

OPA18597-Sequence listing

<110> CJ CheilJedang Corporation
 <120> Novel polypeptide and method of producing IMP using the same
 <130> OPA18597
 <150> KR10-2017-0173505
 <151> 2017-12-15
 <160> 154
 <170> KoPatentIn 3.0
 <210> 1
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 Arg Ile Glu Asp Ala Ala Thr Arg Leu Val Asp Glu Ser Ser Phe Asp
 35 40 45
 Lys Val Thr Ile Glu Glu Ile Cys Glu Ala Ala Gly Ile Ser Arg Arg
 50 55 60
 Thr Phe Phe Asn Tyr Phe Ser Thr Lys Glu Ser Ala Val Ile Gly Ala
 65 70 75 80
 Ser Ser Glu Pro Leu Thr Glu Lys Gln Arg Asn Asp Phe Leu Asn Ala
 85 90 95
 Asp Ala Ser Asn Leu Leu Gln Leu Met Val Glu Gln Ile Lys Gln His
 100 105 110
 Leu Glu Ser Ser His Gln Ser Gln Ala Ile His Asp Arg Arg Gln Arg
 115 120 125
 Ile Phe Ala Asp Pro Asp Val Ala Val Arg Ala Met Ala Phe Arg Lys
 130 135 140
 Glu Arg Ser Arg Glu Thr Met Glu Leu Ile Ala Gln Arg Leu Arg Glu
 145 150 155 160
 His Pro Glu Glu Gln Arg Ala Pro Glu Leu Asp Pro Glu Thr Glu Ala
 165 170 175
 Met Leu Leu Ser Gly Phe Ile Arg Glu Ala Thr Trp Met Ala Ile Ser
 180 185 190
 Arg Pro Asp Arg Asp Cys Ala Leu Pro Val Gly Asp Arg Ile Tyr Arg
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OPA18597-Sequence listing

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

OPA18597-Sequence listing

Ala Ala Ile Ala Ile Thr Thr Ser Thr Leu Ile Leu Leu Thr Thr Trp
245 250 255

Gly Gly Ser Glu Tyr Glu Trp Thr Ser Pro Thr Ile Leu Ser Met Ala
260 265 270

Ala Val Val Ile Val Gly Ala Leu Leu Thr Val Phe Ile Glu Ser Arg
275 280 285

Ala Ser Gln Pro Leu Ile Pro Val Gln Leu Phe Lys Asn Arg Asn Met
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Val Leu Thr Thr Leu Ala Gly Thr Val Leu Gly Leu Ala Met Met Gly
305 310 315 320

Val Leu Gly Tyr Met Pro Thr Tyr Leu Gln Met Val His Thr Leu Thr
325 330 335

Pro Thr Glu Ala Gly Leu Met Met Ile Pro Met Met Val Gly Met Ile
340 345 350

Gly Val Ser Thr Gly Val Gly Phe Ile Ile Ala Lys Thr Gly Asn Tyr
355 360 365

Lys Tyr Tyr Pro Ile Ala Gly Leu Ala Ile Thr Ala Phe Ala Leu Trp
370 375 380

Trp Met Ser Gln Met Thr Val Glu Thr Ser Leu Thr Gly Ile Gly Val
385 390 395 400

Arg Phe Leu Val Phe Gly Val Gly Leu Gly Phe Val Met Gln Val Leu
405 410 415

Val Leu Ile Val Gln Asn Ser Phe Pro Val Ser Gln Val Gly Thr Ala
420 425 430

Thr Ala Ala Asn Asn Phe Phe Arg Gln Ile Gly Ser Ala Leu Gly Ala
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Ser Ile Val Gly Ser Met Phe Ile His Asn Met Gln Asn Glu Met Ala
450 455 460

Thr Arg Leu Pro Asp Ala Leu Ala Ser Leu Gly Lys Glu Gly Ala Ala
465 470 475 480

Ile Ser Gln Gln Phe Gln Gly Ala Asp Ala Ala Asn Ser Leu Thr Pro
485 490 495

His Ala Val Ala Glu Leu Pro Asp Val Leu Arg Asp Ala Ile Leu Asn
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Ser Tyr Asn Asp Gly Leu Thr Pro Val Ile Gly Met Met Val Pro Leu
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OPA18597-Sequence listing

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 attccccgac gcacctttt taattattc agcacgaaag aaagcgccgt tattggcgcg 240
 tcctcggaac cgttgacgga aaagcaacgc aatgacttct tgaatgctga cgccagcaat 300
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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
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 accggacgtg caatccaggg ctccggtgcc ggcatcatga tgatttctc gcagtcgatt 480

OPA18597-Sequence listing

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OPA18597-Sequence listing

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OPA18597-Sequence listing

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OPA18597-Sequence listing

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OPA18597-Sequence listing

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OPA18597-Sequence listing

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OPA18597-Sequence listing

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OPA18597-Sequence listing

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OPA18597-Sequence listing

gagcatcctg aattccaacg cgcccca 27

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OPA18597-Sequence listing

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OPA18597-Sequence listing

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OPA18597-Sequence listing

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<210> 80
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<210> 81
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OPA18597-Sequence listing

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OPA18597-Sequence listing

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<400> 90

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OPA18597-Sequence listing

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OPA18597-Sequence listing

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<400> 101
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<210> 102
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OPA18597-Sequence listing

<210> 105
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OPA18597-Sequence listing

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OPA18597-Sequence listing

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OPA18597-Sequence listing

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<210> 129
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OPA18597-Sequence listing

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OPA18597-Sequence listing

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<400> 138
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<210> 139
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<210> 140
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<400> 140
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<210> 141
 <211> 221
 <212> PRT
 <213> Unknown

<220>
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 Gly Ser Asp Leu Gly Leu Arg Glu Gln Lys Arg Leu Ala Thr Lys His
 20 25 30
 Arg Ile Glu Asp Ala Ala Thr Arg Leu Val Asp Glu Ser Ser Phe Asp
 35 40 45
 Lys Val Thr Ile Glu Glu Ile Cys Glu Ala Ala Gly Ile Ser Arg Arg

OPA18597-Sequence listing

50 55 60
 Thr Phe Phe Asn Tyr Phe Ser Thr Lys Glu Ser Ala Val Ile Gly Ala
 65 70 75 80
 Ser Ser Glu Pro Leu Thr Glu Lys Gln Arg Asn Asp Phe Leu Asn Ala
 85 90 95
 Asp Ala Ser Asn Leu Leu Gln Leu Met Val Glu Gln Ile Lys Gln His
 100 105 110
 Leu Glu Ser Ser His Gln Ser Gln Ala Ile His Asp Arg Arg Gln Arg
 115 120 125
 Ile Phe Ala Asp Pro Asp Val Ala Val Arg Ala Met Ala Phe Arg Lys
 130 135 140
 Glu Arg Ser Arg Glu Thr Met Glu Leu Ile Ala Gln Arg Leu Arg Glu
 145 150 155 160
 His Pro Glu Lys Gln Arg Ala Pro Glu Leu Asp Pro Glu Thr Glu Ala
 165 170 175
 Met Leu Leu Ser Gly Phe Ile Arg Glu Ala Thr Trp Met Ala Ile Ser
 180 185 190
 Arg Pro Asp Arg Asp Cys Ala Leu Pro Val Gly Asp Arg Ile Tyr Arg
 195 200 205
 Ala Met Glu Leu Val Lys Asn Tyr Thr Lys Gly Leu Glu
 210 215 220

<210> 142
 <211> 549
 <212> PRT
 <213> Unknown

<220>
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<400> 142
 Met Ile Ala Lys Asn Ser Thr Pro Ser Thr Ala Gly His Ala Ser Ala
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 His Thr Ala Glu Glu Phe Pro Val Ala Asn Ala Glu Met Ala Thr Pro
 20 25 30
 Ser Ala Ile Asp Pro Asn His Gly Lys Lys Thr Ala Asp Asn Val Gly
 35 40 45
 Ile Ile Phe Ala Ala Leu Met Leu Thr Met Leu Met Ser Ser Leu Glu
 50 55 60
 Gln Met Ile Phe Gly Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly
 65 70 75 80
 Gly Val Asp Gln Met Ser Trp Val Ile Ser Ala Phe Met Val Thr Met
 85 90 95

OPA18597-Sequence listing

Thr Ile Ala Met Pro Leu Ala Gly Gln Leu Gly Asp Arg Met Gly Arg
100 105 110

Lys Trp Val Tyr Ile Ser Gly Ile Ser Ile Phe Val Ile Gly Ser Thr
115 120 125

Leu Gly Gly Phe Ala Asn Gly Met Gly Met Leu Ile Thr Gly Arg Ala
130 135 140

Ile Gln Gly Phe Gly Ala Gly Ile Met Met Ile Ser Ser Gln Ser Ile
145 150 155 160

Val Ala Glu Val Val Ser Ala Arg Glu Arg Gly Lys Phe Met Gly Ile
165 170 175

Met Gly Gly Val Phe Gly Val Ser Ser Val Leu Gly Pro Val Leu Gly
180 185 190

Gly Trp Phe Thr Asp Gly Pro Gly Trp Arg Trp Gly Leu Trp Ile Asn
195 200 205

Ile Pro Leu Gly Leu Leu Ala Ile Ile Val Cys Ala Phe Val Leu Lys
210 215 220

Leu Arg Val Gly Glu Gln Gly Phe Lys Gly Phe Asp Trp Met Gly Phe
225 230 235 240

Ala Ala Ile Ala Ile Thr Thr Ser Thr Leu Ile Leu Leu Thr Thr Trp
245 250 255

Gly Gly Ser Glu Tyr Glu Trp Thr Ser Pro Thr Ile Leu Ser Met Ala
260 265 270

Ala Val Val Ile Val Gly Ala Leu Leu Thr Val Phe Ile Glu Ser Arg
275 280 285

Ala Ser Gln Pro Leu Ile Pro Val Gln Leu Phe Lys Asn Arg Asn Met
290 295 300

Val Leu Thr Thr Leu Ala Gly Thr Val Leu Gly Leu Ala Met Met Gly
305 310 315 320

Val Leu Gly Tyr Met Pro Thr Tyr Leu Gln Met Val His Thr Leu Thr
325 330 335

Pro Thr Glu Ala Gly Leu Met Met Ile Pro Met Met Val Gly Met Ile
340 345 350

Gly Val Ser Thr Gly Val Gly Phe Ile Ile Ala Lys Thr Gly Asn Tyr
355 360 365

Lys Tyr Tyr Pro Ile Ala Gly Leu Ala Ile Thr Ala Phe Ala Leu Trp
370 375 380

Trp Met Ser Gln Met Thr Val Glu Thr Ser Leu Thr Gly Ile Gly Val
385 390 395 400

Arg Phe Leu Val Phe Gly Val Gly Leu Gly Phe Val Met Gln Val Leu
405 410 415

Val Leu Ile Val Gln Asn Ser Phe Pro Val Ser Gln Val Gly Thr Ala

OPA18597-Sequence listing

420 425 430
 Thr Ala Ala Asn Asn Phe Phe Arg Gln Ile Gly Ser Ala Leu Gly Ala
 435 440 445
 Ser Ile Val Gly Ser Met Phe Ile His Asn Met Gln Asn Glu Met Ala
 450 455 460
 Thr Arg Leu Pro Asp Ala Leu Ala Ser Leu Gly Lys Glu Gly Ala Ala
 465 470 475 480
 Ile Ser Gln Gln Phe Gln Gly Ala Asp Ala Ala Asn Ser Leu Thr Pro
 485 490 495
 His Ala Val Ala Glu Leu Pro Asp Val Leu Arg Asp Ala Ile Leu Asn
 500 505 510
 Ser Tyr Asn Asp Gly Leu Thr Pro Val Ile Gly Met Met Val Pro Leu
 515 520 525
 Ala Ile Val Ala Met Leu Ile Leu Phe Pro Leu Arg Gln Glu Arg Leu
 530 535 540
 Lys Glu Thr Ile Glu
 545

<210> 143
 <211> 669
 <212> DNA
 <213> Unknown

<220>
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 ttggttgatg aatcgagctt tgacaaagta acaattgaag aaatttgca agccgccggg 180
 atttcccgac gcacctttt taattatttc agcacgaaag aaagcgccgt tattggcgcg 240
 tcctcggaac cggtgacgga aaagcaacgc aatgacttct tgaatgctga cgccagcaat 300
 ctctgcagc tgatgggtga gcagatcaaa caacacttgg agtcttctca ccagagtcaa 360
 gcgattcacg accgtcgtca gcgaatcttt gcggatccgg atgtcgcggt acgtgcaatg 420
 gcgtttcgca aggaacgctc acgggaaacc atggagctaa tcgctcaacg tcttcgggag 480
 catcctgaaa aacaacgcgc cccagaattg gatccggaag cagaggcgat gctgctgagc 540
 ggattcattc gcgaagccac ctggatggct atctcacgac ccgatcgtga ttgtgactg 600
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 gaatgatag 669

OPA18597-Sequence listing

<210> 144
<211> 1650
<212> DNA
<213> Unknown

<220>
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aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
agctctttgg agcagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300
ccactagccg gtcagctcgg tgaccgcatg ggccgcaagt ggggtctacat ctcaggtatc 360
tccattttcg ttattggctc gacgctcggt ggctttgccaa atggcatggg catgctgac 420
accggacgtg caatccaggg ctccggtgcc ggcatcatga tgattcctc gcagtcgatt 480
gtggctgagg ttgtctccgc acgtgagcgc ggcaagtcca tgggtattat gggcggcgctc 540
tttggcgtct cctccgtact ggggccagtt ctcggtggct gggtcaccga tgggtccggt 600
tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
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gcggccatcg caatcacgac cagcaccttg attctgctca ccacttgggg cggaagcgaa 780
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aaccgcaaca tggttttgac caccctcgcc ggtactgttt tgggtctggc catgatgggc 960
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aatgagatgg ctaccggttt gcctgatgcc ctgcatcgt tgggcaagga aggcgcgct 1440
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OPA18597-Sequence listing

gagcttcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc 1560
 gtgattggca tgatgggtgcc actggccatt gttgcaatgc tgattttgtt cccactgcgc 1620
 caagagcgct tgaaggaaac catcgaataa 1650

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 <211> 222
 <212> PRT
 <213> Unknown

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

OPA18597-Sequence listing

<210> 146
<211> 669
<212> DNA
<213> Unknown

<220>
<223> ImpE1 NT-164K

<400> 146
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gggtaaggg agcagaagcg attggcaacc aagcatcgca tcgaagacgc cgcgacacgg 120
ttggttgatg aatcgagctt tgacaaagta acaattgaag aaatttgca agccgccggg 180
attccccgac gcacctttt taattattc agcacgaaag aaagcgccgt tattggcgcg 240
tcctcggaac cgttgacgga aaagcaacgc aatgacttct tgaatgctga cgccagcaat 300
ctcctgcagc tgatgggtga gcagatcaaa caacacttgg agtcttctca ccagagtcaa 360
gcgattcacg accgtcgtca gcgaatctt gcggatccgg atgtcgcggt acgtgcaatg 420
gcgttcgca aggaacgctc acgggaaacc atggagctaa tcgctcaacg tcttcgggag 480
catcctgaaa aacaacgcgc cccagaattg gatccggaaa cagaggcgat gctgctgagc 540
ggattcattc gcgaagccac ctggatggct atctcacgac ccgatcgtga ttgtgactg 600
ccagtgggtg accgcatcta tcgcgcgatg gaattggtaa agaattacac gaaaggactg 660
gaatggtag 669

<210> 147
<211> 549
<212> PRT
<213> Unknown

<220>
<223> ImpE2 - V2I

<400> 147
Met Ile Ala Lys Asn Ser Thr Pro Ser Thr Ala Gly His Ala Ser Ala
1 5 10 15
His Thr Ala Glu Glu Phe Pro Val Ala Asn Ala Glu Met Ala Thr Pro
20 25 30
Ser Ala Ile Asp Pro Asn His Gly Lys Lys Thr Ala Asp Asn Val Gly
35 40 45
Ile Ile Phe Ala Ala Leu Met Leu Thr Met Leu Met Ser Ser Leu Gly
50 55 60
Gln Met Ile Phe Gly Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly
65 70 75 80

OPA18597-Sequence listing

Gly Val Asp Gln Met Ser Trp Val Ile Ser Ala Phe Met Val Thr Met
85 90 95

Thr Ile Ala Met Pro Leu Ala Gly Gln Leu Gly Asp Arg Met Gly Arg
100 105 110

Lys Trp Val Tyr Ile Ser Gly Ile Ser Ile Phe Val Ile Gly Ser Thr
115 120 125

Leu Gly Gly Phe Ala Asn Gly Met Gly Met Leu Ile Thr Gly Arg Ala
130 135 140

Ile Gln Gly Phe Gly Ala Gly Ile Met Met Ile Ser Ser Gln Ser Ile
145 150 155 160

Val Ala Glu Val Val Ser Ala Arg Glu Arg Gly Lys Phe Met Gly Ile
165 170 175

Met Gly Gly Val Phe Gly Val Ser Ser Val Leu Gly Pro Val Leu Gly
180 185 190

Gly Trp Phe Thr Asp Gly Pro Gly Trp Arg Trp Gly Leu Trp Ile Asn
195 200 205

Ile Pro Leu Gly Leu Leu Ala Ile Ile Val Cys Ala Phe Val Leu Lys
210 215 220

Leu Arg Val Gly Glu Gln Gly Phe Lys Gly Phe Asp Trp Met Gly Phe
225 230 235 240

Ala Ala Ile Ala Ile Thr Thr Ser Thr Leu Ile Leu Leu Thr Thr Trp
245 250 255

Gly Gly Ser Glu Tyr Glu Trp Thr Ser Pro Thr Ile Leu Ser Met Ala
260 265 270

Ala Val Val Ile Val Gly Ala Leu Leu Thr Val Phe Ile Glu Ser Arg
275 280 285

Ala Ser Gln Pro Leu Ile Pro Val Gln Leu Phe Lys Asn Arg Asn Met
290 295 300

Val Leu Thr Thr Leu Ala Gly Thr Val Leu Gly Leu Ala Met Met Gly
305 310 315 320

Val Leu Gly Tyr Met Pro Thr Tyr Leu Gln Met Val His Thr Leu Thr
325 330 335

Pro Thr Glu Ala Gly Leu Met Met Ile Pro Met Met Val Gly Met Ile
340 345 350

Gly Val Ser Thr Gly Val Gly Phe Ile Ile Ala Lys Thr Gly Asn Tyr
355 360 365

Lys Tyr Tyr Pro Ile Ala Gly Leu Ala Ile Thr Ala Phe Ala Leu Trp
370 375 380

Trp Met Ser Gln Met Thr Val Glu Thr Ser Leu Thr Gly Ile Gly Val
385 390 395 400

Arg Phe Leu Val Phe Gly Val Gly Leu Gly Phe Val Met Gln Val Leu

OPA18597-Sequence listing

405 410 415
Val Leu Ile Val Gln Asn Ser Phe Pro Val Ser Gln Val Gly Thr Ala
420 425 430
Thr Ala Ala Asn Asn Phe Phe Arg Gln Ile Gly Ser Ala Leu Gly Ala
435 440 445
Ser Ile Val Gly Ser Met Phe Ile His Asn Met Gln Asn Glu Met Ala
450 455 460
Thr Arg Leu Pro Asp Ala Leu Ala Ser Leu Gly Lys Glu Gly Ala Ala
465 470 475 480
Ile Ser Gln Gln Phe Gln Gly Ala Asp Ala Ala Asn Ser Leu Thr Pro
485 490 495
His Ala Val Ala Glu Leu Pro Asp Val Leu Arg Asp Ala Ile Leu Asn
500 505 510
Ser Tyr Asn Asp Gly Leu Thr Pro Val Ile Gly Met Met Val Pro Leu
515 520 525
Ala Ile Val Ala Met Leu Ile Leu Phe Pro Leu Arg Gln Glu Arg Leu
530 535 540
Lys Glu Thr Ile Glu
545

<210> 148
<211> 1650
<212> DNA
<213> Unknown

<220>
<223> ImpE2 NT - V2I

<400> 148
atgatagcta aaaactccac cccaagcacg gccggccacg ccagtgtca cactgcggaa 60
gaattcccag tggccaatgc tgaatggca acgccttcag caatcgaccc aaaccacggt 120
aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
agctctttgg ggcagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300
ccactagccg gtcagctcgg tgaccgcatg ggccgcaagt ggggtctacat ctgaggtatc 360
tccattttcg ttattggctc gacgctcggg ggctttgccca atggcatggg catgctgac 420
accggacgtg caatccaggg ctccggtgcc ggcatcatga tgatttcctc gcagtcgatt 480
gtggctgagg ttgtctccgc acgtgagcgc ggcaagtcca tgggtattat gggcggcgctc 540
tttggcgtct cctccgtact ggggtccagtt ctcggtggct gggtcaccga tgggtccggt 600
tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660

OPA18597-Sequence listing

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 gcggccatcg caatcacgac cagcaccctg attctgctca ccactgggg cggaagcgaa 780
 tacgagtga cttcccaac tttttgtcc atggctgcc tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
 aaccgcaaca tggtttgac caccctcgcc ggtactgttt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgag atgggtgcaca ccctgacgcc aactgaagca 1020
 ggcttgatga tgatcccgat gatggtcggc atgatcgggtg tctccactgg tgttggttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcgt cgggcctggc catcacggcg 1140
 ttgctttgt ggtggatgtc ccagatgacc gttgagactt cattgaccgg tatcgagatt 1200
 cgcttccttg tttcgggtgt cggcttgggc tttgtcatgc aggtactggg gctgattgtt 1260
 caaaactcct tccctgtatc gcaggtcggg actgccacgg cggctaataa cttcttcgc 1320
 cagattggtt cggcattggg tgcttcatc gtgggttcga tgttcattca caatatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc ctgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagctcccg atgtctccg tgacgctatc taaattcct acaatgacgg tctgaccccc 1560
 gtgattggca tgatgggtgcc actggccatt gttgcaatgc tgattttgtt cccactgcgc 1620
 caagagcgct tgaaggaaac catcgaataa 1650

<210> 149
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> ImpE2 - G64E

<400> 149
 Met Val Ala Lys Asn Ser Thr Pro Ser Thr Ala Gly His Ala Ser Ala
 1 5 10 15
 His Thr Ala Glu Glu Phe Pro Val Ala Asn Ala Glu Met Ala Thr Pro
 20 25 30
 Ser Ala Ile Asp Pro Asn His Gly Lys Lys Thr Ala Asp Asn Val Gly
 35 40 45
 Ile Ile Phe Ala Ala Leu Met Leu Thr Met Leu Met Ser Ser Leu Glu
 50 55 60
 Gln Met Ile Phe Gly Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly
 65 70 75 80

OPA18597-Sequence listing

Gly Val Asp Gln Met Ser Trp Val Ile Ser Ala Phe Met Val Thr Met
85 90 95

Thr Ile Ala Met Pro Leu Ala Gly Gln Leu Gly Asp Arg Met Gly Arg
100 105 110

Lys Trp Val Tyr Ile Ser Gly Ile Ser Ile Phe Val Ile Gly Ser Thr
115 120 125

Leu Gly Gly Phe Ala Asn Gly Met Gly Met Leu Ile Thr Gly Arg Ala
130 135 140

Ile Gln Gly Phe Gly Ala Gly Ile Met Met Ile Ser Ser Gln Ser Ile
145 150 155 160

Val Ala Glu Val Val Ser Ala Arg Glu Arg Gly Lys Phe Met Gly Ile
165 170 175

Met Gly Gly Val Phe Gly Val Ser Ser Val Leu Gly Pro Val Leu Gly
180 185 190

Gly Trp Phe Thr Asp Gly Pro Gly Trp Arg Trp Gly Leu Trp Ile Asn
195 200 205

Ile Pro Leu Gly Leu Leu Ala Ile Ile Val Cys Ala Phe Val Leu Lys
210 215 220

Leu Arg Val Gly Glu Gln Gly Phe Lys Gly Phe Asp Trp Met Gly Phe
225 230 235 240

Ala Ala Ile Ala Ile Thr Thr Ser Thr Leu Ile Leu Leu Thr Thr Trp
245 250 255

Gly Gly Ser Glu Tyr Glu Trp Thr Ser Pro Thr Ile Leu Ser Met Ala
260 265 270

Ala Val Val Ile Val Gly Ala Leu Leu Thr Val Phe Ile Glu Ser Arg
275 280 285

Ala Ser Gln Pro Leu Ile Pro Val Gln Leu Phe Lys Asn Arg Asn Met
290 295 300

Val Leu Thr Thr Leu Ala Gly Thr Val Leu Gly Leu Ala Met Met Gly
305 310 315 320

Val Leu Gly Tyr Met Pro Thr Tyr Leu Gln Met Val His Thr Leu Thr
325 330 335

Pro Thr Glu Ala Gly Leu Met Met Ile Pro Met Met Val Gly Met Ile
340 345 350

Gly Val Ser Thr Gly Val Gly Phe Ile Ile Ala Lys Thr Gly Asn Tyr
355 360 365

Lys Tyr Tyr Pro Ile Ala Gly Leu Ala Ile Thr Ala Phe Ala Leu Trp
370 375 380

Trp Met Ser Gln Met Thr Val Glu Thr Ser Leu Thr Gly Ile Gly Val
385 390 395 400

Arg Phe Leu Val Phe Gly Val Gly Leu Gly Phe Val Met Gln Val Leu

OPA18597-Sequence listing

405 410 415
Val Leu Ile Val Gln Asn Ser Phe Pro Val Ser Gln Val Gly Thr Ala
420 425 430
Thr Ala Ala Asn Asn Phe Phe Arg Gln Ile Gly Ser Ala Leu Gly Ala
435 440 445
Ser Ile Val Gly Ser Met Phe Ile His Asn Met Gln Asn Glu Met Ala
450 455 460
Thr Arg Leu Pro Asp Ala Leu Ala Ser Leu Gly Lys Glu Gly Ala Ala
465 470 475 480
Ile Ser Gln Gln Phe Gln Gly Ala Asp Ala Ala Asn Ser Leu Thr Pro
485 490 495
His Ala Val Ala Glu Leu Pro Asp Val Leu Arg Asp Ala Ile Leu Asn
500 505 510
Ser Tyr Asn Asp Gly Leu Thr Pro Val Ile Gly Met Met Val Pro Leu
515 520 525
Ala Ile Val Ala Met Leu Ile Leu Phe Pro Leu Arg Gln Glu Arg Leu
530 535 540
Lys Glu Thr Ile Glu
545

<210> 150
<211> 1650
<212> DNA
<213> Unknown

<220>
<223> ImpE2 NT - G64E

<400> 150
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gaattcccag tggccaatgc tgaatggca acgccttcag caatcgaccc aaaccacggt 120
aaaaagaccg cggataacgt cggcattatc ttgctgcct tgatgtcac catgtgatg 180
agctctttgg agcagatgat ttcggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300
ccactagccg gtcagctcgg tgaccgcatg ggccgcaagt ggggtctacat ctgaggtatc 360
tcattttcg ttattggctc gacgctcggg ggctttgcc aatggcatggg catgctgac 420
accggacgtg caatccaggg ctccggtgcc ggcatcatga tgatttcctc gcagtcgatt 480
gtggctgagg ttgtctccgc acgtgagcgc ggcaagtcca tgggtattat gggcggcgctc 540
tttggcgtct cctccgtact ggggtccagtt ctcggtggct gggtcaccga tgggtccggt 600
tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660

OPA18597-Sequence listing

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ttcgactga agctgcgcgt gggcgagcaa ggcttaagg gcttgactg gatgggttt 720
gcggccatcg caatcacgac cagcaccctg attctgctca ccactgggg cggaagcgaa 780
tacgagtga cttccccaac tttttgtcc atggctgcc tagtcatcgt cggcgcgctg 840
ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
aaccgcaaca tggtttgac caccctcgcc ggtactgttt tgggtctggc catgatgggc 960
gtgctcggct acatgccaac ctacctgag atggcgaca ccctgacgcc aactgaagca 1020
ggcttgatga tgatcccgat gatggtcggc atgatcggg tctccactgg tgttggttc 1080
atcatcgcta agaccggcaa ctacaagtac taccatcg cgggcctggc catcacggcg 1140
ttgctttgt ggtggatgtc ccagatgacc gttgagactt cattgaccgg tatcgagtt 1200
cgcttcctg tattcgggtg cggttgggc ttgtcatgc aggtactgg gctgattgt 1260
caaaactcct tccctgtatc gcaggtcgg actgccacgg cggctaataa ctcttcgc 1320
cagattggtt cggcattggg tgcttcatc gtgggttca tgttattca caatatgcag 1380
aatgagatgg ctaccggtt gcctgatgcc ctgcatcgt tgggaagga aggcgccgt 1440
atttcgcagc agttccaagg tgcagatgcc gccaactcct tgactccgca cgcagtcga 1500
gagctcccg atgtctccg tgacgctatc taaattcct acaatgacgg tctgaccccc 1560
tgattggca tgatgggtgcc actggccatt gttgcaatgc tgatttgtt cccactgcgc 1620
caagagcgct tgaaggaaac catcgaataa 1650

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<210> 151
<211> 549
<212> PRT
<213> Artificial Sequence

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<220>
<223> ImpE2 - G64D

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<400> 151
Met Val Ala Lys Asn Ser Thr Pro Ser Thr Ala Gly His Ala Ser Ala
 1         5         10        15
His Thr Ala Glu Glu Phe Pro Val Ala Asn Ala Glu Met Ala Thr Pro
      20        25        30
Ser Ala Ile Asp Pro Asn His Gly Lys Lys Thr Ala Asp Asn Val Gly
      35        40        45
Ile Ile Phe Ala Ala Leu Met Leu Thr Met Leu Met Ser Ser Leu Asp
      50        55        60
Gln Met Ile Phe Gly Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly
      65        70        75        80

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OPA18597-Sequence listing

Gly Val Asp Gln Met Ser Trp Val Ile Ser Ala Phe Met Val Thr Met
85 90 95

Thr Ile Ala Met Pro Leu Ala Gly Gln Leu Gly Asp Arg Met Gly Arg
100 105 110

Lys Trp Val Tyr Ile Ser Gly Ile Ser Ile Phe Val Ile Gly Ser Thr
115 120 125

Leu Gly Gly Phe Ala Asn Gly Met Gly Met Leu Ile Thr Gly Arg Ala
130 135 140

Ile Gln Gly Phe Gly Ala Gly Ile Met Met Ile Ser Ser Gln Ser Ile
145 150 155 160

Val Ala Glu Val Val Ser Ala Arg Glu Arg Gly Lys Phe Met Gly Ile
165 170 175

Met Gly Gly Val Phe Gly Val Ser Ser Val Leu Gly Pro Val Leu Gly
180 185 190

Gly Trp Phe Thr Asp Gly Pro Gly Trp Arg Trp Gly Leu Trp Ile Asn
195 200 205

Ile Pro Leu Gly Leu Leu Ala Ile Ile Val Cys Ala Phe Val Leu Lys
210 215 220

Leu Arg Val Gly Glu Gln Gly Phe Lys Gly Phe Asp Trp Met Gly Phe
225 230 235 240

Ala Ala Ile Ala Ile Thr Thr Ser Thr Leu Ile Leu Leu Thr Thr Trp
245 250 255

Gly Gly Ser Glu Tyr Glu Trp Thr Ser Pro Thr Ile Leu Ser Met Ala
260 265 270

Ala Val Val Ile Val Gly Ala Leu Leu Thr Val Phe Ile Glu Ser Arg
275 280 285

Ala Ser Gln Pro Leu Ile Pro Val Gln Leu Phe Lys Asn Arg Asn Met
290 295 300

Val Leu Thr Thr Leu Ala Gly Thr Val Leu Gly Leu Ala Met Met Gly
305 310 315 320

Val Leu Gly Tyr Met Pro Thr Tyr Leu Gln Met Val His Thr Leu Thr
325 330 335

Pro Thr Glu Ala Gly Leu Met Met Ile Pro Met Met Val Gly Met Ile
340 345 350

Gly Val Ser Thr Gly Val Gly Phe Ile Ile Ala Lys Thr Gly Asn Tyr
355 360 365

Lys Tyr Tyr Pro Ile Ala Gly Leu Ala Ile Thr Ala Phe Ala Leu Trp
370 375 380

Trp Met Ser Gln Met Thr Val Glu Thr Ser Leu Thr Gly Ile Gly Val
385 390 395 400

Arg Phe Leu Val Phe Gly Val Gly Leu Gly Phe Val Met Gln Val Leu

OPA18597-Sequence listing

405 410 415
Val Leu Ile Val Gln Asn Ser Phe Pro Val Ser Gln Val Gly Thr Ala
420 425 430
Thr Ala Ala Asn Asn Phe Phe Arg Gln Ile Gly Ser Ala Leu Gly Ala
435 440 445
Ser Ile Val Gly Ser Met Phe Ile His Asn Met Gln Asn Glu Met Ala
450 455 460
Thr Arg Leu Pro Asp Ala Leu Ala Ser Leu Gly Lys Glu Gly Ala Ala
465 470 475 480
Ile Ser Gln Gln Phe Gln Gly Ala Asp Ala Ala Asn Ser Leu Thr Pro
485 490 495
His Ala Val Ala Glu Leu Pro Asp Val Leu Arg Asp Ala Ile Leu Asn
500 505 510
Ser Tyr Asn Asp Gly Leu Thr Pro Val Ile Gly Met Met Val Pro Leu
515 520 525
Ala Ile Val Ala Met Leu Ile Leu Phe Pro Leu Arg Gln Glu Arg Leu
530 535 540
Lys Glu Thr Ile Glu
545

<210> 152
<211> 1650
<212> DNA
<213> Artificial Sequence

<220>
<223> ImpE2 NT - G64D

<400> 152
atggtagcta aaaactccac cccaagcacg gccggccacg ccagtgtca cactgcggaa 60
gaattcccag tggccaatgc tgaatggca acgccttcag caatcgaccc aaaccacggt 120
aaaaagaccg cggataacgt cggcattatc ttgctgcct tgatgtcac catgtgatg 180
agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300
ccactagccg gtcagctcgg tgaccgcatg ggccgcaagt ggggtctacat ctcaggtatc 360
tcattttcg ttattggctc gacgctcggg ggctttgccca atggcatggg catgctgac 420
accggacgtg caatccaggg ctccggtgcc ggcatcatga tgatttctc gcagtcgatt 480
gtggctgagg ttgtctccgc acgtgagcgc ggcaagtcca tgggtattat gggcggcgctc 540
tttggcgtct cctccgtact ggggtccagtt ctccggtggct gggtcaccga tgggtccggt 600
tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660

OPA18597-Sequence listing

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 gggccatcg caatcacgac cagcaccctg attctgctca ccactgggg cggaagcgaa 780
 tacgagtga cttcccaac tttttgtcc atggctgcc tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggtca gctatttaag 900
 aaccgcaaca tggtttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgag atggcgaca cctgacgcc aactgaagca 1020
 ggcttgatga tgatccgat gatggcggc atgatcggg tctccactgg tgttggttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcg cgggcctggc catcacggcg 1140
 ttgctttgt ggtggatgc ccagatgacc gttgagactt cattgaccgg tatcgagtt 1200
 cgcttcctg tattcgggtg cggcttggc tttgtcatgc aggtactgg gctgattgt 1260
 caaaactcct tccctgtatc gcaggctgg actgccacgg cggctaataa cttcttcgc 1320
 cagattggtt cggcattggg tgctccatc gtgggtcga tgttcattca caatatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc ctgcatcgt tgggcaagga aggcgccgt 1440
 atttcgcagc agttccaagg tgcagatgcc gccaactcct tgactccgca cgcagtcgca 1500
 gagctcccg atgtctccg tgacgctatc taaattcct acaatgacgg tctgaccccc 1560
 tgattggca tgatgggcc actggccatt gttgcaatgc tgatttgtt cccactgcgc 1620
 caagagcgt tgaaggaaac catcgaataa 1650

<210> 153
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
 <223> ImpE2 NT - V2I G64E

<400> 153
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 gaattccag tggccaatgc tgaaatggca acgccttcag caatcgaccc aaaccacggt 120
 aaaaagaccg cggataacgt cggcattatc ttcgtgcct tgatgctcac catgctgatg 180
 agctcttgg agcagatgat ttcgggtcc gctctgcaa ccatcgtcgg cgagctcggc 240
 ggctggacc agatgagctg ggtaattca gcatttatgg tcaccatgac cattgctatg 300
 ccactagccg gtcagctcgg tgaccgcatg ggccgcaagt gggctacat ctcaggtatc 360
 tccatttcg ttattggctc gacgctcggg ggcttgcca atggcatggg catgctgac 420
 accggacgtg caatccaggg ctcgggtgcc ggcatcatga tgatttcctc gcagtcgatt 480

OPA18597-Sequence listing

gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
 ttggcgtct cctccgtact ggggccagtt ctcggtggct gggtcaccga tgggtccgggt 600
 tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttctactga agctgcgcgt gggcgagcaa ggcttaagg gctttgactg gatgggtttt 720
 ggggccatcg caatcacgac cagcaccctg attctgtca ccactgggg cggaagcgaa 780
 tacgagtga cttcccaac tttttgtcc atggctgcc tagtcatcgt cggcgcgctg 840
 ctaccgtgt tcattgagtc gcgtgcatcc cagccgtga tcccgggtca gctatttaag 900
 aaccgcaaca tggtttgac caccctgcc ggtactgttt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgag atggcgaca ccctgacgcc aactgaagca 1020
 ggcttgatga tgatcccgat gatggtcggc atgacgggtg tctccactgg tgttggttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcg cgggcctggc catcacggcg 1140
 ttgctttgt ggtggatgtc ccagatgacc gttgagactt cattgaccgg tatcggagtt 1200
 cgcttcttg tattcgggtg cggcttgggc ttgtcatgc aggtactggg gctgattgtt 1260
 caaaactcct tccctgtatc gcaggtcggg actgccacgg cggctaataa ctcttccgc 1320
 cagattgggt cggcattggg tgcttccatc gtgggttcca tgttcattca caatatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc ctgcatcgt tgggcaagga aggcgccgct 1440
 atttcgacg agttccaagg tgcagatgcc gccaactcct tgactccgca cgcagtcgca 1500
 gagctcccg atgtcctccg tgacgctatc taaattcct acaatgacgg tctgaccccc 1560
 gtgattggca tgatgggtgcc actggccatt gttgcaatgc tgattttgtt cccactgcgc 1620
 caagagcgt tgaaggaaac catcgaataa 1650

<210> 154
 <211> 2312
 <212> DNA
 <213> Unknown

<220>
 <223> ImpE NT - CJI0323

<400> 154
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 ggggtaaggg agcagaagcg attggcaacc aagcatcgca tcgaagacgc cgcgacacgg 120
 ttggttgatg aatcgagctt tgacaaagta acaattgaag aaatttgcga agccgccggg 180
 atttcccgac gcacctttt taattattc agcacgaaag aaagcgccgt tattggcgcg 240
 tcctcggaac cgttgacgga aaagcaacgc aatgacttct tgaatgctga cgccagcaat 300

OPA18597-Sequence listing

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OPA18597-Sequence listing

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