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SEQUENCE LISTING

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

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

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<170> PatentIn version 3.5

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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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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 Gly₂₉₀ Phe Phe Pro Val Gly₂₉₅ Ala Val Ile Leu Gly₃₀₀ Pro Glu Leu Ala
Lys₃₀₅ 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 Gly₃₇₀ Glu Tyr Arg Gly Ile₃₇₅ Gly Phe Met Trp Ala₃₈₀ Leu Glu Ala Val
Lys₃₈₅ 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
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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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195

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205

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 Val Met Gly Ala Gly Gly Val Ile Pro Pro Ala Lys Gly Tyr Phe Gln
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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
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 Ala Gly Phe Phe Pro Val Gly Ala Val Ile Leu Gly Pro Glu Leu Ser
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Tyr Leu Asp Ala Asn Ser Gly Leu Tyr Asn Met Val Ala Gly Phe Asp
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His Lys Gly Leu Ile Asp Ala Ala Lys Ala Gln Tyr Glu Arg Phe Pro
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Gly Tyr His Ser 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
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Thr Gly Leu Pro His Asn Ser Val Phe Gly Leu Pro Leu Pro Gly Phe
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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
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260 265 270

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

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

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

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

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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
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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
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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
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eolf-seq1

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gtgccgggta	tctggacgaa	agagcagggt	gaggcctgga	aaccgatcgt	cgacgcgggtg	300
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gattttcagc	cgaacggcga	agatccgatt	tcctgtactg	accgcggcct	gaccccgag	420
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<210> 10
 <211> 1362
 <212> DNA
 <213> Artificial Sequence

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

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ggttaccata	gcttcttcg	tcgtatgtct	gatcaaactg	ttatgctgag	cgagaaactg	300
gtagagggtg	ctccattcga	cagcggtcgc	gtgttctata	ctaactccgg	ctccgaggct	360
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eof-seq1

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

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

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gccggcttcg accacaaggg tctgatcgac gcagcaaagg cccagtacga acgcttcccg	240
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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

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gtggtggacg tcaacggtcg	ccgttacctg gacgcaaact	ccggcctgta caatatgggtt 180
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eolf-seq1

ctggagaagg ctctggacaa agtctttgcg gaggtggcgt aa 1362

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

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

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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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<210> 15

<211> 1362

<212> DNA

<213> Artificial Sequence

<220>

<223> Modification of *Vibrio fluvialis* enzyme

<400> 15

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gccggcttcg accacaaggg tctgatcgac gcagcaaagg ccagtacga acgcttccc	240
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eol-f-seq1						
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