

eolf-seq1
SEQUENCE LISTING

<110> PFIZER IRELAND PHARMACEUTICALS
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DEBARGE, SEBASTIEN
ERDMAN, DAVID THOMAS
KUMAR, RAJESH
KARMILOWICZ, MICHAEL JOHN

<120> PROCESS

<130> PC71999A

<150> US 61/805786
<151> 2013-03-27

<160> 15

<170> PatentIn version 3.5

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<212> PRT
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Tyr Gly Phe Thr Asp Met Pro Ser Leu His Xaa Arg Gly Thr Val Val
20 25 30

Val Thr His Gly Glu Gly Pro Tyr Xaa Val Asp Val Xaa 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 Ser Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95

Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110

Tyr Thr Asn Ser Gly Ser Glu Ala Asn Asp Thr Met Val Lys Met Leu
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115						120						125			
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	130					135					140				
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Thr	Gly	Xaa	Pro	Xaa	Asn	Ser	Val	Phe	Gly	Leu	Pro	Leu	Pro	Gly	Phe
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Val	His	Leu	Xaa	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
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Thr Gly Leu Pro Tyr₁₆₅ Asn Ser Val Phe Gly₁₇₀ Leu Pro Leu Pro Gly₁₇₅ Phe
Val His Leu Thr₁₈₀ Cys Pro His Tyr Trp₁₈₅ Arg Tyr Gly Glu Glu₁₉₀ Gly Glu
Thr Glu Glu₁₉₅ Gln Phe Val Ala Arg₂₀₀ Leu Ala Arg Glu Leu₂₀₅ Glu Glu Thr
Ile Gln Arg Glu Gly Ala Asp₂₁₅ Thr Ile Ala Gly Phe₂₂₀ Phe Ala Glu Pro
Val Met Gly Ala Gly Gly₂₃₀ Val Ile Pro Pro Ala₂₃₅ Lys Gly Tyr Phe Gln₂₄₀
Ala Ile Leu Pro Ile₂₄₅ Leu Arg Lys Tyr Asp₂₅₀ Ile Pro Val Ile Ser₂₅₅ Asp
Glu Val Ile Cys₂₆₀ Gly Phe Gly Arg Thr₂₆₅ Gly Asn Thr Trp Gly₂₇₀ Cys Val
Thr Tyr Asp₂₇₅ Phe Thr Pro Asp Ala₂₈₀ Ile Ile Ser Ser Lys₂₈₅ Asn Leu Thr
Ala Gly Phe Phe Pro Val Gly₂₉₅ Ala Val Ile Leu Gly₃₀₀ Pro Glu Leu Ala
Lys Arg Leu Glu Thr Ala₃₁₀ Ile Glu Ala Ile Glu₃₁₅ Glu Phe Pro His Gly₃₂₀
Phe Thr Ala Ser Gly₃₂₅ His Pro Val Gly Cys₃₃₀ Ala Ile Ala Leu Lys₃₃₅ Ala
Ile Asp Val Val₃₄₀ Met Asn Glu Gly Leu₃₄₅ Ala Glu Asn Val Arg₃₅₀ Arg Leu
Ala Pro Arg₃₅₅ Phe Glu Glu Arg Leu₃₆₀ Lys His Ile Ala Glu₃₆₅ Arg Pro Asn
Ile Gly Glu Tyr Arg Gly Ile₃₇₅ Gly Phe Met Trp Ala₃₈₀ Leu Glu Ala Val
Lys Asp Lys Ala Ser Lys₃₉₀ Thr Pro Phe Asp Gly₃₉₅ Asn Leu Ser Val Ser₄₀₀
Glu Arg Ile Ala Asn₄₀₅ Thr Cys Thr Asp Leu₄₁₀ Gly Leu Ile Cys Ser₄₁₅ Pro
Met Gly Gln Ser₄₂₀ Val Ile Leu Cys Pro₄₂₅ Pro Phe Ile Leu Thr₄₃₀ 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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<213> Artificial Sequence

<220>
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Met Asn Lys Pro Gln Ser Trp Glu Ala Arg Ala Glu Thr Tyr Ser Leu
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Tyr Gly Phe Thr Asp Met Pro Ser Leu His Glu Arg Gly Thr Val Val
20 25 30

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

Tyr Leu Asp Ala Asn Ser Gly Leu 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 Ser Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
85 90 95

Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110

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

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

Thr Arg Asn Asn Ala Tyr His Gly Val 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

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

Val Thr His Gly Glu Gly Pro Tyr Val Val Asp Val Asn 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 Ser Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu
 85 90 95

Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
 100 105 110

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

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

Thr Arg Gln Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
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Thr Gly Leu Pro His Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
 165 170 175

Val His Leu Thr Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
 180 185 190

Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
 195 200 205

Ile Gln Arg Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
 210 215 220

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

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Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255

Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270

Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285

Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300

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

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

Lys Arg Ile Ala Asn Thr Cys Gln Asp Leu Gly Leu Ile Cys Ser Ala
405 410 415

Leu Gly Gln Ser Val Ile Leu Ser Pro Pro Phe Ile Leu Thr Glu Ala
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Phe Ala Glu Val Ala
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275

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285

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

Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335

Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350

Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn
355 360 365

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

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

Lys Arg Ile Ala Asn Thr Cys Gln Asp Leu Gly Leu Ile Cys Ser Ala
405 410 415

Met Gly Gln Ser Val Ile Leu Ser Pro Pro Phe Ile Leu Thr Glu Ala
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Phe Ala Glu Val Ala
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35 40 45

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

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

Lys Arg Ile Ala Asn Thr Cys Gln Asp Leu Gly Leu Ile Cys Ala Ala
405 410 415

Met Gly Gln Ser Val Ile Leu Ser 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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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 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 Ser Phe Phe Gly Arg Met Ser Asp Gln Thr Val Met Leu

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85

90

95

Ser Glu Lys Leu Val Glu Val Ser Pro Phe Asp Ser Gly Arg Val Phe
100 105 110

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

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

Thr Arg Gln Asn Ala Tyr His Gly Val Thr Ala Val Ser Ala Ser Met
145 150 155 160

Thr Gly Leu Pro His Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
165 170 175

Val His Leu Ser Cys Pro His Tyr Trp Arg Tyr Gly Glu Glu Gly Glu
180 185 190

Thr Glu Glu Gln Phe Val Ala Arg Leu Ala Arg Glu Leu Glu Glu Thr
195 200 205

Ile Gln Arg Glu Gly Ala Asp Thr Ile Ala Gly Phe Phe Ala Glu Pro
210 215 220

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

Ala Ile Leu Pro Ile Leu Arg Lys Tyr Asp Ile Pro Val Ile Ser Asp
245 250 255

Glu Val Ile Cys Gly Phe Gly Arg Thr Gly Asn Thr Trp Gly Cys Val
260 265 270

Thr Tyr Asp Phe Thr Pro Asp Ala Ile Ile Ser Ser Lys Asn Leu Thr
275 280 285

Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
290 295 300

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

Phe Thr Ala Gly Gly His Pro Val Gly Cys Ala Ile Ala Leu Lys Ala
325 330 335

Ile Asp Val Val Met Asn Glu Gly Leu Ala Glu Asn Val Arg Arg Leu
340 345 350

Ala Pro Arg Phe Glu Glu Arg Leu Lys His Ile Ala Glu Arg Pro Asn

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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

Lys Arg Ile Ala Asn Thr Cys Gln Asp Leu Gly Leu Ile Cys Ser Ala
405 410 415

Met Gly Gln Ser Val Ile Leu Ser Pro Pro Phe 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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His Ala Ile Leu His Tyr Ser Gln Arg Ser Thr Asn Gly Gly Leu Leu
50 55 60

Ile Gly Glu Ala Thr Val Ile Ser Glu Thr Gly Ile Gly Tyr Lys Asp
65 70 75 80

Val Pro Gly Ile Trp Thr Lys Glu Gln Val Glu Ala Trp Lys Pro Ile
85 90 95

Val Asp Ala Val His Ala Lys Gly Gly Ile Phe Phe Cys Gln Ile Trp
100 105 110

His Val Gly Arg Val Ser Asn Lys Asp Phe Gln Pro Asn Gly Glu Asp
115 120 125

Pro Ile Ser Cys Thr Asp Arg Gly Leu Thr Pro Gln Ile Arg Ser Asn
130 135 140

eo1f-seq1

Gly Ile Asp Ile Ala His Phe Thr Arg Pro Arg Arg Leu Thr Thr Asp
145 150 155 160

Glu Ile Pro Gln Ile Val Asn Glu Phe Arg Val Ala Ala Arg Asn Ala
165 170 175

Ile Glu Ala Gly Phe Asp Gly Val Glu Ile His Gly Ala His Gly Tyr
180 185 190

Leu Ile Asp Gln Phe Met Lys Asp Gln Val Asn Asp Arg Ser Asp Lys
195 200 205

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

Glu Ala Val Ala Asn Glu Ile Gly Ser Asp Arg Val Gly Ile Arg Ile
225 230 235 240

Ser Pro Phe Ala His Tyr Asn Glu Ala Gly Asp Thr Asn Pro Thr Ala
245 250 255

Leu Gly Leu Tyr Met Val Glu Ser Leu Asn Lys Tyr Asp Leu Ala Tyr
260 265 270

Cys His Val Val Glu Pro Arg Met Lys Thr Ala Trp Glu Lys Ile Glu
275 280 285

Cys Thr Glu Ser Leu Val Pro Met Arg Lys Ala Tyr Lys Gly Thr Phe
290 295 300

Ile Val Ala Gly Gly Tyr Asp Arg Glu Asp Gly Asn Arg Ala Leu Ile
305 310 315 320

Glu Asp Arg Ala Asp Leu Val Ala Tyr Gly Arg Leu Phe Ile Ser Asn
325 330 335

Pro Asp Leu Pro Lys Arg Phe Glu Leu Asn Ala Pro Leu Asn Lys Tyr
340 345 350

Asn Arg Asp Thr Phe Tyr Thr Ser Asp Pro Ile Val Gly Tyr Thr Asp
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Tyr Pro Phe Leu Glu Thr Met Thr
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aaaaccgcct gggaaaagat tgagtgcacc gaaagcctgg tgccgatgcg taaagcctac	900
aaaggcacct tcatcgtagc tgggtggctac gaccgtgaag acggttaaccg cgctctgac	960
gaagaccgtg ccgacctggt tgcgtacggc cgtctgttca tcagcaaccc agacctgccg	1020
aagcgttttg aactgaacgc tccgctgaac aaatacaacc gtgacacttt ctacacttcc	1080
gacccgatcg ttggttacac cgattaccg tttctggaaa ctatgactta ataa	1134

<210> 10
 <211> 1362
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Modification of *Vibrio fluvialis* enzyme

<400> 10	
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atcgtggacg tcaacggtcg ccgttacctg gacgcaaact cgggcctgta caatatgggt	180
gccggcttcg accacaaggg tctgatcgac gcagcaaagg cccagtacga acgcttccc	240
ggttaccata gcttcttcg tctgtatgtc gatcaaactg ttatgctgag cgagaaactg	300
gtagagggtg ctccattcga cagcggtcgc gtgttctata ctaactccg ctccgaggct	360
aacgatacta tggtgaaaat gctgtggttt ctgcacgccg cagagggcaa gccgcaaaaa	420
cgaaaaatcc tgactcgtaa caacgcatac cagggtgtaa ctgctgtttc cgcttccatg	480
acgggtctgc cgtacaactc tgtattcggc ctgccgtgc cgggtttcgt tcacctgacc	540
tgtccgcact attggcgtaa cggcgaagaa ggtgaaaccg aagagcagtt tgttgctcgt	600

eof-seq1

ctggccccgcg agctggagga aactatccaa cgtgaaggcg cggacacgat tgcgggcttc	660
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gttatcctgt gcccgccgtt catcctgacc gaggcgcaaa tggatgagat gtttgacaaa	1320
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<210> 11
 <211> 1362
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Modification of *Vibrio fluvialis* enzyme

<400> 11	
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atcgtggacg tcaacggtcg ccgttacctg gacgcaaact cccgcctgta caatatggtt	180
gccggcttcg accacaaggg tctgatcgac gcagcaaagg cccagtacga acgcttcccg	240
ggttaccata gcttcttcgg tcgtatgtct gatcaaactg ttatgctgag cgagaaactg	300
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aacgatacta tggtgaaaat gctgtggttt ctgcacgccg cagagggcaa gccgcaaaaa	420
cgcaaaatcc tgactcgtaa caacgcatac cagggtgtaa ctgctgtttc cgcttccatg	480
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tgtccgcact attggcgta cggcgaagaa ggtgaaaccg aagagcagtt tgttgctcgt	600
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eof-seq1

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<210> 12
 <211> 1362
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Modification of *Vibrio fluvialis* enzyme

<400> 12		
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gtggtggacg tcaacggtcg	ccgttacctg gacgcaaact	ccggcctgta caatatgggt 180
gccggcttcg accacaagg	tctgatcgac gcagcaaagg	cccagtagca acgcttccc 240
ggttaccata gcttcttcgg	tcgtatgtct gatcaaactg	ttatgctgag cgagaaactg 300
gtagagggtg ctccattcga	cagcggctgc gtgttctata	ctaactccgg ctccgaggct 360
aacgatacta tgggtgaaaat	gctgtgggtt ctgcacgccg	cagagggcaa gccgcaaaaa 420
cgcaaaatcc tgactcgta	aaacgcatac caggtgttaa	ctgctgtttc cgcttccatg 480
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gttatcctga gcccgccgtt	catcctgacc gaggcgcaaa	tggatgagat gtttgacaaa 1320

eolf-seq1

ctggagaagg ctctggacaa agtctttgcg gaggtggcgt aa 1362

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

<220>
 <223> Modification of *Vibrio fluvialis* enzyme

<400> 13
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 atcgtggacg tcaacggtcg ccgttacctg gacgcaaact ccggcctgta caatatgggt 180
 gccggcttcg accacaaggg tctgatcgac gcagcaaagg ccagtacga acgcttcccg 240
 gggtaccata gcttcttcgg tcgtatgtct gatcaaactg ttatgctgag cgagaaactg 300
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 aacgatacta tgggtgaaaat gctgtggttt ctgcacgccg cagagggcaa gccgcaaaaa 420
 cgcaaaatcc tgactcgtca aaacgcatac cacggtgtaa ctgctgtttc cgcttccatg 480
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<210> 14
 <211> 1362
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Modification of *Vibrio fluvialis* enzyme

<400> 14

eof-seq1

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gtggtggacg tcaacggtcg ccgttacctg gacgcaaact ccggcctgta caatatggtt	180
gccggcttcg accacaaggg tctgatcgac gcagcaaagg cccagtacga acgcttccc	240
ggttaccata gcttcttcgg tcgtatgtct gatcaaactg ttatgctgag cgagaaactg	300
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aacgatacta tgggtgaaaat gctgtggttt ctgcacgccg cagagggcaa gccgcaaaaa	420
cgcaaaatcc tgactcgtca aaacgcatac cacggtgtaa ctgctgtttc cgcttccatg	480
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ctggagaagg ctctggacaa agtctttgcg gaggtggcgt aa	1362

<210> 15

<211> 1362

<212> DNA

<213> Artificial Sequence

<220>

<223> Modification of *Vibrio fluvialis* enzyme

<400> 15

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atcgtggacg tccacggtcg ccgttacctg gacgcaaact ccggcctgta caatatggtt	180
gccggcttcg accacaaggg tctgatcgac gcagcaaagg cccagtacga acgcttccc	240
ggttaccata gcttcttcgg tcgtatgtct gatcaaactg ttatgctgag cgagaaactg	300
gtagagggtg ctccattcga cagcggtcgc gtgttctata ctaactccgg ctccgaggct	360

eol-f-seq1						
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cgcaaaatcc	tgactcgtca	aaacgcatac	cacggtgtaa	ctgctgtttc	cgcttccatg	480
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