

CX2-105USP1-ST25
SEQUENCE LISTING

<110> Codexis, Inc.
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SMITH, Derek
CROWE, Michael
COLLIER, Steven

<120> BIOCATALYSTS AND METHODS FOR SYNTHESIZING DERIVATIVES OF
TRYPTAMINE AND TRYPTAMINE ANALOGS

<130> CX2-105USP1

<160> 154

<170> Patentin version 3.5

<210> 1
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimized transaminase gene from Vibrio fluvialis

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<213> *Vibrio fluvialis*

<400> 2

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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
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Gly Tyr His Ala Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
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Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
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Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
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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 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

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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
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 <213> Artificial Sequence

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

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25
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Val Thr His Gly Gln Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
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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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Phe 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
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<211> 453

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<213> Artificial Sequence

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<223> Engineered variant of V. fluvialis transaminase

<400> 6

Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
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Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
385 390 395 400

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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 Ala Pro Pro Tyr Ile Leu Thr Glu Ala
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Phe Ala Glu Val Ala
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<213> Artificial Sequence

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<223> Engineered variant of V. fluvialis transaminase

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<210> 8

<211> 453

<212> PRT

<213> Artificial sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 8

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Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Ile 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
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210

215

Val Met Gly Ala Gly Gly Val Ile Thr Pro Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr Ile Leu Thr Glu Ala
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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> 9
<211> 1362
<212> DNA
<213> Artificial Sequence

<220> Engineered variant of V. fluvialis transaminase

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<211> 453

<212> PRT

<213> Artificial Sequence

<220> Engineered variant of V. fluvialis transaminase

<400> 10

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met Val
20 25 30

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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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
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 Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
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 Thr Gly Arg Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
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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 Thr Pro Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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

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Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Asp His Gly
 305 310 315 320

Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr Ile Leu Thr Glu Ala
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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
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<210> 11
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 <212> DNA
 <213> Artificial Sequence

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

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

<220>
<223> Engineered variant of V. fluvialis transaminase
<400> 12

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Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Asp 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Phe 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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
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 Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
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 Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Asp His Gly
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 Phe Thr Thr 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
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 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 Val 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 Ala Pro Pro Tyr Ile Leu Thr Glu Ala
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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> 13

<211> 1362

<212> DNA

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 13

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<210> 14
<211> 453
<212> PRT
<213> Artificial Sequence

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

<400> 14

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Val 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 Thr Pro Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr 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> 15
<211> 1362
<212> DNA

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

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120

atcgttgatg tgcattgccc tcgttatctg gatgcgaaca gcggccctgtg gaaacatgtg

180

gcgggcttgg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgtttccg

240

ggctatcatg cgtttacgg cctgatgagc gatcagaccg tgatgctgtc tgaaaaaactg

300

gtggaagtga gccctgttga tagcggccgt gtgtttctga ccaacagcgg cagcgaaagg

360

aacgatacca tgttgaaaat gctgtgtttt cgtcatctgt cggaaaggcaa accgcagaaa

420

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540

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600

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660

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720

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780

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840

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900

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960

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1020

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1080

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1140

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1362

<210> 16

<211> 453

<212> PR1

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 16

Met Asn Lys Pro Gln Ser Trp Gln Thr Arg Ala Gln Thr Val Ser Leu

10

15

Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Thr Met Val

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 Leu 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

Leu Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125

Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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

Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Asp His Gly
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Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr 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> 17
<211> 1362
<212> DNA
<213> Artificial Sequence

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

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cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480

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<210> 18
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Engineered variant of V. fluvialis transaminase
 <400> 18

Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Val Ser Leu
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Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met 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

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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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Val Val
 370 375 380

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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 Ala Pro Pro Tyr 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> Engineered variant of V. fluvialis transaminase

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

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

<400> 20

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 1 5 10 15

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met Val
 20 25 30

Thr 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 Leu 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

Leu Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
 115 120 125

Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Leu 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
 Page 26

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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
 305 310 315 320

Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr Ile Leu Thr Glu Ala
 420 425 430

Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Glu
 435 440 445

Phe Ala Glu Val Ala
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<210> 21

<211> 1362
<212> DNA

<213> Artificial Sequence

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

<400> 21

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120
atcgtgatg tgcattgccg tcgttatctg gatgcgaaca gcggccctgtg gaaacatgtg
180
gagggttctg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgtttccg
240
ggctatcatg cgtttacgg cgcattgagc gatcagaccg tgaatgctgtc tgaaaaactg
300
gtggaagtga gccgtttga tagcggccgt gtgtttctga ccaacagcgg cagcggaagcg
360
aacgatacca tggtaaaaat gctgtggttt ctgcacgtg cggaaaggca accgcagaaa
420
cgtaaaatc tgaccctgaa gcaggcgtat catggtcca ccgctgtgag cgcgagcatg
480
accggcatcc cgtataacag cgtgtttgc ctgcgcctgc cggctttct gcatctgacc
540
tgcccgcat attgcgta tggcgaaaga ggcgaaccg aagaacagt tgtcgcgcgt
600
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660
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720
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780
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840
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900
ccggaactga gcaaacgtc ggaaccgcg attgaagcga tcgaagaatt tgcattagt
960
tttaccacag gcggccatcc ggtgggtgt gctattgcgc tgaagcgat tgaatgtgtg
1020
atgaacgaag gcttggccga aacgtgcgt cgtctggccc cgcgttttga aagaactgt
1080
aaacatatg cggaaacgtc gaacatggc gaatatctgt gtattgacct tatgtggcg
1140
ctggaagtgt tgaagataa agcgagcaaa gcccggttg atgcacaact gagcgtgagc
1200
gaaacttat cgaacacctg caccgatctg ggaactgtt gccgaccgtt ggccagagc
1260
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1320
ctggaaaaag cgtggataa agtgtttgcg gaagtgcgt aa
1362

<210> 22

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 22

1
Met Asn Lys Pro Gln Ser Trp Gln Thr Arg Ala Gln Thr Val Ser Leu
10
15

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Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met 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 Ala 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
 Leu Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
 115 120 125
 Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Gln Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Ile 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 Ser 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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

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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 Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr 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> 23
<211> 1362
<212> DNA
<213> Artificial Sequence

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

<400> 23
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atcgtggatg tgcattggcg tcgttatctg gatgcgaaca gcggcctgtt caacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg cctgatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttctga ccaacagcgg cagcgaagcg 360
aacgatacca tgggtgaaaat gctgtggttt ctgcatcgtg cggaaggcaa accgcagaaa 420

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accggcatcc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatc attggcggtt tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggccccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggatgatggg tgcgggcggt gttattaccc cgccaaaagg ctattttcag 720
gcgattctga ccatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
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aaacatattg cggaactgcc gaacattggc gaatatcgtg gtattggctt tatgtgggag 1140
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gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260
gtggttctgg caccgccgta cattctgacc gaagcgaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agagtgtgag gaagtggcgt aa 1362

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

<220>
<223> Engineered variant of V. fluvialis transaminase
<400> 24

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Leu 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

Leu Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125

Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Gln Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val Val

370

375

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 Ala Pro Pro Tyr Ile Leu Thr Glu Ala
420 425 430

Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Glu
435 440 445

Phe Ala Glu Val Ala
450

<210> 25
<211> 1362
<212> DNA
<213> Artificial Sequence

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

<400> 25
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atcgtggatg tgcattggccg 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 tgggtgaaaat gctgtggttt ctgcatcgtg cggaaggcaa accgcagaaa 420
cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
accggccttc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcattctgacc 540
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ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cgggtgatggg tgcgggcggt gttattacc cgcctaaaagg ctattttcag 720
gcgattctga ccattcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggtc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccag taggagcggg gattttgggg 900
ccggaactga gcaaactct ggaaaccgcg attgaagcga tcgaagaatt tgatcatggt 960
tttaccacag gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080

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aaacatatattg cggaacgtcc gaacattggc gaatatcgtg gtattggcctt tatgtgggctg 1140
ctggaagtgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260
gtggttcttg caccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 26
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered variant of V. fluvialis transaminase
<400> 26

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu 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 Thr Pro Pro Lys Gly Tyr Phe Gln
 225 230 235
 Ala Ile Leu Thr 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 Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr 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> Engineered variant of V. fluvialis transaminase

<400> 27

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120 atcgttgatg tgcattggccg tgcattatcg gatgcgaaca gcggccttgg gaacatgttg

180 gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttcgg

240 ggctatacg cgtttacgg cgcctagagc gatcagaccg tgaatgctgc tgaaaaaatg

300 gtggaagtga gcccgtrtga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg

360 aacgatacca tgttgaaaat gctgtgttt ctcgcatcgtg cggaaaggcaa accgcagaaa

420 cgtaaaaatc tgaccctgaa gcaggcgtat catgctcca cgcggttga cgcgagcatg

480 accggcatcc cgtataacag cgtgtttggc ctgcgcctgc cggctttct gcatctgacc

540 tgcgccgatc attgcgta tggcgaagaa ggcgaaccg aagaacagtt tgtcgcgcgt

600 ctggcccggt aactggaaga aaccttcag aaggaaaggc cgtataccat tgcgggcttt

660 ttgcgggaac cgtgtatggg tgcgggcgt gtattacc cgcgaagg ctattttcag

720 gcatcttga ccatcctcg caaatatgat attccggtga tcagcagatga agtgatttc

780 ggctttgttc gtaccggcaa cacttgggc tgcgtgacct atgattttac cccgagtcg

840 atattagca gtaaaaaact aaccgcgggt ttttttcag taggaagcgt gattttgggg

900 ccggaactga gcaaacgtct ggaaccgcg attgaagcga tcgaagaaat tgatcatgtg

960 tttaaccag gcggccatcc ggtgggtgt gcgattgcgc tgaagcgat tgatgtgtg

1020 atgaacgaag gcttgccga aacgtgcgt gctctggccc cgcgttttga agaacgtctg

1080 aaacatattg cggaaacgtcc gaacatggc gaatatcgtg gtattggcct tatgtggcgg

1140 ctggaagtgg tgaagataa agcgaagcaa gcccggtttg atggcaacct gagcgtgagc

1200 gaaagtatt cgaacacctg caccgatctg ggaatgatt gccgaccgtt ggcccaagc

1260 gtgttcttg caccgcgtga catctgacc gaagcgcaga tggatgaaat gttcgataaa

1320 ctggaaaaag cgtggataa agtgtttcg gaagtggcgt aa

1362

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1 5 10 15
 Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met 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 Ala 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Gln Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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
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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 Asp His Gly
 305 310 315 320

Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr 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> 29

<211> 1362

<212> DNA

<213> Artificial Sequence

<220>

<223> Engineered variant of *V. fluvialis* transaminase

<400> 29

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atcgtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180

gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240

ggctatcatg cgttttacgg cctgatgagc gatcagaccg tgatgctgtc tgaaaaactg 300

gtggaagtga gcccgtttga tagcggccgt gtgtttgtga ccaacagcgg cagcgaagcg 360

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 accggccttc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcattctgacc 540
 tgcccgcatt attggcgta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
 ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
 tttgcggaac cggatgatggg tgcgggagggt gttattaccc cgccaaaagg ctattttcag 720
 gcgattctga ccatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
 ggctttggtc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
 attattagca gtaaaaacct aaccgcgggt ttttttccag taggagcggg gattttgggg 900
 ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tgatcatggt 960
 tttaccacag gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
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 aaacatattg cggaacgtcc gaacattggc gaatatcgtg gtattggctt tatgtgggcg 1140
 ctggaagtgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
 gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260
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 ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 30

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 30

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

Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met 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 Leu 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

Val Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125

Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
305 310 315 320

Phe Thr Thr 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

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Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Val 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 Ala Pro Pro Tyr 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> Engineered variant of V. fluvialis transaminase

<400> 31
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tttaccacag gcggccatcc ggtgggttgt gcgattgctc tgaaagcgat tgatgtggtg 1020

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 ctggaagtgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
 gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260
 gtggttctgg caccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
 ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

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

<220>
 <223> Engineered variant of V. fluvialis transaminase
 <400> 32

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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

Val Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
 115 120 125

Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Gln Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Leu 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
 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr Ile Leu Thr Glu Ala
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 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

<210> 33
<211> 1362
<212> DNA
<213> Artificial Sequence
<220>
<223> Engineered variant of V. fluvialis transaminase
<400> 33

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120
atcgtgatg tgcattgcg tcttatctg gatgcgaaca gcggccgtt caacatgtg
180
gcgggcttg atcataaagg cctgattgat gcggcgaagg cgcagtatga acgtttccg
240
ggctatcatg cgtttacgg cgtatgagc gatcagaccg tgaatgctgc tgaaaaactg
300
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360
aacgatatac tgtgtgaaat gctgtgttt ctcacatcgt cgaagcga accgcaga
420
cgtaaaatc tgaccctga gcaaggcgtat catgctcca ccgcggtgag cgcgaagcatg
480
accggcatcc cgtataacag cgtgtttgac ctcgcgcctgc cgggctttct gcattcgacc
540
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600
ctggcccggt aactggaaga aaccattcag aaggaagcgc cggataccat tgcgggcttt
660
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720
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780
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840
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900
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960
tttaccacag gcggccatcc ggtgtgtgt gcgattgcgc tgaagcgtat tgatgtgtg
1020
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1080
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1140
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1200
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1260
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1362

<210> 34
<211> 453
<212> PRT
<213> Artificial Sequence
<220>
<223> Engineered variant of V. fluvialis transaminase
<400> 34

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

Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Gln Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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
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 Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr 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> Engineered variant of V. fluvialis transaminase

<400> 35

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atcgtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180

gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240

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tgcccgcatc attggcggtt tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
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gcatctctga ccacctcgtc caaatatgat attccggtga tcagcgatga agtgatttgc 780
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gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260
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ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 36
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered variant of V. fluvialis transaminase
<400> 36

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

Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met 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
Page 47

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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
305 310 315 320

Phe Thr Thr 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
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355

360

365

Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Val 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 Ala Pro Pro Tyr 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> 37
 <211> 1362
 <212> DNA
 <213> Artificial Sequence

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

<400> 37
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 cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
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 ctggccccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
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 ggcttttggtc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
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 ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tgatcatggt 960

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

<220>
<223> Engineered variant of V. fluvialis transaminase
<400> 38

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

Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met 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

Leu Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125

Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu 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 Thr Pro Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr 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

39 <210>

1362

DNA

Artificial Sequence

 $\langle 220 \rangle$

<223>

Engineered variant of V. fuvialis transaminase

39 <400>

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1320	gtgtgttcgc	caccgcgcta	catttcgacc	ggaagcgaga	tgatgaaat
1260	gaaagtattg	cgaaacacctg	caccgatctg	ggaactgattt	gcccgaacctt
1200	ctggaagtgg	tgaagaataa	agcgagcaaa	gccccgtttg	atgccaacct
1140	aaacatatatg	cggaacgtcc	gaaacattgbc	gaaatatcgtg	gtattggcctt
1080	atgaaacgaag	gacctgcccga	aaaagtcgct	cgctcgtcccc	cgcggtttga
1020	tttaaccag	gcgcccatcc	ggttggttgt	gcgattgcgc	tgaagcgat
960	cggaaactga	gcaaacgtct	ggaaacccgc	attgaagcga	tcgaagaaat
900	attattagca	gtaaaaacct	aaccgcgggt	ttttttccag	tagagcggt
840	ggtcttggtc	gtaccgcgaa	cacctgggbc	tgcgtgacct	atgattttac
780	gcatctctga	ccatctctgc	caaatatgat	attccggtga	tcagcgatga
720	tttgcggaac	cggtgatggg	tgcggcggt	gtatttcccc	cgccaagaag
660	ctggccccgc	aactggaaga	aaccattcag	aaggaagcgc	cgatatccat
600	tgcgccgatt	attgcggtta	tggcggaagaa	ggcggaaccg	aagaaacgtt
540	accgcatcc	cgataaacag	cggtgttgc	ctgcgcctgc	cggtctttct
480	cgtaaatcc	tgaacctga	gaaagcgtaa	catgctcca	ccgcggtgag
420	aacgatacca	tgttgaaaaat	gctgtgtttt	ctgcatactg	cggaagcca
360	gtggaagtga	gccccgttga	tagcgccggt	gtgttttata	ccaacagcgg
300	ggctatcatg	cgttttacgg	ccgtatgagc	gatcagaccg	tgatgctgtc
240	gcggtctttg	atcataaagg	cctgattgat	gcggcgaaag	cgcatatga
180	atcgttgatg	tgcattgcgc	tctttatactg	gatgcgaaaca	gcggtccctg
120	cacatgcgga	gcctacgtca	gcgtgcccac	atgtgtgtga	cccatggcga
60	atgaaacaaa	cgacagctg	ggaaacgcgt	gcggaaacgc	tgaagcctga

<210> 40

453

PRT

Art

Artificial Sequence

<220>

<223>

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<400> 40

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

Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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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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 Asp His Gly
 305 310 315 320

Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr 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> 41
 <211> 1362
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Engineered variant of v. fluvialis transaminase

<400> 41
 atgaacaaac cgcagagctg ggaaacgcgt gcggaaaccg tgagcctgta tgcctttacc 60
 cacatgccga gcctacgtca gcgtggcacc atggtggtga cccatggcga aggcccgtat 120
 atcgtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgtt caacatggtg 180
 gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240

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ggctatcatg cgttttacgg cctgatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
 gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
 aacgatacca tggtgaaaat gctgtggttt ctgcatcgtg cggaaggcaa accgcagaaa 420
 cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
 accggcatcc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcattctgacc 540
 tgcccgcatc attggcggtt tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
 ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
 tttgcggaac cggtgatggg tgcgggcggt gttattacc cgcctaaaagg ctattttcag 720
 gcgattctga ccatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
 ggctttggtc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
 attattagca gtaaaaaacct aaccgcgggt ttttttccag taggagcggg gattttgggg 900
 ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tgatcatggt 960
 tttaccacag gcggccatcc ggtgggttgt gcgattgctc tgaaagcgat tgatgtggtg 1020
 atgaacgaag gcctggccga aaacgtgctg cgtctggccc cgcgttttga agaacgtctg 1080
 aaacatattg cggaacgtcc gaacattggc gaatatcgtg gtattggctt tatgtgggcg 1140
 ctggaagtgg tgaaagataa agcgagcaaa gcccgtttg atggcaacct gagcgtgagc 1200
 gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260
 gtggttcttg caccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
 ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

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

<220>
 <223> Engineered variant of V. fluvialis transaminase
 <400> 42

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

Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met 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

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Gly Tyr His Ala Phe Tyr Gly Leu 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
305 310 315 320

Phe Thr Thr 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

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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 Val 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 Ala Pro Pro Tyr 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> Engineered variant of V. fluvialis transaminase

<400> 43
atgaacaaac cgcagagctg ggaaacgcgt gcggaaaccg tgagcctgta tgcctttacc 60
cacatgccga gcctacgtca gcgtggcacc atggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgtttttccg 240
ggctatcatg cgtttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgtttgtga ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgcatcgtg cggaaggcaa accgcagaaa 420
cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
accggcatcc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatc attggcggtt tggcgaagaa ggcgaaaccg aagaacagtt tgcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattacc cgcctaaaagg ctattttcag 720
gcgattctga ccatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggcttttggtc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccag taggagcggg gattttgggg 900

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ccggaactga gcaaactgtct ggaaaccgcg attgaagcga tcgaagaatt tgatcatggt 960
 tttaccacag gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
 atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaactgtctg 1080
 aaacatattg cggaactgcc gaacattggc gaatatcgtg gtattggctt tatgtgggcg 1140
 ctggaagtgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
 gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260
 gtggttctgg caccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
 ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 44

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 44

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

Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met 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

Val Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
 115 120 125

Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Ile Pro Tyr Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
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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 Thr Pro Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr Ile Leu Thr Glu Ala
 420 425 430
 Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Val

<210> 45
<211> 1362
<212> DNA
<213> Artificial Sequence

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

<400> 45
atgaacaac ccagagctg ggaacgcgt gcggaaccc tgaacctga tgccttaac
cacatgccga gccatagtca gcgtggcacc atgttgttaa cccatggcga aggcccgat
atcgttgatg tgcattggccg tcgttatctg gatgcgaaca gccgcctgtt caacatgtg
gcgggccttg atcataagg cctgattgat gcggcgaaag cgcagtatga acgtttccg
ggctatcatg cgtttacgg cctgattgagc gatcagaacc tgatgctgtc tgaaaaaatg
gtggaagtga gcccggttga tagcggccgt gtgtttctga ccaacagcg cagcgaagcg
aagatatcca tggttgaaat gctgtgttt ctcgactctg cggagggcaa accgcagaaa
cgtaaaaatc tgaccctgaa gcaggcgtat catggtcca ccgcggtgag cgcgagcatg
accggcatcc cgtataacag cgtgtttgac ctgccgctgc cgggccttct gcatctgacc
tgcgcccat attgcgctta tggcgaagaa gcggaaccc aagaacagt tgtcgcgcgt
ctggcccggt aactggaaag aaccattcag aaggaaagcg cggataccat tgcgggcttt
tttgcggaac cgtgtatggg tgcgggcggt gtatttaacc cggcaaaaag ctattttcag
gcgattctga ccatcttcgc caatatgat attccggtga tcagcgatga agtgattgc
ggccttggc gtaaccggcaa caccctgggc tgcgtgacct atgattttac cccggaatgcg
attatagca gtaaaaaacc aaccgcgggt ttttttccag tagagcggt gattttggg
ccgaactga gcaaacgctt ggaacccgcg attgaagcga tcgaagaaat tgatcatgtg
tttaaccacag gcggccatcc ggtgggtgt gctgttcgc tgaagcgat tgatgtgtg
atgaacgaag gccctggccga aaacgtgcgt cgtctggccc cgcgttttga aagaacgtctg
aaacatatg cggaacgctc gaacatggc gaatatctg gtattgacct tatgtggcg
aaacatatg cggaacgctc gaacatggc gaatatctg gtattgacct tatgtggcg
ctggaagtga tgaagatga agcgaagcaaa gccccggttg atgcacaacc gagcgtgagc
gaaacttatg cgaacacctg caccgactg ggactgatt gccgaaccgt ggccagagc
gtgttcttg caccgctga catctgacc gaagcgcaga tggatgaaat gttcgataa
ctggaaaaag cgtggatga agtgtttcg gaagtgcgt aa

<210> 46
<211> 453
<212> PRT
<213> Artificial Sequence

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<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 46

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

Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met 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 Leu 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

Leu Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125

Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Gln Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr 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> Engineered variant of *V. fluvialis* transaminase

<400> 47
atgaacaaac cgagagctg ggaaacgcgt gcggaaaccg tgagcctgta tgcctttacc 60
cacatgccga gcctacatca gcgtggcacc atggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgtt caacatggtg 180

gagggtttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttcg
ggctacatg cgtttacgg cctgattgag gatcagaccg tgattgctgtc tgaaaaaactg
gtggaagtga gccgtttga tagcggcgt gtgttttata ccaacagcgg cagcgaagcg
aagatacca tggtaaaaat gctgtgttt ctcgattcgt cggaaaggcaa accgcagaaa
cgtaaaaatc tgaacctgaa gcaggcgtat catggtctca ccggcgttag ccgagcatg
accggcatcc cgtataacaa cgtgtttgc ctgccgctgc cgggtttct gcatctgacc
tgcccgcat attggcgtta tggcgaagaa ggcgaaacg aagaacagt tgtcgcgcgt
ctggcccggt aactggaaga aacatcag aaggaaggcg cgtataccat tgcgggctt
tttcgggaac cgttgatggg gtatataccc cgcgaaaagg ctattttcag
ggattctga ccatcctgcg caaatatgat attccggtga tcagcgtatga agtgatttgc
ggctttgtc gtaccggcaa cactgggc tgcttgacct atgatttac ccggatgcg
atatatga gtaaaaaact aaccgcgggt tttttccag taggagcgt gattttggg
ccggaactga gcaaacgtct ggaaccgcg atgaagcga tcgaagaaat tgatcatgt
tttaccag gcggccatcc ggtgggtgt gcgattgcgc tgaagcgat tgatgtgtg
atgaacgaag gcttgccga aacgtgcgt gctctggccc cgcgtttga agaactctg
aaacatatg cggaaactcc gaacatggc gaatatcgt gtattgctt tatgtggcg
ctggaagtg tgaagataa agcgaagcaa gcccggttg atgcaacct gagcgtgagc
gaactatg cgaacacctg caccgatctg ggaactgatt gccgaaccgt ggccagagc
gtgttcttg caccgccta catctgacc gaagcgcaga tggatgaaat gttcgataa
ctgaaaaag cgttgataa agtttgcg aa

<210> 48
<211> 453
<212> PRT
<213> Artificial Sequence
<220>
<223> Engineered variant of V. fluvialis transaminase
<400> 48

Met Asn Lys Pro Gln Ser Trp Gln Thr Arg Ala Gln Thr Val Ser Leu
1
5
10
15

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met Val
20
25
30
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 Lys Ala Gln Tyr Gln Arg Phe Pro
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65

70

75

80

Gly Tyr His Ala Phe Tyr Gly Leu 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Gln Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
305 310 315 320

Phe Thr Thr 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
Page 64

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 Val 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 Ala Pro Pro Tyr 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> 49

<211> 1362

<212> DNA

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 49

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accggccttc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc	540
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ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt	660
tttgcggaac cggatgatggg tgcgggagggt gttattaccc cgccaaaagg ctattttcag	720
gcgattctga ccatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc	780
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ccggaactga gcaaactgtct ggaaaccgcg attgaagcga tcgaagaatt tgatcatggt	960
tttaccacag gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg	1020
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aaacatattg cggaacgtcc gaacattggc gaatatcgtg gtattggctt tatgtgggcg	1140
ctggaagtgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc	1200
gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc	1260
gtgggttctg caccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa	1320
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<210> 50

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 50

Met	Asn	Lys	Pro	Gln	Ser	Trp	Glu	Thr	Arg	Ala	Glu	Thr	Val	Ser	Leu
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Tyr	Ala	Phe	Thr	His	Met	Pro	Ser	Leu	Arg	Gln	Arg	Gly	Thr	Met	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	Leu	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		

Val	Thr	Asn	Ser	Gly	Ser	Glu	Ala	Asn	Asp	Thr	Met	Val	Lys	Met	Leu
		115					120					125			

Trp	Phe	Leu	His	Arg	Ala	Glu	Gly	Lys	Pro	Gln	Lys	Arg	Lys	Ile	Leu
	130					135					140				

Thr	Leu	Lys	Arg	Ala	Tyr	His	Gly	Ser	Thr	Ala	Val	Ser	Ala	Ser	Met
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Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr Ile Leu Thr Glu Ala
 420 425 430

CX2-105USPL-ST25
Gln Met Asp Gln Met Phe Asp Lys Leu Gln Lys Ala Leu Asp Lys Val
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Phe Ala Gln Val Ala
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<210> 51
<211> 1362
<212> DNA
<213> Artificial Sequence
<220>
<223> Engineered variant of V. fluvialis transaminase
<400> 51

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240 ggctatcatg cgtttacgg cgcattgagc gatcagaccg tgaatgctgtc tgaaaaaatg
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360 aacgatacca tgtgtgaaat gctgtgtttt ctgcattctg cggaaaggcaa accgcagaaa
420 cgtaaaaatc tgaacccgaa gaacgcgtat catgctcca ccgcggtgag cgcgagcatg
480 accggcatcc cgtataacag cgtgtttggc ctgcgcctgc cggccttct gcatctgacc
540 tgcgcccat attgcgtaa tggcgaaaga ggcgaacccg aagaacagtt tgtcgcgcgt
600 ctggcccggt aactggaaga aaccatcag aaggaaaggc cgcataccat tgcgggcttt
660 ttgcccgaac cgtgatggg tgcgggcggt gtatatcccc cgcgaaaaagg ctattttcag
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1080 aaacatatg cggaaacgtcc gaacatggc gaatatctg gtattggctt tatgtgggcg
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1260 gtgttcttg caccgcctga catctgacc gaagcgccaga tggatgaaat gttcgataaa
1320 ctggaaaaaa gcctggatga agtgtttgcg gaagtggcgt aa
1362

<210> 52
<211> 453
<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 52

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Ala 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

Val Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
 115 120 125

Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240

Ala Ile Leu Thr Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
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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 Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr 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> 53
<211> 1362
<212> DNA
<213> Artificial Sequence

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

<400> 53
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 420
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<210> 54
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Engineered variant of V. fluvialis transaminase
 <400> 54

Met Asn Lys Pro Gln Ser Trp Gln Thr Arg Ala Gln Thr Val Ser Leu
 1
 Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met Val
 20
 Val Thr His Gly Gln Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
 35
 Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp
 50
 55
 60

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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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr Ile Leu Arg Lys Tyr Ala 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 Asp His Gly
 305 310 315 320
 Phe Thr Thr Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
 325 330 335

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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 Val 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 Ala Pro Pro Tyr 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> 55
<211> 1362
<212> DNA
<213> Artificial Sequence

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

<400> 55
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tttgcggaac cggatgatggg tgcgggcggt gttattacc cgcctaaaagg ctattttcag 720
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CX2-105USP1_ST25

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ctggaaaaag cgctggataa agtgtttgcm gaagtggcmg aa	1362

<210> 56

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 56

Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Val Ser Leu	
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Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met 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 Leu 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	

Leu Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu	
115 120 125	

Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu	
130 135 140	

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met	
---	--

145 150 155 160
 Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Asp His Gly
 305 310 315 320
 Phe Thr Thr Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
 325 330 335
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 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 Val 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 Ala Pro Pro Tyr Ile Leu Thr Glu Ala
 420 425 430 435 440 445 450

Gln Met Asp Gln Met Phe Asp Lys Leu Gln Lys Ala Leu Asp Lys Val
435 440 445

Phe Ala Gln Val Ala
450

<210> 57

<211> 1362

<212> DNA

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 57

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120
atcgttgatg tgcattgccc tcttatctg gatgcgaaca gcggcctgtt caacatgtg
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540
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660
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720
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<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 58

Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Val Ser Leu
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Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Ala 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

Leu Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
 115 120 125

Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Leu 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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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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240

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Ala Ile Leu Thr Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
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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 Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr Ile Leu Thr Glu Ala
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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> 59
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
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<400> 59
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420 aacgatacca tgggtgaatat gctgtgtttt ctcgatctgtg cggaaaggcaa accgcagaaa
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<210> 60
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<400> 60

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Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gln Thr Met 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
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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 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

Leu Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125

Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Arg Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
305 310 315 320

Phe Thr Thr Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
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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 Val 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 Ala Pro Pro Tyr 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> 61

<211> 1362

<212> DNA

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 61

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accggcatcc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc	540
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<210> 62

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 62

Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Val Ser Leu
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Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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

Leu Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
 115 120 125

Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

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Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
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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 Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr Ile Leu Thr Gln Ala
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Gln Met Asp Gln Met Phe Asp Lys Leu Gln Lys Ala Leu Asp Lys Val
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Phe Ala Gln Val Ala
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<210> 63
<211> 1362
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<220>
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CX2-105USP1_ST25

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

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

<400> 64

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Leu 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Ile Pro Tyr Asn Ser Val Phe Gly Leu Pro Ala 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 Pro Lys Gly Tyr Phe Gln
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<210> 66
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<212> PRT
<213> Artificial Sequence
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<223> Engineered variant of V. fluvialis transaminase
<400> 66

Met Asn Lys Pro Gln Ser Trp Gln Thr Arg Ala Gln Thr Tyr Ser Leu
1
Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met Val
20
Thr Thr His Gly Gln Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35
40
45

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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 Leu 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Phe Pro Tyr Asn Ser Val Phe Gly Leu Pro Ala 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
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 Val Met Gly Ala Gly Gly Val Ile Thr Pro Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
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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 Ala 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 Asp His Gly
 305 310 315 320

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Phe Thr Thr 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 Gly
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 Ala Pro Pro Tyr 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> 67
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<213> Artificial Sequence

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<223> Engineered variant of V. fluvialis transaminase

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ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660

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ggctttggtc	gtaccggcaa	cacctggggc	tgcgtgacct	atgattttac	cccggatgcg	840
attattagca	gtaaaaacct	aaccgcgggt	ttttttccag	taggagcggt	gattttgggg	900
ccggaactga	gcaaacgtct	ggaaaccgcg	attgaagcga	tcgaagaatt	tgatcatggt	960
tttaccacac	acggccatcc	ggtgggttgt	gcgattgcg	tgaaagcgat	tgatgtggtg	1020
atgaacgaag	gcctggccga	aaacgtgctg	cgtctggccc	cgcgttttga	agaacgtctg	1080
aaacatattg	cggaacgtcc	gaacattggc	gaatatcgtg	gtattggctt	tatgtgggcg	1140
ctggaagtgg	tgaaagataa	agcgagcaaa	gccccgtttg	atggcaacct	gagcgtgggt	1200
gaacgtattg	cgaacacctg	caccgatctg	ggactgattt	gccgaccgtt	gggccagagc	1260
gtggttctgg	caccgccgta	cattctgacc	gaagcgcaga	tggatgaaat	gttcgataaa	1320
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<210> 68
<211> 453
<212> PRT
<213> Artificial Sequence
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<220>
<223> Engineered variant of V. fluvialis transaminase
<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 Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Asp 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
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130

135

140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Phe 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
 305 310 315 320

Phe Thr Thr His 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 Val Val
 370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Gly
 385 390 395 400

Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
 Page 91

Leu Gly Gln Ser Val Val Leu Ala Pro Pro Tyr 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> Engineered variant of V. fluvialis transaminase

<400> 69
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atcgtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcggggctttg atcataaaagg cctgattgat gcggcgaaaag cgcagtatga acgttttccg 240
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aacgatacca tgggtgaaaat gctgtggttt ctgcatcgtg cggaaggcaa accgcagaaa 420
cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
accggctttc cgtataacag caagtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcggtt tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggatgatgg tgcgggcggt gttattacc cgcctaaaagg ctattttcag 720
gcgattctga ccatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
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gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260
gtggttcttg caccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320

ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa

1362

<210> 70

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 70

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

Ala Ile Leu Thr 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 Ala 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 Asp His Gly
305 310 315 320

Phe Thr Thr His 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 Gly
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 Ala Pro Pro Tyr 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> 71

<211> 1362

<212> DNA

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

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atcgtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg      180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg      240
ggctatcatg cgtttgatgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg      300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg      360
aacgatacca tggtgaaaat gctgtggttt ctgcatcgtg cggaaggcaa accgcagaaa      420
cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg      480
accggctttc cgtataacag cgtgtttggc ctgccggctc cgggctttct gcattctgacc      540
tgcccgcatc attggcgcta tggcgaagaa ggcgaaaccg aagaacagtt tgcgcgcgt      600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt      660
tttgcggaac cggatgatggg tgcgggcggt gttattaccg cgccaaaagg ctattttcag      720
gcgattctga ccattcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc      780
ggctttggtc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg      840
attattagcg ccaaaaacct aaccgcgggt ttttttccag taggagcggg gattttgggg      900
ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tgatcatggt      960
tttaccacac acggccatcc ggtgggttgt gcgattgctc tgaaagcgat tgatgtggtg     1020
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aaacatattg cggaacgtcc gaacattggc gaatatcgtg gtattggctt tatgtgggcg     1140
ctggaagtgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc     1200
gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc     1260
gtggttcttg caccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa     1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa                          1362

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<210> 72
<211> 453
<212> PRT
<213> Artificial Sequence

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

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<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

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Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met Val
          20           25           30

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Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg

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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 Asp 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Phe Pro Tyr Asn Ser Val Phe Gly Leu Pro Ala 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Ala 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 Asp His Gly
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305 310 315 320

Phe Thr Thr His 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 Val 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 Ala Pro Pro Tyr 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>	73
<211>	1362
<212>	DNA
<213>	Artificial Sequence

<220>
<223> Engineered variant of *V. fluvialis* transaminase

<400>	73								
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atcgtggatg	tgcattggccg	tcgttatctg	gatgcgaaca	gcggcctgtg	gaacatgggtg				180
gcgggctttg	atcataaagg	cctgattgat	gcggcgaaag	cgcagtatga	acgttttccg				240
ggctatcatg	cgtttgatgg	ccgtatgagc	gatcagaccg	tgatgctgtc	tgaaaaactg				300
gtggaagtga	gcccgtttga	tagcggccgt	gtgttttata	ccaacagcgg	cagcgaagcg				360
aacgatacca	tggtgaaaat	gctgtggttt	ctgcatcgtg	cggaggcaa	accgcagaaa				420
cgtaaaattc	tgaccctgaa	gaacgcgtat	catggctcca	ccgcggtgag	cgcgagcatg				480
accggctttc	cgtataacag	cgtgtttggc	ctgccgctgc	cgggctttct	gcatctgacc				540
tgcccgcat	attggcggtta	tggcgaagaa	ggcgaaaccg	aagaacagtt	tgtcgcgcgt				600

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 gcgattctga ccatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
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 ccggaactga gcaaactgtc ggaaaccgcg attgaagcga tcgaagaatt tgatcatggt 960
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 gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260
 gtggttctgg caccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
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<210> 74

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 74

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Asp 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Phe 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Gly
 385 390 395 400

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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 Ala Pro Pro Tyr 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> 75
<211> 1362
<212> DNA
<213> Artificial Sequence

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

<400> 75
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gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttgatgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
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cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
accggctttc cgtataacag cgtgtttggc ctgccggctc cgggctttct gcattctgacc 540
tgcccgcatc attggcgcta tggcgaagaa ggcgaaaccg aagaacagtt tgcgcgcgt 600
ctggccccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggatgatggg tgcgggcggt gttattacc cgcctaaagg ctattttcag 720
gcgattctga ccatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggtc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
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tttaccacag gcggccatcc ggtgggttgt gcgattgctc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaactgtc 1080
aaacatattg cggaactgcc gaacattggc gaatatcgtg gtattggctt tatgtgggcg 1140
ctggaagtgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgggt 1200
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gtgggttctgg caccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320

ctggaaaaaag cgctggataa agagtttgcg gaagtggcgt aa 1362

<210> 76

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 76

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Asp 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Phe Pro Tyr Asn Ser Val Phe Gly Leu Pro Ala 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
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210

215

Val Met Gly Ala Gly Gly Val Ile Thr Pro Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Gly
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 Ala Pro Pro Tyr Ile Leu Thr Glu Ala
420 425 430

Gln Met Asp Glu Met Phe Asp Lys Leu Glu Lys Ala Leu Asp Lys Glu
435 440 445

Phe Ala Glu Val Ala
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<210> 77
<211> 1362
<212> DNA
<213> Artificial Sequence

<220> Engineered variant of V. fluvialis transaminase

<400> 77

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120 atcgttgatg tgcattgccg tgcattatcg gatgcgaaca gcggccctgtg gaacatgtg

180 gcgggcttg atcataaagg cctgattgat gcggcggaag cgcagtatga acgtttccg

240 ggctatcatg cgtttgatgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaaatg

300 gtggaagtga gccggttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg

360 aacgatacca tggtagaata gctgtgttt ctcgcatcgtg cggaaaggca accgcagaaga

420 cgtaaaaatc tgaccctgaa gaacgcgtat catggtcca cgcggttgag cgcgagcatg

480 accgcttcc cgtataacag cgtgtttgac ctcgcgctgc cggcttct gcatctgacc

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600 ctggcccttg aactggaaga aaccattcag aaggaaagcg cgtataccat tgcgggcttt

660 ttgtcggaac cgttgatggg tgcgggcgt gtattatccc cgcgaagaag ctattttcag

720 gcatcttga ccatcctgc caaatatgat atccggtga tcagcgtatga agtgatttgc

780 ggccttgtc gtaaccggca cactggggc tgcgtgacct atgattttac cccgagatcg

840 attatagcg ccaaaaaact aaccgcgggt ttttttcag tagagcgtt gattttgggg

900 ccggaactga gcaaacgtct ggaacccgc attgaagcga tcgaagaaat tgatcatgtg

960 tttaaccac accgccatcc ggtgggtgt gcgattgcgc tgaagcgat tgatgtgtg

1020 atgaacgaag gcttgccga aacgttgcgt cgtctggccc cgcgttttga agaacgtctg

1080 aaacatatg cggaaacgtcc gaacatggc gaatatcgtg gtatttgctt tatgtggcg

1140 ctggaagtgg tgaagataa agcgaagcaaa gcccggtttg atggcaacct gagcgttgggt

1200 gaacgtatg cgaacacctg caccgatctg ggaactgatt gccgaacctt ggccagaagc

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1362

<210> 78

<211> 453

<212> PRT

<213> Artificial sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 78

Met Asn Lys Pro Gln Ser Trp Gln Thr Arg Ala Gln Thr Tyr Ser Leu
1

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met Val
20

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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 Asp 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Phe 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Ala 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

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Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Asp His Gly
 305 310 315 320

Phe Thr Thr His 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 Val Val
 370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Gly
 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 Ala Pro Pro Tyr 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> Engineered variant of V. fluvialis transaminase

<400> 79
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 gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
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 gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
 aacgatacca tgggtgaaaat gctgtggttt ctgcatcgtg cggaaggcaa accgcagaaa 420
 cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
 accggctttc cgtataacag cgtgtttggc ctgccggctc cgggctttct gcatctgacc 540

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ggctttg	gtc	gtaccgg	caa	cacct	ggggc	tg	cg	tgac	ct	at	gatttt	tac	cccggat	840
attattag	cg	ccaaaa	ac	ct	aaccgc	gggt	tttttt	ccag	taggag	cggt	gatttt	gggg		900
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tttaccac	ac	acggcc	atcc	ggtggg	ttgt	gc	gattgc	gc	tg	aaag	cgat	tgat	gtggtg	1020
atgaacga	ag	gcctgg	ccga	aa	acgtgc	gt	cttg	gccc	cg	cg	tttt	ga	agaacgtctg	1080
aaacatatt	g	cggaac	gtcc	ga	acattgg	c	gaat	atcgtg	gtatt	ggctt	tat	gtggg	cg	1140
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gaacgtatt	g	cgaac	acctg	cacc	gatctg	gg	actgat	ttt	gcc	gacc	gct	ggg	ccagagc	1260
gtggttct	gg	caccg	ccgta	catt	ctgacc	ga	agcgc	aga	tggat	gaaat	gttc	gataaa		1320
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<210> 80

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 80

Met	Asn	Lys	Pro	Gln	Ser	Trp	Glu	Thr	Arg	Ala	Glu	Thr	Tyr	Ser	Leu
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Tyr	Ala	Phe	Thr	His	Met	Pro	Ser	Leu	His	Gln	Arg	Gly	Thr	Met	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	Asp	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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Phe Pro Tyr Asn Ser Val Phe Gly Leu Pro Ala 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240

Ala Ile Leu Thr 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 Ala 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 Asp His Gly
 305 310 315 320

Phe Thr Thr His 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 Val Val
 370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Gly
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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 Ala Pro Pro Tyr 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
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<220>
<223> Engineered variant of *V. fluvialis* transaminase

[illegible]

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gtggttcttg caccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gatgtggcgt aa 1362

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

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

<400> 82

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met Val
20 25 30

Val Thr His Gly Glu Gly Pro Tyr Leu Val Asp Val His Gly Arg Arg
35 40 45

Tyr Leu Asp Ala Asn Ser Gly Leu Tyr Asn Met Val Ala Gly Phe Asp
50 55 60

His Lys Gly Leu Ile Ala 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 Pro 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 Phe Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu 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 Thr Pro Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asn Glu Glu Phe Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Val 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 Ala Pro Pro Tyr 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 Asp Val Ala
450

<210> 83
<211> 1362
<212> DNA

<213> Artificial Sequence

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

<400> 83

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120

ctgtgtgatg tgcattgcaa ccgttatctg gatgcgaaca gcggcctga taacatgtg

180

gcgggcttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgtttccg

240

ggctatcatg cgttttacgg cgtatgagc gatcagaccg tcatgctgtc tgaaaaaatg

300

gtggaagtga gccggttga tagcggcgt gtttttata ccaacagcgg cagcgaagcg

360

aacgatacca tggtagaaat gctgtgttt ctcgcatcgt cggaaggcaa accgcagaaa

420

cgtaaaaatc tgaccctgaa gaacgcgtat catgctcca ccgctgtgag cgcgagcatg

480

accggccttc cgtataacag cgtgtttgac ctgcgcctgc cggcttct gcatctgacc

540

tgcgcgcatt attgcggtta tggcgaagaa ggcgaacacg aagaacagt tgtcgcgcgt

600

ctggcccttg aactggaaga aacattcag aaggaagcgg cgcataccat tgcggcctt

660

tttcgggaac cgtgtatggg tgcgggcgt gttattaccc cgcgaagg ctatttcag

720

gcgattctga ccatcctcgg caaatatgat attccggtga tcagcgtatga agtgattgc

780

ggctttgttc gtaccggcaa cactggggc tgcgtgacct atgatttac ccgcatgcg

840

attattagca gtaaaaaact aacgcgggt ttttttcag tagagcgtt gattttggg

900

ccggaactga gcaaacgctt ggaacccgc attgaagcga ttggggaatt tgatcatggt

960

tttaaccacag gcggccatcc ggtgggtgt gcgattgcgc tgaagcgcgt tgatgtgtg

1020

atgaacgaag gcttggccga aacgtgctgt cgtctggccc cgcgtttga agaacgtctg

1080

aaacatatg cggaaacgtc gaacattgac gaatatcgtg gtattgctt tatgtggcg

1140

ctggaagtgg tgaagatata agcagcaaa gcccgcttg atgtaacct ggtgtgagc

1200

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1260

gtgttatcg cgcgcgcgtt cattctgacc gaagcgcaga tggatgaaat gttcgataaa

1320

ctggaaaaaa gcctggatata agttttgcg gaagtgcgt aa

1362

<210> 84

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 84

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gln Thr Met Val
Page 111

Val Thr His Gly Glu Gly Pro Tyr Leu Val Asp Val His Gly Asn Arg
 35 40 45

Tyr Leu Asp Ala Asn Ser Gly Leu Tyr 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240

Ala Ile Leu Thr 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
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290

295

Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Gly Glu Phe Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Val 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 Ile Ala Pro Pro Tyr 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> 85
<211> 1362
<212> DNA
<213> Artificial Sequence

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

<400> 85
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cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480

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ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt	660
tttgcggaac cggatgatggg tgcgggagggt gttattaccc cgccaaaagg ctattttcag	720
gcgattctga ccatacctgcg caaatatgat attccgggtga tcagcgatga agtgatttgc	780
ggctttggtc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg	840
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ccggaactga gcaaacgtct ggaaaccgcg attgaagcga ttggggaatt tgatcatggt	960
tttaccacag gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg	1020
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gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc	1260
gtggttctgg cgccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa	1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa	1362

<210> 86

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 86

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

Tyr	Ala	Phe	Thr	His	Met	Pro	Ser	Leu	His	Gln	Arg	Gly	Thr	Met	Val
			20					25					30		

Val	Thr	His	Gly	Glu	Gly	Pro	Tyr	Leu	Val	Asp	Val	His	Gly	Arg	Arg
		35					40					45			

Tyr	Leu	Asp	Ala	Asn	Ser	Gly	Leu	Tyr	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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Gly Glu Phe Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Val Val
 370 375 380

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Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Val 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 Ala Pro Pro Tyr 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> Engineered variant of V. fluvialis transaminase

<400> 87
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ctggtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgta taacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttcc aagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgtttcgtg cggaaggcaa accgcagaaa 420
cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
accggccttc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcattctgacc 540
tgcccgcatt attggcgta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggatgatggg tgcgggagggt gttattaccc cgccaaaagg ctattttcag 720
gcgattctga ccattcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
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ccggaactga gcaaactgtt ggaaaccgcg attgaagcga ttggggaatt tgatcatggt 960
tttaccacag gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaactctg 1080
aaacatattg cggaactgcc gaacattggc gaatatcgtg gtattggctt tatgtgggcg 1140

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ctggaagtgg tgaaagataa agcgagcaaa gccccgtttg atccaaacct gtgggtgagc 1200
 gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260
 gtggttctgg cgccgccgta cattctgacg gaagcgaga tggatgaaat gttcgataaa 1320
 ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 88
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Engineered variant of V. fluvialis transaminase
 <400> 88

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met Val
 20 25 30

Val Thr His Gly Glu Gly Pro Tyr Leu Val Asp Val His Gly Arg Arg
 35 40 45

Tyr Leu Asp Ala Asn Ser Gly Leu Tyr 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 Pro 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 Phe Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Leu 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 Thr Pro Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Gly Glu Phe Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Val Val
 370 375 380
 Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Pro Asn Leu Trp 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 Ala Pro Pro Tyr 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> 89

<211> 1362
<212> DNA

<213> Artificial Sequence

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

<400> 89

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ctgttggtatg tgcattggccg tctgtatctg gatgcgaaca gcggcctgtg gaacatgtg
gggggcttg atcataaagg cctgattgat gggcggaag cgcgatatga acgtttccg
ggctatcatg cgtttacgg ccgtatgagc gatcagaccg tcatgtctgtc tgaaaaaatg
gtggaagtga gccgcttcc aagcggcgt gtgttttata ccaacagcgg cagcgaagcg
aagatatacca tgtgtgaaat gctgtgtgtt ctgtttcgtg cggaaaggca accgcagaaa
cgtaaaaatc tgaacctga gaaagcgtat catggctcca ccggtgtgag cgcgagcatg
accggccttc cgtataacag cgtgtttgc ctggcgttc cgcgtttct gcatctgacc
tgcccgcat attgcggtta tggcgaagaa ggcaaacgg aagaacagt tgtcgcgcgt
ctggcccggt aactggaaga aaccttcag aaggaaggcg cggataccat tgcgggcttt
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gcatcttcga caatatgat attccggtga tcaagcgtga agtatttgc
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atattagca gtaaaaaact aaccgcgggt ttttttcag tagagcgtt gattttggg
ccggaactga gcaaacgtct ggaacccgg attgaagcga ttgaagaatt tgcattggt
ttataccag gcggccatcc ggtgggtgt gcgattgcgc tgaagcgtat tcatgtgtg
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aaacatatg cggaaacgtcc gaacatggc gaatatctg gtattgctt tatgtggcg
aaacgtatg cgaacacctg caccgatctg ggaactgatt gccgaaccgt ggcccaagc
gtgttcttg cgcgcgcgt catcttgacc gaagcgcaga tgcattgaat gttcgaataa
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60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1080 1140 1200 1260 1320 1362

<210> 90
<211> 453
<212> PRT

<213> Artificial Sequence

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

<400> 90

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

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Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met Val
 20 25 30
 Val Thr His Gly Glu Gly Pro Tyr Leu 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 Pro 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 Phe Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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

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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 Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Val 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 Ala Pro Pro Tyr 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 Asp Val Ala
450

<210> 91
<211> 1362
<212> DNA
<213> Artificial Sequence

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

<400> 91
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ctggtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgta taacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttcc aagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tggtgaaaat gctgtggttt ctgtttcgtg cggaaggcaa accgcagaaa 420

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tgcccgcatt attggcggtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
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gcgattctga ccatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
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gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260
gtggttatcm cgcgcccmga cattctgacc gaagcmcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgtcgataa agtgtttcmg gatgtggcmg aa 1362

<210> 92

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of v. fluvialis transaminase

<400> 92

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met Val
20 25 30

Val Thr His Gly Glu Gly Pro Tyr Leu Val Asp Val His Gly Arg Arg
35 40 45

Tyr Leu Asp Ala Asn Ser Gly Leu Tyr 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 Pro Ser Gly Arg Val Phe
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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 Phe Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asn Gly Glu Phe Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val Val
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375

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Val 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 Ile Ala Pro Pro Tyr 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 Asp Val Ala
450

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

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

<400> 93
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ctggtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgta taacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttcc aagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tgggtgaaaat gctgtggttt ctgtttctgt cggaaggcaa accgcagaaa 420
cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
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tgcccgcatt attggcgta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggtgatggg tgcgggcggt gttattacc ccgcaaaagg ctattttcag 720
gcgattctga ccatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
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tttaccacag gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080

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aaacatattg cggaacgtcc gaacattggc gaatatcgtg gtattggctt tatgtgggcg 1140
ctggaagtgg tgaaagataa agcgagcaaa gccccgtttg atggtaacct ggttgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260
gtggttatcg cgccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 94
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered variant of v. fluvialis transaminase

<400> 94

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met Val
20 25 30

Val Thr His Gly Glu Gly Pro Tyr Leu Val Asp Val His Gly Arg Arg
35 40 45

Tyr Leu Asp Ala Asn Ser Gly Leu Tyr 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 Pro 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 Phe Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu 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 Thr Pro Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Gly Glu Phe Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Val 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 Ile Ala Pro Pro Tyr 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>	95	
<211>	1362	
<212>	DNA	
<213>	Artificial Sequence	
<220>		Engineered variant of V. fluvialis transaminase
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180		ctgtgtgatg tgcattggccg tcgttatctg gatgcgaaca gcggccctgta taacatggtg
240		gcgggctttg atcataaagg cctgattcgc gcggcgaagg cgcagtatga acgttttcgcg
300		ggctatcatg cgttttacgg cgtatgagc gatcagaccg tgatgctgtc tgaaaaaactg
360		gtggaagtga gcccgcttc aagcggccgt gtgttttata ccaacagcgg cagcgaagcg
420		aacgatacca tggtagaaat gctgtgttt cgttttcgtg cggaaaggca accgcagaaga
480		cgtaaaatc tgaccctgaa gaacgcgtat catgctcca ccgcggtgag cgcgagcatg
540		accggccttc cgtataacag cgtgtttgc ctgcgcctgc cggctttct gcatctgacc
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660		ctggcccggt aactggaaga aaccttcag aaggaaaggc cgtataccat tgcgggcttt
720		tttgcggaac cgtgtatggg tgcgggcgtg gtatatccc cgcgaagg ctattttcag
780		gcgattctga ccatcctcgc caaatatgat attccggtga tcagcagatga agtgatttgc
840		ggctttgttc gtaccggcaa cacttgggc tgcgtgacct atgattttac cccgagtcg
900		attatagca gtaaaaaact aaccgcgggt ttttttcag taggaagcgt gattttgggg
960		ccggaactga gcaaacgtct ggaacccgc attgaagcga atgaagaaat tgatcatggt
1020		tttaccacag gcggccatcc ggtgggtgt gcgatggcgc tgaagcgcat tgatgtgtg
1080		atgaacgaag gcttggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg
1140		aaacatatg cggaaacgtcc gaacatggc gaatatcgtg gtattggcct tatgtgggcg
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1260		gaacgtatg cgaacacctg caccgatctg ggaatgatt gccgaacctt ggagcagcagc
1320		gtgttcttgg cgcgcctgta catctgacc gaagcgcaga tggatgaaat gttcgaataa
1362		ctggaaaaag cgttgataa agttgttcg gaagtgcgt aa

1 5 10 15
 Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met Val
 20 25 30
 Val Thr His Gly Glu Gly Pro Tyr Leu Val Asp Val His Gly Arg Arg
 35 40 45
 Tyr Leu Asp Ala Asn Ser Gly Leu Tyr Asn Met Val Ala Gly Phe Asp
 50 55 60
 His Lys Gly Leu Ile Ala 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 Pro 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 Phe Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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
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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 Asn Glu Glu Phe Asp His Gly
 305 310 315 320

Phe Thr Thr 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 Val Val
 370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Trp 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 Ser Ser Val Val Leu Ala Pro Pro Tyr Ile Leu Thr Glu Ala
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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> 97

<211> 1362

<212> DNA

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 97

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atcgtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgtt caacatggtg 180

gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240

ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300

gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360

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 accggcatcc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
 tgcccgcatc attggcggtt tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
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<210> 98

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of v. fluvialis transaminase

<400> 98

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

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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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asn Glu Glu Phe Asp His Gly
305 310 315 320

Phe Thr Thr 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 Leu 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

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Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Pro Asn Leu Trp 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 Ala Pro Pro Tyr 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 Asp Val Ala
450

<210> 99
<211> 1362
<212> DNA
<213> Artificial Sequence

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

<400> 99
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aacgatacca tgggtgaaaat gctgtggttt ctgcatcgtg cggaaggcaa accgcagaaa 420
cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
accggcatcc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatc attggcggtt tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggatgatggg tgcgggcggt gttattacc cgcctaaaagg ctattttcag 720
gcgattctga ccatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggtc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
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ccggaactga gcaaactgtt ggaaaccgcg attgaagcga ttggggaatt tgatcatggt 960
tttaccacag gcggccatcc ggtgggttgt gcgattgctg tgaaagcgat tgatgtggtg 1020

CX2-105USP1_ST25

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

<220>
<223> Engineered variant of V. fluvialis transaminase
<400> 100

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Ser 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Ile 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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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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Gly Glu Phe Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Leu 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 Val Val
 370 375 380
 Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Leu 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 Ser Ser Val Val Leu Ala Pro Pro Tyr 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

<210> 101
 <211> 1362
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Engineered variant of V. fluvialis transaminase

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<210> 102
 <211> 453
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Engineered variant of V. fluvialis transaminase
 <400> 102

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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 Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Ser Val
 20 25 30
 Val Thr His Gly Glu Gly Pro Tyr Leu 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 Ala 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Ile Pro Tyr Asn Ser Ser 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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
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 Asp His Gly
305 310 315 320

Phe Thr Thr 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 Leu 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 Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Val 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 Ala Pro Pro Tyr 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 Asp Val Ala
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<210> 103
<211> 1362
<212> DNA
<213> Artificial sequence

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

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ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300

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gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggcagcagc 1260
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<210> 104
<211> 453
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<220>
<223> Engineered variant of V. fluvialis transaminase
<400> 104

Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
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Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Ser 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
Page 138

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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu Pro Tyr Asn Ser Ser 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Gly Glu Phe Asp His Gly
305 310 315 320

Phe Thr Thr 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 Leu 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
Page 139

355 CX2-105USP1_ST25 360 365

Ile Gly Glu Tyr Arg Gly Ile Gly Phe Met Trp Ala Leu Glu Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Val 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 Ser Ser Val Val Leu Ala Pro Pro Tyr 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> 105
<211> 1362
<212> DNA
<213> Artificial Sequence

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

<400> 105
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atcgtggatg tgcattggcg tcgttatctg gatgcgaaca gcggcctggt caacatgggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
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gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tgggtgaaaat gctgtggttt ctgcatcgtg cggaaggcaa accgcagaaa 420
cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
accggccttc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcattctgacc 540
tgcccgcatc attggcggtt tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggatgatggg tgcgggagggt gttattaccg cgccaaaagg ctattttcag 720
gcgattctga ccatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggtc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccag taggagcggg gattttgggg 900
ccggaactga gcaaacgtct ggaaaccgag attgaagcga atgaggaatt tgatcatggt 960

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tttaccacag gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg	1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg	1080
aaacatatattg cggaacgtcc gaacattggc gaatatcgtg gtattggctt tatgtgggcg	1140
ctggaagtgg tgaaagataa agcgagcaaa gccccgtttg atggtaacct gtgggtgagc	1200
gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc	1260
gtggttcttg caccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa	1320
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<210> 106
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Engineered variant of V. fluvialis transaminase
 <400> 106

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Ser 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Leu 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 Thr Pro Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Asn Glu Glu Phe Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Val Val
 370 375 380
 Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Trp 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 Ala Pro Pro Tyr 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

<210> 107
<211> 1362
<212> DNA
<213> Artificial Sequence

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

<400> 107
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atcgtgatg tgcattgccg tcgttatctg gatgcgaaca gcggccctgt caacatggtg
gcgggctttg atcataaagg cctgatgat gcggcgaaag cgcagtatga acgtttccg
ggctatcatg cgtttacgg cgtatgagc gatcagaccg tgaatgctgc tgaataaactg
gtggaagtga gccggttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg
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cgtaaatc tgaccctgaa gaacgcgtat catgctcca ccgcggtgag cgcgagcatg
accggccttc cgtataacag cgtgtttgc cgtccgctgc cgggctttct gcatctgacc
tgcccgcat attgcgtaa tggcgaagaa ggcgaaaccg aagaacagt tgcgcgcgt
ctggcccgctg aactggaaag aacctcag aaggaaaggc cggataccat tgcgggcttt
tttgcggaac cgtgatggg tgcggggcgt gtatttacc ccgcaaaagg ctatttcag
gcgattctga ccatcctgcg caatatgat attccggtga tcagcagtga agtgattgc
ggcttggtc gtaccggcaa cactggggc tgcgtgacct atgattttac cccggtgcg
attattaaga gtaaaaacct aaccgcgggt ttttttccag taggagcgggt gattttgggg
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atgaacgaag gcttggccga aacgtgcgt cgtctggccc cgcgttttga agaacgtctg
aaacatattg cggaaacgtcc gaacattgac gaatatctg gtattggcct tatgtggcgc
ctggaagtgg tgaagataa agcgagcaaa gcccggtttg atggcaacct gagcgtgagc
aaacatattg caccgccgta cattctgacc gaagcgcaga tggatgaat gttcgataaa
ctggaaaaag cgtggataa agtgtttgcg gaagtgcgt aa
1362

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

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

CX2-105USP1_ST25

<400> 108

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Ser 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240

Ala Ile Leu Thr 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 Phe Asp His Gly
 305 310 315 320

Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr 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> Engineered variant of V. fluvialis transaminase

<400> 109

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atcgtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctggt caacatgggtg 180

gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240

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 gtggaagtga gcccggttga tagcggccgt gtgtttttata ccaacagcgg cagcggaagcg
 360 aacgatacca tgytgaaaaat gctgtggttt ctgcatacgtg cggaaagcaca accgcagaanaa
 420 cgtaaaaatc tgaaccctgaa gaacgcgtat catggtctca ccgcggtgag cgcgagcatg
 480 accggcatcc cgtataacag caagtctgc ctgcgcgtgc cgggtcttct gcatctgacc
 540 tgcgccgat attgucgtta tggcgaagaa ggcgaacccg aagaacagtt tgtcgcgcgt
 600 ctggcccggt aactgggaaga aaccattcag aaggaagcgg cggataccat tgcgggcttt
 660 ttgcgggaac cgtgatggg tgcgggcgt gtattacc ccgcaaaagg ctatttcag
 720 gcatcttga ccatccctgc caaatatgat attccggtga tcagcagatga agtgatttgc
 780 ggctttgtc gtaccggcaa cactgggc tgcgtgaact atgatttac ccgcatgcg
 840 atattagca gtaaaaaact aaccgcgggt tttttccag taggaagcgt gattttgggg
 900 ccggaactga gcaaacgtct ggaaccgcg attgaagcga ttggggaatt tgatcatggt
 960 tttaaccacag gcggccatcc ggtgggtgt gcgattgcgc tgaagcgat tgatgtgtg
 1020 atgaacgaag gccctgtga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg
 1080 aaacatatg cggaaacgtcc gaacattgac gaatatcgtg gtattgctt tatgtggcg
 1140 ctggaagtgg tgaagaatga agcgagcaaa gccccggttg atgtaacct gtgggtgagc
 1200 ctggaagtgg tgaagaatga agcgagcaaa gccccggttg atgtaacct gtgggtgagc
 1260 gaacgtatg cgaacacctg caccgatctg ggaactgatt gccgaccggt ggcccaagc
 1320 gtgttctgg cgcgcgcgt catctgacc gaagcgcaga tggatgaat gttcgataaa
 1362 ctggaaaaag cgtggtataa agtgttcg gatgtgcgt aa

<210> 110
 <211> 453
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Engineered variant of V. fluvialis transaminase
 <400> 110

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Ser Val
 20
 25
 30

Val Thr His Gly Gln 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 Gln Arg Phe Pro
 65
 70
 75
 80

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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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Ile Pro Tyr Asn Ser Lys 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Gly Glu Phe Asp His Gly
305 310 315 320

Phe Thr Thr 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 Leu Glu Asn Val Arg Arg Leu
340 345 350

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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 Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Trp 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 Ala Pro Pro Tyr 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 Asp Val Ala
450

<210> 111
<211> 1362
<212> DNA
<213> Artificial Sequence

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

<400> 111
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atcgtggatg tgcattggcg tcgttatctg gatgcgaaca gcggcctggt caacatgggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
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cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
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tgcccgcat attggcggtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
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tttgcggaac cggatgatggg tgcgggagggt gttattacc cgcctaaagg ctattttcag 720
gcgattctga ccattcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggtc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
attattagca gtaaaaacct aaccgcgggt ttttttccag taggagcggg gattttgggg 900

CX2-105USP1_ST25

ccggaactga gcaaactctt ggaaaccgcg attgaagcga atgaggaatt tgatcatggt 960
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 atgaacgaag gcctgctgga aaacgtgcgt cgtctggccc cgcgttttga agaactctg 1080
 aaacatattg cggaactgcc gaacattggc gaatatcgtg gtattggctt tatgtgggag 1140
 ctggaagtgg tgaaagataa agcgagcaaa gccccgtttg atggtaacct ggttgtgagc 1200
 gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260
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<210> 112

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 112

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Ser 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Leu 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 Thr Pro Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asn Glu Glu Phe Asp His Gly
305 310 315 320

Phe Thr Thr 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 Leu 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 Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Val 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 Ala Pro Pro Tyr 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
450

<210> 113
<211> 1362
<212> DNA
<213> Artificial Sequence

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

<400> 113
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120
atcgtgcatg tcgtagccg tcgttatctg gatgcgaaca gcggccctgt caacatgtg
180
gcgggcttg atcataaagg cctgattgat gcggcggaag cgcagtatga acgtttccg
240
ggctatcatg cgtttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg
300
gtggaagtga gcccgttga tagcggccgt gtgttttata ccaacagcgg cagcggaagc
360
aacgatacca tggtagaaat gctgtgttt ctgcattctg cggaaagcaa accgcagaaa
420
cgtaaaatc tgaccctga gaaacgcgtat catgctcca ccgctgtgag cgcgagcatg
480
accgcatcc cgtataacag cgtgtttgc ctgcgcctgc cggcttct gcatttgacc
540
tgcccgcat atggcgtta tggcgaagaa ggcgaacccg aagaacagtt tgtcgcgcgt
600
ctggccctg aactggaaga aaccattcag aaggaaggc cgtataccat tgcgggcttt
660
tttcggaac cgtgtaggg tgcgggcgt gtatatccc gttatccc cgcgaagg ctatttcag
720
gcgattctga ccatcctgc caatatgat attccggtga tcagcgatga agtgatttgc
780
ggctttgtc gtaccggcaa cactgggc tgctgtgacc atgatttac cccgagtcg
840
atatagca gtaaaacct aacgcgcgt tttttccag taggaagcgt gatttgggg
900
ccggaactga gcaaacgtct ggaacccgc attgaagcga ttggggaatt tgatcatggt
960
tttaaccag gcggccatcc ggtgggtgt gcgattgcgc tgaagcgat tgatgtgtg
1020
atgaacgaag gccctgtga aaaacgtgcgt gctctggccc cgcgttttga agaacgtctg
1080
aaacatatg cggaaacgtcc gaacatggc gaatatcgt gtattgctt tatgtgggcg
1140
ctggaagtgg tgaagataa agcgaagcaa gccccgttg atgtaacct gttggtgagc
1200
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1260
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1320
ctggaaaaag cgtggataa agtgttcg gaagtgcgt aa
1362

<210> 114
<211> 453
<212> PRT
<213> Artificial Sequence

<220>

<223> Engineered variant of v. fluvialis transaminase

<400> 114

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Ser 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240

Ala Ile Leu Thr 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
260 270

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 Gly Glu Phe Asp His Gly
305 310 315 320

Phe Thr Thr 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 Leu 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 Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Leu 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 Ala Pro Pro Tyr 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> 115

<211> 1362

<212> DNA

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 115

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cacatgccga gcctacatca gcgtggcacc tcagtggtaa cccatggcga aggcccgtat 120

atcgtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180

240 ggggcttg atcataaagg cctgattgat gcggcggaagg cgcagtatga acgtttccg
 300 ggtatcatg cgtttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaatg
 360 gtggaagtga gccgttga tagcgccgt gtgtttata ccaacagcgg cagcggaagg
 420 aacgatacca tegtgaatat gctgtgttt cgtcatcgtg cggaaaggcaa accgcagaaa
 480 cgtaaaatc tgaacctgaa gaacgcgtat catgctcca ccgcggtgag cgcgagcatg
 540 accggcatcc cgtataacag cgtgttggc ctgcgcgtgc cggcttct gcatctgacc
 600 tgcgccatt attgcgta tggcgaagaa ggcgaacgg aagaacagt tgcgcgcgt
 660 ctggccgtg aactggaaga aacattcag aaggaaaggc cgtataccat tgcggctt
 720 ttgcgggaac cgtgatggg tgccggcggt gtattacc ccgcaaaagg ctatttcag
 780 gcgattctga ccatccctgc caaatatgat attccggtga tcagcgatga agtgattgc
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 900 attatagca gtaaaaact aaccgggt tttttccag taggagcgt gattttggg
 960 ccggaactga gcaaacgtct ggaaccgcg attgaagcga ttggggaatt tgatcatgt
 1020 ttaccacag gcggccatcc ggtgggtgt gcgattgcgc tgaagcgat tgatgtgtg
 1080 atgaacgaag gcctgtgga aaaacgtcgt cgtctggccc cgcgtttga agaacgtctg
 1140 aaacatatg cggaaacgtcc gaacattgyc gaatatcgtg gtattgctt tatgtggcg
 1200 ctggaagtgg tgaagataa agcgaagcaa gccccgttg atgtaacct ggttgtgagc
 1260 gaacgtatg cgaacacctg caccgatctg ggaactgatt gccgaaccgt ggccagagc
 1320 gtgttcttg caccgcgtta catctgacc gaagcgcaga tggatgaaat gttcgataaa
 1362 ctggaaaaag cgtgataa agtttgcg gatgtgcgt aa

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<210> 116
 <211> 453
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Engineered variant of V. fluvialis transaminase
 <400> 116

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Ser Val

Val Thr His Gly Gln Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg

Tyr Leu Asp Ala Asn Ser Gly Leu Trp Asn Met Val Ala Gly Phe Asp

His Lys Gly Leu Ile Asp Ala Lys Ala Gln Tyr Gln 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Gly Glu Phe Asp His Gly
305 310 315 320

Phe Thr Thr 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 Leu Glu Asn Val Arg Arg Leu
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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 Val Val
 370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Val 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 Ala Pro Pro Tyr 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 Asp Val Ala
 450

<210> 117

<211> 1362

<212> DNA

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 117

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atcgtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgtt caacatggtg	180
gcaggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg	240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg	300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg	360
aacgatacca tgggtgaaaat gctgtggttt ctgcatcgtg cggaaggcaa accgcagaaa	420
cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg	480
accggcatcc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc	540
tgcccgcatc attggcggtt tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt	600
ctggcccgtg aactggaaga aaccattcag aaggaaaggc cggataccat tgcgggcttt	660
tttgcggaac cggatgatggg tgcgggaggc gttattacc cgcctaaagg ctattttcag	720
gcgattctga ccatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc	780
ggctttggtc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg	840

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attattagca gtaaaaacct aaccgcgggt ttttttccag taggagcggg gattttgggg      900
ccggaactga gcaaactgtct ggaaaccgcg attgaagcga ttggggaatt tgatcatggt      960
tttaccacag gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg     1020
atgaacgaag gcctgctgga aaacgtgcgt cgtctggccc cgcgttttga agaactgtctg     1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gtattggctt tatgtgggcg     1140
ctggaagtgg tgaaagataa agcgagcaaa gccccgtttg atggtaacct gtgggtgagc     1200
gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc     1260
gtggttctgg cgccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa     1320
ctggaaaaag cgctggataa agtgtttgcg gatgtggcgt aa                          1362

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<210> 118

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 118

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Ser 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

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Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Gly Glu Phe Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Leu 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 Val Val
 370 375 380
 Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Trp 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 Ala Pro Pro Tyr 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 Asp Val Ala
450

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

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

<400> 119
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120 cacatgccga gctacatca gcgtgycacc tcagtgtgtaa cccatgycga aggcccgat
180 atcgttgatg tgcattgccg tcgttatctg gatgcgaaca gcggccttgt caacatgtg
240 gcgggcttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgtttccg
300 ggcatacatg cgtttacgg cgtatgagc gatcagaccg tgatgctgtc tgaaaaaactg
360 gtggaagtga gcccgttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg
420 aacgatacca tggtagaaat gctgtgttt ctcgacatctg cggaaagcaca accgcagaaa
480 cgtaaaatic tgaccctgaa gaacgcgtat catggtcca ccgcggtgag cgcgagcatg
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600 tgcgccgat attgcttta tggcgaagaa ggcgaaccg aagaacagtt tgtcgcgcgt
660 ctggcccggt aactggaaga aaccatcag aaggaaagcg cggataccat tgcgggcttt
720 ttgacggaac cgtgatggg tgcgggcgt gtatatcccc cgcgaagaag ctattttcag
780 gcgattctga ccatcctgcg caaatatgat atcccggtga tcagcgatga agtgatttgc
840 ggccttgctc gtaccggcaa cactggggc tgcgtgacct atgattttac cccgcatgcg
900 attatagca gtaaaaacct aaccgcgggt ttttttcag taggagcgggt gattttgggg
960 ccggaactga gcaaacgtct ggaacccgcg atggaagcga ttgggggaatt tgatcatggt
1020 tttaaccag gcggccatcc ggtgggtgtg gcgattgcgc tgaagcgcat tgatgtgtgtg
1080 atgaacgaag gccctcctga aaaacgtcgt cgtctggccc cgcgttttga agaacgtctg
1140 aaacatatg cggaaacgtcc gaacatggc gaatatcgtg gtattggcct tatgtggggcg
1200 ctggaagtgg tgaagataa agcgaagcaaa gcccggttg atgttaacct ggtgtgtagc
1260 gaaacgtatt cgaacacactg caccgatctg ggaactgatt gccgacccgtt ggccagagagc
1320 gtgttcttg cgcgcgcgta catctgacc gaagcgcaga tggatgaaat gttcgaataa
1362 ctggaaaaag cgttggtataa agtgttgcg gaagtggcgt aa

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 120

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Ser 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240

Ala Ile Leu Thr Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
 Page 160

Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 270

Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 285

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 Gly Glu Phe Asp His Gly
305 310 315 320

Phe Thr Thr 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 Leu 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 Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Val 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 Ala Pro Pro Tyr 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> Engineered variant of *V. fluvialis* transaminase

<400> 121
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atcgttgatg tgcattgccc tgcattatctg gatgcgaaca gcggccctgt caacatggtg
 180
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 240
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 300
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 360
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 420
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 480
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 540
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 600
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 660
 ttgcggaac cgtgatggg tgcggcggt gtatatccc cgcaaaagg ctatttcag
 720
 gcatctga ccatctcg caaatatgat attcggtga tcagcgatga agtgattgc
 780
 ggcttgtc gtaaccgcaa cactgggc tgcgtgacct atgatttac ccggaatcg
 840
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 900
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 960
 ttaccacag gcggccatc ggtgggtgt gcgattgcgc tgaagcgat tgatgtgtg
 1020
 atgaacgaag gcctgtga aaacgtgct cgtctggccc cgcgtttga agaactgtg
 1080
 aaacatattg cggaaactc gaacatgac gaatatctg gtattgctt tatgtggcg
 1140
 ctggaagtgt tgaagataa agcgaagcaa gcccgcttg atgtaacct gttggtgagc
 1200
 gaactgattg cgaacacctg cactgactg ggaactgatt gccgaaccgt ggccagagc
 1260
 gttgtctg gcgcgcgta catctgacc gaagcgcaga tggatgaat gttcgataaa
 1320
 ctggaaaaag cgtgataa agtttgcg gaagtgcgt aa
 1362

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<210> 122
 <211> 453
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Engineered variant of V. fluvialis transaminase
 <400> 122

Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
 1
 Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met Val
 20
 Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
 35
 Tyr Leu Asp Ala Asn Ser Gly Leu Phe Asn Met Val Ala Gly Phe Asp
 50
 55
 60

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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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Asp His Gly
 305 310 315 320
 Phe Thr Thr Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
 325 330 335

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Ile Asp Val Val Met Asn Glu Gly Leu Leu 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 Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Leu 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 Ala Pro Pro Tyr 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> Engineered variant of V. fluvialis transaminase

<400> 123
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cacatgccga gcctacatca gcgtggcacc atggtggtga cccatggcga aggcccgtat 120
atcgtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctggt 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 ctgcatcgtg cggaaggcaa accgcagaaa 420
cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
accggccttc cgtataacag caagtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatt attggcggtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggccccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggatgatggg tgcgggcggt gttattacc cgccaaaagg ctattttcag 720
gcgattctga ccatcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780

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attattagca gtaaaaacct aaccgcgggt ttttttccag taggagcggg gattttgggg      900
ccggaactga gcaaactgtc ggaaaccgcg attgaagcga atgggggaatt tgatcatggt      960
tttaccacag gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg     1020
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aaacatattg cggaacgtcc gaacattggc gaatatcgtg gtattggctt tatgtgggcg     1140
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gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc     1260
gtggttctgg cgccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa     1320
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<210> 124
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Engineered variant of V. fluvialis transaminase
 <400> 124

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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 Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met Val
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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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
          130          135          140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met

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145 150 155 160
 Thr Gly Leu Pro Tyr Asn Ser Lys 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Asn Gly Glu Phe Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Leu 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 Val Val
 370 375 380
 Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Val 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 Ala Pro Pro Tyr Ile Leu Thr Glu Ala
 420 425 430 435 440 445 450

420

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430

Gln Met Asp Gln Met Phe Asp Lys Leu Gln Lys Ala Leu Asp Lys Val
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Phe Ala Gln Val Ala
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<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 125

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180
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240
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360
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480
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1200
gaacgtattg cgaacacctg caccgatctg ggaactgat gccgaacctt ggccagagc
1260
gtgttatctg cgcgcgcgtg catctgacc gaagcgcaga tggatgaat gttcgataaa
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<210> 126

CX2-105USP1_ST25

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 126

Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Tyr Ser Leu
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Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Ser 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

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Ala Ile Leu Thr 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 Gly Glu Phe Asp His Gly
305 310 315 320

Phe Thr Thr 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 Leu 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 Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Val 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 Ile Ala Pro Pro Tyr 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> 127
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> Engineered variant of v. fluvialis transaminase

<400> 127
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180 atcgtggatg tgcattgccc tgcattatcg gatgcgaaca gcggccctgt caacatggtg
240 ggggcttg atcataaagg cctgattgat gcggcgaagg cgcagtatga acgtttccg
300 ggctatcatg cgtttacgg cgtatgagc gatcagaccg tcatgtctgtc tgaaaaaatg
360 gtggaagtga gcccggttga tagcgccgt gtgttttata ccaacagcgg cagcgaagcg
420 aacgatacca tgggtgaatat gctgtgttt ctcgatctgt cgaagcgcaa accgcagaaa
480 cgtaaaaatc tgaccctgaa gaacgcgtat catgctcca ccgggttgag cgcgagcatg
540 accggccttc cgtataacag cgtgtttgac ctcggcctgc cgggcttct gcatctgacc
600 tggcccgcat attgcggtta tggcgaagaa ggcgaaacg aagaacagt tctcgcgcgt
660 ctggcccggt aactggaaag aaccattcag aaggaaagcg cgtataccat tgcgggcttt
720 ttgctgggaa cgtgtatggg tgcgggcgt gtatatcacc cgcgaagaag ctattttcag
780 cgtattctga ccatcctgcg caaatatgat attccggtga tcagcgtatga agtgatttc
840 ggcttgttc gtaaccgcaa cactggggc tgcgtgacct atgattttac cccgattcg
900 attatagca gtaaaaaact aaccgcgggt tttttccag taggagcgtt gattttgggg
960 ccggaactga gcaaacgtct ggaaccgcg attgaagcga atggggaatt tgatcatgt
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1080 atgaacgaag gctcgtgga aacgtgcgt cgtctggccc cgcgttttga agaacgtctg
1140 aaacatatg cggaaactcc gaacatggc gaatatctg gtattgctt tatgtggcg
1200 ctggaagtgg tgaagatata agcagcaaa gccccggttg atgtaacct ggttgtgagc
1260 gaacgtatg cgaacacct caccgatcg ggaactgatt gccgaccgtt ggcagcagc
1320 gtgttcttg cgcgcgcta catctgacc gaagcgcaga tggatggaat gttcgataaa
1362 ctggaaaaag cgtggataa agtgttcg gaagtgcgt aa

<210> 128
<211> 453
<212> PRT
<213> Artificial Sequence
<220>
<223> Engineered variant of V. fluvialis transaminase
<400> 128

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Ser Val
20
25
30

Val Thr His Gly Gln 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
Page 170

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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240

Ala Ile Leu Thr 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 Asn Gly Glu Phe Asp His Gly
 305 310 315 320

Phe Thr Thr Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
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325

330

335

Ile Asp Val Val Met Asn Glu Gly Leu Leu 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 Val Val
 370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Val 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 Ser Ser Val Val Leu Ala Pro Pro Tyr 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> Engineered variant of V. fluvialis transaminase

<400> 129

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 gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
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 accggcatcc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
 tgcccgcatt attggcggtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
 ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
 tttgcggaac cggtgatggg tgcgggcggt gttattaccc cgccaaaagg ctattttcag 720

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tttaccacag gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg	1020
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<210> 130
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Engineered variant of V. fluvialis transaminase
 <400> 130

Met Asn Lys Pro Gln Ser Trp Glu Thr Arg Ala Glu Thr Val Ser Leu	1	5	10	15
Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu	130	135	140	

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Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Ala 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 Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Val Val
 370 375 380
 Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Gly
 385 390 395 400
 Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
 405 410 415

Met Gly Gln Asn Val Val Leu Ala Pro Pro Tyr Ile Leu Thr Gln Ala
420 425 430

Gln Met Asp Gln Met Phe Asp Lys Leu Gln Lys Ala Leu Asp Lys Val
435 440 445

Phe Ala Gln Val Ala
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<210> 131
<211> 1362
<212> DNA
<213> Artificial Sequence
<220>
<223> Engineered variant of V. fluvialis transaminase

<400> 131
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ctggaaaaag cgttgataa agtgtttcg gaagtggcgt aa
1362

CX2-105USP1_ST25

<210> 132
 <211> 453
 <212> PRT
 <213> Artificial Sequence

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

<400> 132

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Leu Pro Tyr Asn Ser Val Phe Gly Leu Pro Ala 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 Pro Lys Gly Tyr Phe Gln
 Page 176

225 230 235 240
 Ala Ile Leu Thr 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 Asp His Gly
 305 310 315 320
 Phe Thr Thr 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 Val Val
 370 375 380
 Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Gly
 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 Ala Pro Pro Tyr 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> 133
 <211> 1362
 <212> DNA
 <213> Artificial Sequence

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

<400> 133

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gaacgtatt cgaacacctg caccgatcg ggaactgatt gccgaaccgt ggcccaagc
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1362

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

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

Met Asn Lys Pro Gln Ser Trp Gln Thr Arg Ala Gln Thr Val Ser Leu
1
Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gln Thr Met Val
20
Val Thr His Gly Gln Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg
35
40
45

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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
 Leu Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
 115 120 125
 Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Ala 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 Asp His Gly
 305 310 315 320

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Phe Thr Thr 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 Val 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 Val Pro Pro Tyr 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> Engineered variant of V. fluvialis transaminase

<400> 135
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atcgtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcggggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgtttttacgg cctgatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgtttttata ccaacagcgg cagcgaagcg 360
aacgatacca tgggtgaaaat gctgtggttt ctgcatcgtg cggaaggcaa accgcagaaa 420
cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
accggccttc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatc attggcggtt tggcgaagaa ggcgaaaccg aagaacagtt tgcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660

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ggcttttggtc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
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tttaccacac acggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
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gaacgtattg cgaacacctg caccgatctg ggactgattt gtcgaccgat gggccagagc 1260
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<210> 136
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered variant of V. fluvialis transaminase
<400> 136

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Leu 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
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130

135

140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
305 310 315 320

Phe Thr Thr His 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 Val Val
370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Gly
385 390 395 400

Glu Arg Ile Ala Asn Thr Cys Thr Asp Leu Gly Leu Ile Cys Arg Pro
Page 182

Met Gly Gln Ser Val Val Leu Ala Pro Pro Tyr Ile Leu Thr Gln Ala 420 425 430
Gln Met Asp Gln Met Phe Asp Lys Leu Gln Lys Ala Leu Asp Lys Val 435 440 445

Phe Ala Gln Val Ala 450

<210> 137
<211> 1362
<212> DNA
<213> Artificial Sequence
<220>
<223> Engineered variant of V. fluvialis transaminase

<400> 137
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120
atcgttgatg tgcattgccg tgcgttatctg gatgcggaaca gcggccctgtt caacatgtgtg
180
gcgggctttg atcataaagg cctgatgtat gcggcggaag cgcagtatga acgttttccg
240
ggctatcatg cgttttaagg cgtatgagc gatcagaacc tgatgctgtc tgaanaactg
300
gtggaagtga gcccgttga tagcggccgt gtgtttctga ccaacagcgg cagcgaagcg
360
aagatatcca tgggtgaaat gctgtgttt ctcgatctg cggaagcga accgcagaaga
420
cgtaaaatc tgaccctgaa gaacgcgtat catggtcca ccgcggtgag cgcgagcatg
480
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540
tgcccgcat attgcggtta tggcggaaga ggcgaaacgg aagaacagtt tgcgcacagt
600
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660
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720
gcgattctga ccatcctgcg caaatatgat attcgggtga tcagcagatga agtgatttgc
780
ggccttgttc gtaccggcaa cactggggc tgcgtgaact atgattttac cccgagtcg
840
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900
ccggaactga gcaaacgtct ggaacccgcg attgaaagcga tcgaagaatt tgatcatggt
960
tttaccacag gcggccatcc ggtgggtgt gcgattgcgc tgaagcgat tgatgtgtgtg
1020
atgaacgaag gccctggccga aacggtgcgt cgtctggccc cgcgttttga agaacgctctg
1080
aaaacatatg cggaaacgtcc gaacatggc gaatatctgt gtatttgctt tatgttggcg
1140
ctggaagtgg tgaagaataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc
1200
gaacgtatg cgaacacactg caccgatctg ggaactgatt gccgaaccgt ggccagagc
1260
gtgttcttgg caccgcccga cattctgacc gaagcgcaga tggatgaaat gttcgataaa
1320

ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa

1362

<210> 138

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 138

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

Ala Ile Leu Thr 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 Ala 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 Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr 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> 139

<211> 1362

<212> DNA

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 139
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ctggaagcgg tgaagataa agcggaaca gcccgcttg atgcacact gagcgtgggt
gaacgtatg cgaacacctg caccgatcg ggaactgatt gccgaacct ggccagagc
gtgttctg caccgcgtg catctgacc gaagcgaga tggatgaat gttcgataa
ctggaaaaag cgttgataa agtttgcg gaagtgcgt aa

1362
1320
1260
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<210> 140
<211> 453
<212> PRT
<213> Artificial Sequence
<220>
<223> Engineered variant of V. fluvialis transaminase
<400> 140

Met Asn Lys Pro Gln Ser Trp Gln Thr Arg Ala Gln Thr Val Ser Leu 1
Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met Val 20
Val Thr His Gly Glu Gly Pro Tyr Ile Val Asp Val His Gly Arg Arg 30

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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Ala 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 Asp His Gly
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305 310 315 320
 Phe Thr Thr 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 Gly
 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 Ala Pro Pro Tyr 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> Engineered variant of V. fluvialis transaminase

<400> 141
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 atcgtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
 gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
 ggctatcatg cgtttttacgg ccgcatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
 gtggaagtga gcccgtttga tagcggccgt gtgtttctga ccaacagcgg cagcgaagcg 360
 aacgatacca tggtgaaaat gctgtggttt ctgcatcgtg cggaaggcaa accgcagaaa 420
 cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
 accggccttc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
 tgcccgcatc attggcggtta tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600

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ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
 tttgcggaac cggatgatggg tgcgggcggt gttattaccc cgccaaaagg ctattttcag 720
 gcgattctga ccattcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
 ggctttggtc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
 attattagca gtaaaaacct aaccgcgggt ttttttccag taggagcggt gattttgggg 900
 ccggaactga gcaaactgtc ggaaaccgcg attgaagcga tcgaagaatt tgatcatggt 960
 tttaccacag gcggccatcc ggtgggttgt gcgattgcmc tgaaagcgat tgatgtgggtg 1020
 atgaacgaag gcctggccga aaacgtgcmg cgtctggccc cgcgttttga agaacgtctg 1080
 aaacatattg cggaacgtcc gaacattggc gaatatcmg gtattggctt tatgtgggcmg 1140
 ctggaagccg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcmgtgagc 1200
 gaacgtattg cgaacacctg caccgatcmg ggactgattt gccgaccgtt gggccagagc 1260
 gtggttctgg tgccgcmgta cattctgacc gaagcmgaga tggatgaaat gttcgataaa 1320
 ctggaaaaag cmctggataa agtgtttcmg gaagtggcmg aa 1362

<210> 142
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Engineered variant of V. fluvialis transaminase
 <400> 142

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

Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met 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

Leu 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Asp His Gly
 305 310 315 320
 Phe Thr Thr 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

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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 Val Pro Pro Tyr 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> 143
<211> 1362
<212> DNA
<213> Artificial Sequence

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

<400> 143
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atcgtggatg tgcattggccg tcgttatctg gatgcgaaca gcggcctgtg gaacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg cctgatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgttttata ccaacagcgg cagcgaagcg 360
aacgatacca tgggtgaaaat gctgtggttt ctgcatcgtg cggaaggcaa accgcagaaa 420
cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
accggccttc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
tgcccgcatc attggcggtt tggcgaagaa ggcgaaaccg aagaacagtt tgtcgcgcgt 600
ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
tttgcggaac cggatgatggg tgcgggcggt gttattacc cgcctaaaagg ctattttcag 720
gcgattctga ccattcctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
ggctttggtc gtaccggcaa cacctggggc tgcgtgacct atgattttac cccggatgcg 840
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ccggaactga gcaaacgtct ggaaaccgcg attgaagcga tcgaagaatt tgatcatggt 960
tttaccacag gcggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtggtg 1020
atgaacgaag gcctggccga aaacgtgcgt cgtctggccc cgcgttttga agaacgtctg 1080
aaacatattg cggaacgtcc gaacattggc gaatatcgtg gtattggctt tatgtgggcg 1140
ctggaagtgg tgaaagataa agcgagcaaa gccccgtttg atggcaacct gagcgtgagc 1200
gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260

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gtgggttctgg caccgccgta cattctgacc gaagcgaga tggatgaaat gttcgataaa 1320

ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 144

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of v. fluvialis transaminase

<400> 144

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Leu 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu 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

Val Met Gly Ala Gly Gly Val Ile Thr Pro Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr 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> 145
<211> 1362
<212> DNA
<213> Artificial Sequence

<220> Engineered variant of V. fluvialis transaminase

<400> 145

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 atcgttgatg tgcattgcc tgcattatc gatgcgaaca gcggcctgtg gaacatgtg
 ggggcttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgtttccg
 ggtatcatg cgtttacgg cgtatgagc gatcagacc tgaatcctgc tgaataactg
 gtggaagtga gccgtttga tagcgccgt gtgtttata ccaacagcgg cagcgaagcg
 aagatatcca tggtagaaat gctgtgtrt ctcacatcgt cgaagcga accgcaga
 cgtaaaatc tgaccctga gacggcgtat catgctcca ccgggtgag cgcagcatg
 accgcaccc cgtataacag cgtgttggc ctgcgcctgc cggccttct gcatctgacc
 tgcccgcat attggcgtta tggcgaagaa ggcgaaccg aagaacagtt tgcgcgcgt
 ctggccctg aactggaaga aaccttcag aaggaagcg cgtataccat tgcggcctt
 ttgcggaac cgtgatggg tgcggcggt gtatatccc cgcgaagg ctatttcag
 gcatctga ccatcctcg caatatgat atccggtga tcagcgtga agtgattgc
 gctttgtc gtaaccgcaa cactgggc tgcgtgacct atgatttac ccgcatgcg
 attatagc ccaaaact aaccgcgggt tttttccag taggaagcgt gatttgggg
 ccggaactga gcaacgtct ggaaccgcg atgaagcga tcgaagaatt tgatcatgt
 ttaccacag gcggccacc ggtggtgt gcatgtgcg tgaagcgtat tgatgtgtg
 1020
 atgaacgaag gctggccga aacgtgtcgt cgtctggccc cgcgtttga aagaactg
 1080
 aacatattg cggaaactc gaacatgtc gaatatcgt gtattgctt tatgtggcg
 1140
 ctggaagcgg tgaagataa agcgaagcaa gcccgcttg atgcaacct gagcgtgggt
 1200
 gaactatg cgaacacct caccgatcg ggaactgt gtcgacct gggccagaac
 1260
 gtgttctgg caccgccgt catctgacc gaagcgcaga tggatgaat gttcgataa
 1320
 ctggaaaaag cgttgataa agtttgcg gaagtgcgt aa
 1362

<210> 146

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 146

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

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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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Gln Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Ile 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Ala 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

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Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Asp His Gly
305 310 315 320

Phe Thr Thr 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 Gly
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 Ala Pro Pro Tyr 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> Engineered variant of V. fluvialis transaminase

<400> 147
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atcgtggatg tgcattggcg tcgttatctg gatgcgaaca gcggcctggt caacatggtg 180
gcgggctttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgttttccg 240
ggctatcatg cgttttacgg ccgtatgagc gatcagaccg tgatgctgtc tgaaaaactg 300
gtggaagtga gcccgtttga tagcggccgt gtgtttctga ccaacagcgg cagcgaagcg 360
aacgatacca tgggtgaaaat gctgtggttt ctgcatcgtg cggaaggcaa accgcagaaa 420
cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480
accggccttc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540

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tgcccgcat	attggcgta	tggcgaaga	ggcgaaaccg	aagaacagtt	tgtcgcgcgt	600
ctggcccgtg	aactggaaga	aaccattcag	aaggaaggcg	cggataccat	tgcgggcttt	660
tttgcggaac	cggtgatggg	tgcgggcggt	gttattaccc	cgccaaaagg	ctattttcag	720
gcgattctga	ccatcctgcg	caaatatgat	attccgggtga	tcagcgatga	agtgatttgc	780
ggctttggtc	gtaccggcaa	cacctggggc	tgcgtgacct	atgattttac	cccggatgcg	840
attattagca	gtaaaaacct	aaccgcgggt	ttttttccag	taggagcggt	gatttttggg	900
ccggaactga	gcaaacgtct	ggaaaccgcg	attgaagcga	tcgaagaatt	tgatcatggt	960
tttaccacag	gcggccatcc	ggtgggttgt	gcgattgcgc	tgaaagcgat	tgatgtggtg	1020
atgaacgaag	gcctggccga	aaacgtgcgt	cgtctggccc	cgcgttttga	agaacgtctg	1080
aaacatattg	cggaacgtcc	gaacattggc	gaatatcgtg	gtattggctt	tatgtgggcg	1140
ctggaagtgg	tgaaagataa	agcgagcaaa	gccccgtttg	atggcaacct	gagcgtgagc	1200
gaacgtattg	cgaacacctg	caccgatctg	ggactgattt	gccgaccggt	gggccagagc	1260
gtggttctgg	caccgccgta	cattctgacc	gaagcgcaga	tggatgaaat	gttcgataaa	1320
ctggaaaaag	cgctggataa	agtgtttg	gcg	gaagtggcgt	aa	1362

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

<220>
 <223> Engineered variant of V. fluvialis transaminase
 <400> 148

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

Tyr	Ala	Phe	Thr	His	Met	Pro	Ser	Leu	His	Gln	Arg	Gly	Thr	Met	Val
			20					25					30		

Thr	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		

Leu	Thr	Asn	Ser	Gly	Ser	Glu	Ala	Asn	Asp	Thr	Met	Val	Lys	Met	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115

120

125

Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160

Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
 305 310 315 320

Phe Thr Thr 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 Val Val
 370 375 380

Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Ser
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<400>	149						
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gcgggctttg	atcataaagg	cctgattgat	gcggcgaaaag	cgcagtatga	acgtttttccg		240
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accggcatcc	cgtataacag	cgtgtttggc	ctgccggctc	cgggcctttct	gcatctgacc		540
tgcccgcatt	attggcggtta	tggcgaagaa	ggcgaaacccg	aagaacagtt	tgtcgcgcgt		600
ctggcccgtg	aactggaaga	aaccattcag	aagggaaggcg	cggataccat	tgccgggcttt		660
tttgccgaac	cggtgatggg	tgcgggcggt	gttattatcc	cgccaaaagg	ctatttttcag		720
gcgatttctga	ccatcctgcg	caaatatgat	attccgggtga	tcagcgatga	agtgatttgc		780
ggcttttgtc	gtaccggcaa	cacctggggc	tgcgtgacct	atgattttac	cccggatgcg		840
attatttagca	gtaaaaacct	aaccgcgggt	ttttttccag	taggagcggt	gattttgggg		900
ccggaactga	gcaaactgtc	ggaaaccgcg	attgaagcga	tcgaagaatt	tgatcatggt		960
tttaccacag	gcggccatcc	ggtgggttgt	gcgattgcgc	tgaaagcgat	tgatgtggtg		1020
atgaacgaag	gcctggccga	aaacgtgcgt	cgtctggccc	cgcgttttga	agaacgtctg		1080
aaacatatg	cggaacgtcc	gaacattggc	gaatatcgtg	gtattggctt	tatgtgggcg		1140
ctggaagccg	tgaaagataa	agcgagcaaa	gccccgtttg	atggcaacct	gagcgtgggt		1200

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gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260
gtggttctgg caccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 150
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered variant of V. fluvialis transaminase
<400> 150

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met 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 Leu 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

Leu Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
115 120 125

Trp Phe Leu His Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Gln Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Ile Pro Tyr Asn Ser Val Phe Gly Leu Pro Ala 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 Thr Pro Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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 Asp His Gly
305 310 315 320

Phe Thr Thr 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 Gly
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 Ala Pro Pro Tyr 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> Engineered variant of V. fluvialis transaminase

<400> 151

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caatgcgga gccatcata gcgtggcacc atgttgtga ccatggcga aggcccgat

120

atcgtgagt tgcattgcc tgcattatc gatgcgaaca gcggcctgt caacatgtg

180

gcgggcttg atcataaagg cctgattgat gcggcgaaag cgcagtatga acgtttccg

240

ggctacatg cgtttacgg cgtatgagc gatcagacc tgaatcctgc tgaaaaactg

300

gtggaagtga gccgttga tagcgccgt gtgtttata ccaacagcgg cagcgaagcg

360

aacgatacca tgttgaaat gctgtggtt ctcgcatctg cggaaagcga accgcaga

420

cgtaaaatc tgaccctga gaacgcgtat catgctcca ccgcgttga cgcgaagcatg

480

accggccttc cgtatacag cgtgtttgc tcgcgcctgc cggccttct gcatctgacc

540

tgcgcccat attgcgta tgcgaagaa ggcgaacgg aagaacagt tgcgcgcgt

600

ctggcccgta aactggaaga aacatcag aaggaagcg cgcataccat tgcggcctt

660

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720

gcgattctga ccatcctcga caatatgat attccggtga tcagcgtatga agtgatttc

780

ggctttgtc gtaaccgcaa cactgggc tcggtgacct atgatttac cccgattcg

840

attatagca gtaaaaact aaccgcgggt tttttccag taggaagcgt gattttgggg

900

ccggaactga gcaaacgtct ggaaccgcg atggaagcga tcgaagaaat tgatcatgt

960

tttaaccag gcggccatcc gttgggtgt gcgattgcgc tgaagcgat tgatgtgtg

1020

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1080

aaacatatg cggaaactcc gaacatggc gaatatcgt gtattggcct tatgtggcg

1140

ctggaagtgg tgaagataa agcgaagcaa gccccgttg atgcgaact gagcgtgagc

1200

gaactatg cgaacacctg caccgatctg ggaactgatt gccgaaccgt ggccagagc

1260

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1320

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1362

<210> 152

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered variant of V. fluvialis transaminase

<400> 152

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

Tyr Ala Phe Thr His Met Pro Ser Leu His Gln Arg Gly Thr Met Val
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20

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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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
130 135 140

Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
225 230 235 240

Ala Ile Leu Thr 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
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290

295

Lys Arg Leu Glu Thr Ala Ile Glu Ala Ile Glu Glu Phe Asp His Gly
305 310 315 320

Phe Thr Thr 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 Val 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 Ala Pro Pro Tyr 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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<213> Artificial Sequence

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<223> Engineered variant of V. fluvialis transaminase

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atcgtggatg tgcattggccg 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 ctgcatcgtg cggaaggcaa accgcagaaa 420
cgtaaaattc tgaccctgaa gaacgcgtat catggctcca ccgcggtgag cgcgagcatg 480

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accggccttc cgtataacag cgtgtttggc ctgccgctgc cgggctttct gcatctgacc 540
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 ctggcccgtg aactggaaga aaccattcag aaggaaggcg cggataccat tgcgggcttt 660
 tttgcggaac cggatgatggg tgcgggcggt gttattaccc cgccaaaagg ctattttcag 720
 gcgattctga ccattctgcg caaatatgat attccggtga tcagcgatga agtgatttgc 780
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 tttaccacac acggccatcc ggtgggttgt gcgattgcgc tgaaagcgat tgatgtgggt 1020
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 aaacatattg cggaacgtcc gaacattggc gaatatctg gtattggctt tatgtgggcg 1140
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 gaacgtattg cgaacacctg caccgatctg ggactgattt gccgaccgtt gggccagagc 1260
 gtggttctgg caccgccgta cattctgacc gaagcgcaga tggatgaaat gttcgataaa 1320
 ctggaaaaag cgctggataa agtgtttgcg gaagtggcgt aa 1362

<210> 154
 <211> 453
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Engineered variant of V. fluvialis transaminase
 <400> 154

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

Tyr Ala Phe Thr His Met Pro Ser Leu Arg Gln Arg Gly Thr Met 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 Arg Ala Glu Gly Lys Pro Gln Lys Arg Lys Ile Leu
 130 135 140
 Thr Leu Lys Asn Ala Tyr His Gly Ser Thr Ala Val Ser Ala Ser Met
 145 150 155 160
 Thr Gly Leu 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 Pro Lys Gly Tyr Phe Gln
 225 230 235 240
 Ala Ile Leu Thr 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 Ala 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 Asp His Gly
 305 310 315 320
 Phe Thr Thr His 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 Val Val
 370 375 380

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Lys Asp Lys Ala Ser Lys Ala Pro Phe Asp Gly Asn Leu Ser Val Gly
 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 Ala Pro Pro Tyr 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