Val	Ala	Arg	Leu	Ala	Arg	Glu	Leu	Glu	Glu	Thr
		195					200					205			
Ile	Gln	Lys	Glu	Gly	Ala	Asp	Thr	Ile	Ala	Gly	Phe	Phe	Ala	Glu	Pro
	210					215					220				
Val	Met	Gly	Ala	Gly	Gly	Val	Ile	Pro	Pro	Ala	Lys	Gly	Tyr	Phe	Gln
225					230					235					240
Ala	Ile	Leu	Pro	Ile	Leu	Arg	Lys	Tyr	Asp	Ile	Pro	Val	Ile	Ser	Asp
				245					250					255	
Glu	Val	Ile	Cys	Gly	Phe	Gly	Arg	Thr	Gly	Asn	Thr	Trp	Gly	Cys	Val
			260					265					270		
Thr	Tyr	Asp	Phe	Thr	Pro	Asp	Ala	Ile	Ile	Ser	Ser	Lys	Asn	Leu	Thr
		275					280					285			
Ala	Gly	Phe	Phe	Pro	Val	Gly	Ala	Val	Ile	Leu	Gly	Pro	Glu	Leu	Ser
	290					295					300				
Lys	Arg	Leu	Glu	Thr	Ala	Ile	Glu	Ala	Ile	Glu	Glu	Phe	Pro	His	Gly
305					310					315					320
Phe	Thr	Ala	Gly	Gly	His	Pro	Val	Gly	Cys	Ala	Ile	Ala	Leu	Lys	Ala
				325					330					335	
Ile	Asp	Val	Val	Met	Asn	Glu	Gly	Leu	Ala	Glu	Asn	Val	Arg	Arg	Leu
			340					345					350		
Ala	Pro	Arg	Phe	Glu	Glu	Arg	Leu	Lys	His	Ile	Ala	Glu	Arg	Pro	Asn
		355					360					365			
Ile	Gly	Glu	Tyr	Arg	Gly	Ile	Gly	Phe	Met	Trp	Ala	Leu	Glu	Ala	Val
	370					375					380				
Lys	Asp	Lys	Ala	Ser	Lys	Ala	Pro	Phe	Asp	Gly	Asn	Leu	Ser	Val	Ser
385					390					395					400

Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Cys Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 109
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 109
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttcatgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
cgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
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ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgac cggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
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<210> 110
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 110
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Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe His Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu

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        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Arg Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Thr Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 111
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 111
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttgta ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840

attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgagagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgtg tggccagagc 1260
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ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 112
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 112

Met	Asn	Lys	Pro	Gln	Ser	Trp	Glu	Thr	Arg	Ala	Glu	Thr	Tyr	Ser	Leu
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Tyr	Gly	Phe	Thr	Asp	Met	Pro	Ser	Leu	His	Gln	Arg	Gly	Thr	Val	Val
			20					25					30		
Val	Thr	His	Gly	Glu	Gly	Pro	Tyr	Ile	Val	Asp	Val	His	Gly	Arg	Arg
		35					40					45			
Tyr	Leu	Asp	Ala	Asn	Ser	Gly	Leu	Trp	Asn	Met	Val	Ala	Gly	Phe	Asp
	50					55					60				
His	Lys	Gly	Leu	Ile	Asp	Ala	Ala	Lys	Ala	Gln	Tyr	Glu	Arg	Phe	Pro
65					70					75					80
Gly	Tyr	His	Ala	Phe	Tyr	Gly	Arg	Met	Ser	Asp	Gln	Thr	Val	Met	Leu
				85					90					95	
Ser	Glu	Lys	Leu	Val	Glu	Val	Ser	Pro	Phe	Asp	Ser	Gly	Arg	Val	Phe
			100					105					110		
Cys	Thr	Asn	Ser	Gly	Ser	Glu	Ala	Asn	Asp	Thr	Met	Val	Lys	Met	Leu
		115					120					125			
Trp	Phe	Leu	His	Ala	Ala	Glu	Gly	Lys	Pro	Gln	Lys	Arg	Lys	Ile	Leu
	130					135					140				
Thr	Arg	Trp	Asn	Ala	Tyr	His	Gly	Val	Thr	Ala	Val	Ser	Ala	Ser	Met
145					150					155					160
Thr	Gly	Lys	Pro	Tyr	Asn	Ser	Val	Phe	Gly	Leu	Pro	Leu	Pro	Gly	Phe
				165					170					175	
Leu	His	Leu	Thr	Cys	Pro	His	Tyr	Trp	Arg	Tyr	Gly	Glu	Glu	Gly	Glu
			180					185					190		
Thr	Glu	Glu	Gln	Phe	Val	Ala	Arg	Leu	Ala	Arg	Glu	Leu	Glu	Glu	Thr
		195					200					205			
Ile	Gln	Lys	Glu	Gly	Ala	Asp	Thr	Ile	Ala	Gly	Phe	Phe	Ala	Glu	Pro
	210					215					220				
Val	Met	Gly	Ala	Gly	Gly	Val	Ile	Pro	Pro	Ala	Lys	Gly	Tyr	Phe	Gln
225					230					235					240
Ala	Ile	Leu	Pro	Ile	Leu	Arg	Lys	Tyr	Asp	Ile	Pro	Val	Ile	Ser	Asp
				245					250					255	
Glu	Val	Ile	Cys	Gly	Phe	Gly	Arg	Thr	Gly	Asn	Thr	Trp	Gly	Cys	Val
			260					265					270		
Thr	Tyr	Asp	Phe	Thr	Pro	Asp	Ala	Ile	Ile	Ser	Ser	Lys	Asn	Leu	Thr
		275					280					285			
Ala	Gly	Phe	Phe	Pro	Val	Gly	Ala	Val	Ile	Leu	Gly	Pro	Glu	Leu	Ser
	290					295					300				
Lys	Arg	Leu	Glu	Thr	Ala	Ile	Glu	Ala	Ile	Glu	Glu	Phe	Pro	His	Gly
305					310					315					320
Phe	Thr	Ala	Gly	Gly	His	Pro	Val	Gly	Cys	Ala	Ile	Ala	Leu	Lys	Ala
				325					330					335	
Ile	Asp	Val	Val	Met	Asn	Glu	Gly	Leu	Ala	Glu	Asn	Val	Arg	Arg	Leu
			340					345					350		
Ala	Pro	Arg	Phe	Glu	Glu	Arg	Leu	Lys	His	Ile	Ala	Glu	Arg	Pro	Asn
		355					360					365			
Ile	Gly	Glu	Tyr	Arg	Gly	Ile	Gly	Phe	Met	Trp	Ala	Leu	Glu	Ala	Val
	370					375					380				

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Arg Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Cys Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 113
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 113
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgct taacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
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tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
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aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
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<210> 114
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 114
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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                   10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Leu Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
```

```
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Cys Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Leu Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 115
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 115
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtt taacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaatt gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720

```
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacgt atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgtg tggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                     1362
```

<210> 116
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 116

```
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Phe Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Leu Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
```

```
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Cys Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 117
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 117

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atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg gttgaagcga ccgaagaatt cccgcacggt 960
ttcaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt ga                    1362
```

<210> 118
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 118

```
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                   10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
```

```
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Val Glu Ala Thr Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 119
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 119
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc cgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgatttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600

```
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaact cccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
```

<210> 120
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 120

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Ile
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Leu Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
```

```
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 121
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 121

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atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cggcatacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgtgg gaacgcgtat catggcgcca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccac cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
```

<210> 122
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 122

```
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                   10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
```

65 70 75 80
Gly Tyr His Ala Ala Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Gly Asn Ala Tyr His Gly Ala Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 123
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 123
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga gcgttttccg 240
ggctatcatg cgtcttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480

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accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaagg cgctggataa agtgtttgcg gaagtggcgt aa                    1362


<210> 124
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 124
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Ser Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
```

```
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 125
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 125

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atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcaaaca gcggcctgct taacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttttcgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattacac cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgac cggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 126
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 126

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                   10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Leu Asn Met Val Ala Gly Phe Asp
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50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Thr Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Thr Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 127
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 127
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtcttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360

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aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgcca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattacac cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
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ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362


<210> 128
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 128
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Ser Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Ala Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Thr Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
```

Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 129
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 129
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgat taacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cggcacatgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgtg tggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 130
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 130
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg

```
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Ile Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Ala His Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Cys Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 131
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 131
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240

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ggctatcatg cggcatacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggctcga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgag cggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 132
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 132

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

```
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Ser Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 133
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 133

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atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgag caacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattctgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccggt gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
```

<210> 134
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 134

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                   10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
```

```
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Ser Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Leu Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Val Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 135
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 135
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120

```
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgag caacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttggcgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgtg cggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                     1362


<210> 136
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 136
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Ser Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Gly Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
```

```
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Cys Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 137
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 137

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atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tggcggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaact gccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgtg cggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 138
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 138

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
```

```
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Gly Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Leu Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Cys Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 139
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 139

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atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctggc gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcagca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tggccatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
```

<210> 140
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 140

```
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Ala Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
```

```
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Gly His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 141
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 141

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atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtt taacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttcatgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggccaga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 142
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 142

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Phe Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe His Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Gln Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 143
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 143
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgat taacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttttgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatgcg 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 144
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 144
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Ile Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255

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Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Ala
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 145
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 145

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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtt taacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttttgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggccaga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 146
<211> 453
<212> PRT
<213> Artificial Sequence

<220>

<223> variant of transaminase from V. fluvialis

<400> 146
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Phe Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Gln Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 147
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 147
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctggc gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggctgca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
ctgaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
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gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 148
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 148
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Ala Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Cys Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240

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Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Leu Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 149
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 149

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gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttttgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tcgtcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccggc gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 150
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 150
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Arg His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Ala Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 151
<211> 1362
<212> DNA

<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 151
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tggcggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tggccatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgtg cggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 152
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 152
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220

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Val Met Gly Gly Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Gly His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Cys Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 153
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 153

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gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg caacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttagcgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgac cggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 154
<211> 453

<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 154

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Cys Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Ser Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Thr Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 155

<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 155
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttttgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggctgca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggc gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 156
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 156
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Cys Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205

```
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Ala Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 157
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 157

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atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttagcgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcacca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgtgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggc gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 158
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 158

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Ser Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Thr Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Ala Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
```

<210> 159
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 159
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcagca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tcgtcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgga aggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 160
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

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

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Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Arg His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Glu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 161
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 161

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gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttcatgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattctgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccggc gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 162
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 162
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe His Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Leu Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Ala Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala

450

<210> 163
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 163
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggctgca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattctgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tcgtcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 164
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 164
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Cys Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175

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Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Leu Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Arg His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 165
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 165

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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg caacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttgcggg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgatttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
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tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
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aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
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gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
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gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 166
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 166
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Cys Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Ala Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Leu Pro His Gly
305 310 315 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val

435 440 445
Phe Ala Glu Val Ala
450

<210> 167
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 167
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttaacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tggcggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaact gccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 168
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 168
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Asn Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160

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Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Gly Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Leu Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 169
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 169

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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcacca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tggcggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
ctgaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
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ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 170
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 170

Met	Asn	Lys	Pro	Gln	Ser	Trp	Glu	Thr	Arg	Ala	Glu	Thr	Tyr	Ser	Leu
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Tyr	Gly	Phe	Thr	Asp	Met	Pro	Ser	Leu	His	Gln	Arg	Gly	Thr	Val	Val
			20					25					30		
Val	Thr	His	Gly	Glu	Gly	Pro	Tyr	Ile	Val	Asp	Val	His	Gly	Arg	Arg
		35					40					45			
Tyr	Leu	Asp	Ala	Asn	Ser	Gly	Leu	Trp	Asn	Met	Val	Ala	Gly	Phe	Asp
	50					55					60				
His	Lys	Gly	Leu	Ile	Asp	Ala	Ala	Lys	Ala	Gln	Tyr	Glu	Arg	Phe	Pro
65					70					75					80
Gly	Tyr	His	Ala	Phe	Tyr	Gly	Arg	Met	Ser	Asp	Gln	Thr	Val	Met	Leu
				85					90					95	
Ser	Glu	Lys	Leu	Val	Glu	Val	Ser	Pro	Phe	Asp	Ser	Gly	Arg	Val	Phe
			100					105					110		
Tyr	Thr	Asn	Ser	Gly	Ser	Glu	Ala	Asn	Asp	Thr	Met	Val	Lys	Met	Leu
		115					120					125			
Trp	Phe	Leu	His	Ala	Ala	Glu	Gly	Lys	Pro	Gln	Lys	Arg	Lys	Ile	Leu
	130					135					140				
Thr	Arg	Trp	Asn	Ala	Tyr	His	Gly	Thr	Thr	Ala	Val	Ser	Ala	Ser	Met
145					150					155					160
Thr	Gly	Lys	Pro	Tyr	Asn	Ser	Val	Phe	Gly	Leu	Pro	Leu	Pro	Gly	Phe
				165					170					175	
Leu	His	Leu	Thr	Cys	Pro	His	Tyr	Trp	Arg	Tyr	Gly	Glu	Glu	Gly	Glu
			180					185					190		
Thr	Glu	Glu	Gln	Phe	Val	Ala	Arg	Leu	Ala	Arg	Glu	Leu	Glu	Glu	Thr
		195					200					205			
Ile	Gln	Lys	Glu	Gly	Ala	Asp	Thr	Ile	Ala	Gly	Phe	Phe	Ala	Glu	Pro
	210					215					220				
Val	Met	Gly	Gly	Gly	Gly	Val	Ile	Pro	Pro	Ala	Lys	Gly	Tyr	Phe	Gln
225					230					235					240
Ala	Ile	Leu	Pro	Ile	Leu	Arg	Lys	Tyr	Asp	Ile	Pro	Val	Ile	Ser	Asp
				245					250					255	
Glu	Val	Ile	Cys	Gly	Phe	Gly	Arg	Thr	Gly	Asn	Thr	Trp	Gly	Cys	Val
			260					265					270		
Thr	Tyr	Asp	Phe	Thr	Pro	Asp	Ala	Ile	Ile	Ser	Ser	Lys	Asn	Leu	Thr
		275					280					285			
Ala	Gly	Phe	Phe	Pro	Val	Gly	Ala	Val	Ile	Leu	Gly	Pro	Glu	Leu	Ser
	290					295					300				
Lys	Arg	Leu	Glu	Thr	Ala	Ile	Glu	Ala	Ile	Glu	Glu	Phe	Pro	His	Gly
305					310					315					320
Leu	Thr	Ala	Gly	Gly	His	Pro	Val	Gly	Cys	Ala	Ile	Ala	Leu	Lys	Ala
				325					330					335	
Ile	Asp	Val	Val	Met	Asn	Glu	Gly	Leu	Ala	Glu	Asn	Val	Arg	Arg	Leu
			340					345					350		
Ala	Pro	Arg	Phe	Glu	Glu	Arg	Leu	Lys	His	Ile	Ala	Glu	Arg	Pro	Asn
		355					360					365			
Ile	Gly	Glu	Tyr	Arg	Gly	Ile	Gly	Phe	Met	Trp	Ala	Leu	Glu	Ala	Val
	370					375					380				
Lys	Asp	Lys	Ala	Ser	Lys	Ala	Pro	Phe	Asp	Gly	Asn	Leu	Ser	Val	Ser
385					390					395					400
Glu	Arg	Ile	Ala	Asn	Thr	Cys	Thr	Asp	Leu	Gly	Leu	Ile	Cys	Arg	Pro
				405					410					415	
Leu	Gly	Gln	Ser	Val	Val	Leu	Cys	Pro	Pro	Phe	Ile	Leu	Thr	Glu	Ala

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            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 171
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 171
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gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcagca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgatttctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaact gccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgtg cggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 172
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 172
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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
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Thr Arg Trp Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Leu Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Cys Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 173
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 173

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gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtt taacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt ttttcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
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atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgag cggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 174
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 174

Met	Asn	Lys	Pro	Gln	Ser	Trp	Glu	Thr	Arg	Ala	Glu	Thr	Tyr	Ser	Leu
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Tyr	Gly	Phe	Thr	Asp	Met	Pro	Ser	Leu	His	Gln	Arg	Gly	Thr	Val	Val
			20					25					30		
Val	Thr	His	Gly	Glu	Gly	Pro	Tyr	Ile	Val	Asp	Val	His	Gly	Arg	Arg
		35					40					45			
Tyr	Leu	Asp	Ala	Asn	Ser	Gly	Leu	Phe	Asn	Met	Val	Ala	Gly	Phe	Asp
	50					55					60				
His	Lys	Gly	Leu	Ile	Asp	Ala	Ala	Lys	Ala	Gln	Tyr	Glu	Arg	Phe	Pro
65					70					75					80
Gly	Tyr	His	Ala	Phe	Tyr	Gly	Arg	Met	Ser	Asp	Gln	Thr	Val	Met	Leu
				85					90					95	
Ser	Glu	Lys	Leu	Val	Glu	Val	Ser	Pro	Phe	Asp	Ser	Gly	Arg	Val	Phe
			100					105					110		
Tyr	Thr	Asn	Ser	Gly	Ser	Glu	Ala	Asn	Asp	Thr	Met	Val	Lys	Met	Leu
		115					120					125			
Trp	Phe	Leu	His	Ala	Ala	Glu	Gly	Lys	Pro	Gln	Lys	Arg	Lys	Ile	Leu
	130					135					140				
Thr	Arg	Trp	Asn	Ala	Tyr	His	Gly	Val	Thr	Ala	Val	Ser	Ala	Ser	Met
145					150					155					160
Thr	Gly	Lys	Pro	Tyr	Asn	Ser	Val	Phe	Gly	Leu	Pro	Leu	Pro	Gly	Phe
				165					170					175	
Leu	His	Leu	Thr	Cys	Pro	His	Tyr	Trp	Arg	Tyr	Gly	Glu	Glu	Gly	Glu
			180					185					190		
Thr	Glu	Glu	Gln	Phe	Val	Ala	Arg	Leu	Ala	Arg	Glu	Leu	Glu	Glu	Thr
		195					200					205			
Ile	Gln	Lys	Glu	Gly	Ala	Asp	Thr	Ile	Ala	Gly	Phe	Phe	Ala	Glu	Pro
	210					215					220				
Val	Met	Gly	Ala	Gly	Gly	Val	Ile	Pro	Pro	Ala	Lys	Gly	Tyr	Phe	Gln
225					230					235					240
Ala	Ile	Leu	Pro	Ile	Leu	Arg	Lys	Tyr	Asp	Ile	Pro	Val	Ile	Ser	Asp
				245					250					255	
Glu	Val	Ile	Cys	Gly	Phe	Gly	Arg	Thr	Gly	Asn	Thr	Trp	Gly	Cys	Val
			260					265					270		
Thr	Tyr	Asp	Phe	Thr	Pro	Asp	Ala	Ile	Ile	Ser	Ser	Lys	Asn	Leu	Thr
		275					280					285			
Ala	Gly	Phe	Phe	Pro	Val	Gly	Ala	Val	Ile	Leu	Gly	Pro	Glu	Leu	Ser
	290					295					300				
Lys	Arg	Leu	Glu	Thr	Ala	Ile	Glu	Ala	Ile	Glu	Glu	Phe	Phe	His	Gly
305					310					315					320
Phe	Thr	Ala	Gly	Gly	His	Pro	Val	Gly	Cys	Ala	Ile	Ala	Leu	Lys	Ala
				325					330					335	
Ile	Asp	Val	Val	Met	Asn	Glu	Gly	Leu	Ala	Glu	Asn	Val	Arg	Arg	Leu
			340					345					350		
Ala	Pro	Arg	Phe	Glu	Glu	Arg	Leu	Lys	His	Ile	Ala	Glu	Arg	Pro	Asn
		355					360					365			
Ile	Gly	Glu	Tyr	Arg	Gly	Ile	Gly	Phe	Met	Trp	Ala	Leu	Glu	Ala	Val
	370					375					380				
Lys	Asp	Lys	Ala	Ser	Lys	Ala	Pro	Phe	Asp	Gly	Asn	Leu	Ser	Val	Ser
385					390					395					400
Glu	Arg	Ile	Ala	Asn	Thr	Cys	Thr	Asp	Leu	Gly	Leu	Ile	Cys	Arg	Pro

405 410 415
Ser Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 175
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 175
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcacca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccggtgggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
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gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgat tggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 176
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 176
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125

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Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Thr Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro Val Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Ile Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 177
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 177

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gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgct gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttagcgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgcga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
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ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 178
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 178

Met	Asn	Lys	Pro	Gln	Ser	Trp	Glu	Thr	Arg	Ala	Glu	Thr	Tyr	Ser	Leu
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Tyr	Gly	Phe	Thr	Asp	Met	Pro	Ser	Leu	His	Gln	Arg	Gly	Thr	Val	Val
			20					25					30		
Val	Thr	His	Gly	Glu	Gly	Pro	Tyr	Ile	Val	Asp	Val	His	Gly	Arg	Arg
		35					40					45			
Tyr	Leu	Asp	Ala	Asn	Ser	Gly	Leu	Leu	Asn	Met	Val	Ala	Gly	Phe	Asp
	50					55					60				
His	Lys	Gly	Leu	Ile	Asp	Ala	Ala	Lys	Ala	Gln	Tyr	Glu	Arg	Phe	Pro
65					70					75					80
Gly	Tyr	His	Ala	Phe	Ser	Gly	Arg	Met	Ser	Asp	Gln	Thr	Val	Met	Leu
				85					90					95	
Ser	Glu	Lys	Leu	Val	Glu	Val	Ser	Pro	Phe	Asp	Ser	Gly	Arg	Val	Phe
			100					105					110		
Tyr	Thr	Asn	Ser	Gly	Ser	Glu	Ala	Asn	Asp	Thr	Met	Val	Lys	Met	Leu
		115					120					125			
Trp	Phe	Leu	His	Ala	Ala	Glu	Gly	Lys	Pro	Gln	Lys	Arg	Lys	Ile	Leu
	130					135					140				
Thr	Arg	Trp	Asn	Ala	Tyr	His	Gly	Ala	Thr	Ala	Val	Ser	Ala	Ser	Met
145					150					155					160
Thr	Gly	Lys	Pro	Tyr	Asn	Ser	Val	Phe	Gly	Leu	Pro	Leu	Pro	Gly	Phe
				165					170					175	
Leu	His	Leu	Thr	Cys	Pro	His	Tyr	Trp	Arg	Tyr	Gly	Glu	Glu	Gly	Glu
			180					185					190		
Thr	Glu	Glu	Gln	Phe	Val	Ala	Arg	Leu	Ala	Arg	Glu	Leu	Glu	Glu	Thr
		195					200					205			
Ile	Gln	Lys	Glu	Gly	Ala	Asp	Thr	Ile	Ala	Gly	Phe	Phe	Ala	Glu	Pro
	210					215					220				
Val	Met	Gly	Ala	Gly	Gly	Val	Ile	Pro	Pro	Ala	Lys	Gly	Tyr	Phe	Gln
225					230					235					240
Ala	Ile	Leu	Pro	Ile	Leu	Arg	Lys	Tyr	Asp	Ile	Pro	Val	Ile	Ser	Asp
				245					250					255	
Glu	Val	Ile	Cys	Gly	Phe	Gly	Arg	Thr	Gly	Asn	Thr	Trp	Gly	Cys	Val
			260					265					270		
Thr	Tyr	Asp	Phe	Thr	Pro	Asp	Ala	Ile	Ile	Ser	Ser	Lys	Asn	Leu	Thr
		275					280					285			
Ala	Gly	Phe	Phe	Pro	Val	Gly	Ala	Val	Ile	Leu	Gly	Pro	Glu	Leu	Ser
	290					295					300				
Lys	Arg	Leu	Glu	Thr	Ala	Ile	Glu	Ala	Ile	Glu	Glu	Phe	Pro	His	Gly
305					310					315					320
Phe	Thr	Ala	Gly	Gly	His	Pro	Val	Gly	Cys	Ala	Ile	Ala	Leu	Lys	Ala
				325					330					335	
Ile	Asp	Val	Val	Met	Asn	Glu	Gly	Leu	Ala	Glu	Asn	Val	Arg	Arg	Leu
			340					345					350		
Ala	Pro	Arg	Phe	Glu	Glu	Arg	Leu	Lys	His	Ile	Ala	Glu	Arg	Pro	Asn
		355					360					365			
Ile	Gly	Glu	Tyr	Arg	Gly	Ile	Gly	Phe	Met	Trp	Ala	Leu	Glu	Ala	Val
	370					375					380				
Lys	Asp	Lys	Ala	Ser	Lys	Ala	Pro	Phe	Asp	Gly	Asn	Leu	Ser	Val	Ser

385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 179
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 179
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgct gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttttgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaagc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt ttttcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 180
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 180
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1 5 10 15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
20 25 30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35 40 45
Tyr Leu Asp Ala Asn Ser Gly Leu Leu Asn Met Val Ala Gly Phe Asp
50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110

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Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Phe His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 181
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 181

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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcagca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tggcggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
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ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccggt gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 182
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 182

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

```
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Val Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 183
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 183
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattctgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
ctgaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgat tggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa   1362

<210> 184
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 184
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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
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Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Leu Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Leu Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Ile Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 185
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 185
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660

tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaact gcgtcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgac cggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 186
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 186

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

```
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Thr Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 187
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 187

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gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggctgca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaata tccgcagggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 188
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 188

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
```

```
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Cys Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Tyr Pro Gln Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 189
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 189
atgaacaaac cgcagagctg ggaaacgcgt gcggaaacct atagcctgta tggttttacc 60
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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcacca ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540

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tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tggcggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccggc gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362


<210> 190
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 190
Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Thr Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Gly Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
```

```
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Ala Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 191
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 191

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atcgtggatg tgcatggccg tcgttatctg gatgcgaaca gcggcctgtt taacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggtaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccgg taggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tggccatggt 960
tttaccgcgg gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgat tggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 192
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 192

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Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
1               5                   10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Phe Asn Met Val Ala Gly Phe Asp
    50                  55                  60
```

```
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Tyr Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Leu His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Lys Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Gly His Gly
305                 310                 315                 320
Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Ile Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 193
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 193
atgaacaaac cgcagagctg ggaagcgcgt gcgaaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgaacggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttttgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtta gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480

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accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttgt gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtggcgcgt 600
ctggcccgtg aactggaaga aaccattcag cgtgaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gcaaaaacct gaccgcgggt ttttttccga tgggcgcggt gattctgggt 900
ccgaaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcga gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa accccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362


<210> 194
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 194
Met Asn Lys Pro Gln Ser Trp Glu Ala Arg Ala Lys Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val Asn Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Val His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Arg Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Met Gly Ala Val Ile Leu Gly Pro Lys Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
Phe Thr Ala Ser Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
```

```
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Thr Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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<210> 195
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 195

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atgaacaaac cgcagaggtg ggaagcgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgaacggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttttgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatacgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttgt gcatctgacc 540
tgcccgcatt tttggcgtta cggcgaagaa ggcgaaaccg aagaacagtt tgtggcgcgt 600
ctggcccgtg aactggaaga aaccattcag cgtgaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attcaggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gcaaaaacct gaccgcgggt ttttttccga tgggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcgt tcgaagaatt tccgcatggt 960
tttaccgcga gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa accccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362
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<210> 196
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 196

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Met Asn Lys Pro Gln Arg Trp Glu Ala Arg Ala Glu Thr Tyr Ser Leu
1               5                   10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val Asn Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
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50 55 60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65 70 75 80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125
Trp Phe Leu His Thr Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175
Val His Leu Thr Cys Pro His Phe Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205
Ile Gln Arg Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225 230 235 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Gln Val Ile Ser Asp
245 250 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285
Ala Gly Phe Phe Pro Met Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Phe Glu Glu Phe Pro His Gly
305 310 315 320
Phe Thr Ala Ser Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
370 375 380
Lys Asp Lys Ala Ser Lys Thr Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
405 410 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
420 425 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
435 440 445
Phe Ala Glu Val Ala
450

<210> 197
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 197
atgaacaaac cgcagatctg ggaagcgcgt gcggaaacct atagcctgta tggctttacc 60
gatatgccga gcctgcatca gcgtggcacc gtggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgaacggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttttgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360

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aacgatacca tggtgaaaat gctgtggttt ctgcatgcgg cggaaggcaa accgcagaaa 420
cgtaaaattc tgacccgttg gaacgcgtat catggcgtga ccgcggtgag cgcgagcatg 480
accggcaaac cgtataacag cgtgtttggc ctgccgctgc cgggctttgt gcatctgacc 540
tgcccgcatt attggcgtta tggcgaagaa ggcgaaaccg aagaacagtt tgtggcgcgt 600
ctggcccgtg aactggaaga aaccattcag cgtgaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattccgc cggcgaaagg ctattttcag 720
gcgattctgc cgatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggcc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gcaaaaacct gaccgcgggt ttttttccga tgggcgcggt gattctgggt 900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tccgcatggt 960
tttaccgcga gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gcattggctt tatgtgggcg 1140
ctggaagcgg tgaaagataa agcgagcaaa accccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggcctgattt gccgtccgct gggccagagc 1260
gtggttctgt gcccgccgtt tattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                    1362


<210> 198
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> variant of transaminase from V. fluvialis

<400> 198
Met Asn Lys Pro Gln Ile Trp Glu Ala Arg Ala Glu Thr Tyr Ser Leu
1               5                  10                  15
Tyr Gly Phe Thr Asp Met Pro Ser Leu His Gln Arg Gly Thr Val Val
            20                  25                  30
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val Asn Gly Arg Arg
        35                  40                  45
Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
    50                  55                  60
His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
65                  70                  75                  80
Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
                85                  90                  95
Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
            100                 105                 110
Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
        115                 120                 125
Trp Phe Leu His Ala Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
    130                 135                 140
Thr Arg Trp Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145                 150                 155                 160
Thr Gly Lys Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
                165                 170                 175
Val His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
            180                 185                 190
Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
        195                 200                 205
Ile Gln Arg Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
    210                 215                 220
Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
225                 230                 235                 240
Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
                245                 250                 255
Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
            260                 265                 270
Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
        275                 280                 285
Ala Gly Phe Phe Pro Met Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
    290                 295                 300
Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Pro His Gly
305                 310                 315                 320
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Phe Thr Ala Ser Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
                325                 330                 335
Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
            340                 345                 350
Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
        355                 360                 365
Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Ala Val
    370                 375                 380
Lys Asp Lys Ala Ser Lys Thr Pro Phe Asp Gly Asn Leu Ser Val Ser
385                 390                 395                 400
Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
                405                 410                 415
Leu Gly Gln Ser Val Val Leu Cys Pro Pro Phe Ile Leu Thr Glu Ala
            420                 425                 430
Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val
        435                 440                 445
Phe Ala Glu Val Ala
    450
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