

OPA18598-seq list

<110> CJ CheilJedang Corporation
 <120> Novel polypeptide and method of producing IMP using the same
 <130> OPA18598
 <150> KR10-2018-0001399
 <151> 2018-01-04
 <160> 156
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 35 40 45
 Lys Val Thr Ile Glu Glu Ile Cys Glu Ala Ala Gly Ile Ser Arg Arg
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 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
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OPA18598-seq list

Ala Met Glu Leu Val Lys Asn Tyr Thr Lys Gly Leu Glu Trp
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 35 40 45
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 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
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 Lys Trp Val Tyr Ile Ser Gly Ile Ser Ile Phe Val Ile Gly Ser Thr
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 Val Ala Glu Val Val Ser Ala Arg Glu Arg Gly Lys Phe Met Gly Ile
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 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

OPA18598-seq list

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

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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 Gly Tyr Met Pro Thr Tyr Leu Gln Met Val His Thr Leu Thr
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Pro Thr Glu Ala Gly Leu Met Met Ile Pro Met Met Val Gly Met Ile
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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

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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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OPA18598-seq list

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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg ggcagatgat ttccggttcc gctctgcaa ccatcgtcgg cgagctcggc 240
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 tccatttcg ttattggctc gacgctcggg ggctttgcca atggcatggg catgctgac 420
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OPA18598-seq list

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OPA18598-seq list

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OPA18598-seq list

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OPA18598-seq list

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35 40 45
Ile Ile Phe Ala Ala Leu Met Leu Thr Met Leu Met Ser Ser Leu Gly
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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 Cys Val Ile Gly Ser Thr
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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

OPA18598-seq list

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			
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	

OPA18598-seq list

Lys Glu Thr Ile Glu
545

<210> 74
<211> 549
<212> PRT
<213> Unknown

<220>
<223> impE2(I243V)

<400> 74
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 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
Ala Ala Val Ala Ile Thr Thr Ser Thr Leu Ile Leu Leu Thr Thr Trp

OPA18598-seq list

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
 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> 75

OPA18598-seq list

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

<220>
 <223> impE2(S387T)

<400> 75
 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 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
 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

OPA18598-seq list

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
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 Thr Gln Met Thr Val Glu Thr Ser Leu Thr Gly Ile Gly Val		
385	390	395
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		
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
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> 76
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> impE2(F405Y)

OPA18598-seq list

<400> 76
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 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
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

OPA18598-seq list

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 Tyr 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
 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> 77
<211> 549
<212> PRT
<213> Unknown

<220>
<223> impE2(M413T)

<400> 77
Met Val Ala Lys Asn Ser Thr Pro Ser Thr Ala Gly His Ala Ser Ala
1 5 10 15

OPA18598-seq list

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

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

OPA18598-seq list

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 Thr 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
 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> 78
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> impE2(N458K)

<400> 78
 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

OPA18598-seq list

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

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

OPA18598-seq list

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
435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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> 79
<211> 1650
<212> DNA
<213> Unknown

<220>
<223> impE2(F123C)

<400> 79
atggtagcta aaaactccac cccaagcacg gccggccacg ccagtgtca cactgcggaa 60
gaattcccag tggccaatgc tgaaatggca acgccttcag caatcgaccc aaaccacggt 120
aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
agctctttgg ggcagatgat ttccggttcc gctctgccaa ccatcgctcg cgagctcggc 240
ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300
ccactagccg gtcagctcgg tgaccgcatg ggccgcaagt ggggtctacat ctcaggtatc 360
tccatttgcg ttattggctc gacgctcggt ggctttgcca atggcatggg catgctgac 420
accggacgtg caatccaggg cttcggtgcc ggcatcatga tgatttctc gcagtcgatt 480

OPA18598-seq list

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gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc      540
tttggcgtct cctccgtact ggggccagtt ctcggtggct gggtcaccga tggccccggt      600
tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct      660
ttcgtactga agctgcgcgt gggcgagcaa ggctttaagg gctttgactg gatgggtttt      720
gcgggccatcg caatcacgac cagcaccctg attctgctca ccactggggg cggaagcgaa      780
tacgagtggg cttccccaac tttttgtcc atggctgccg 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 taccatcg cgggcctggc catcacggcg     1140
tttgctttgt ggtggatgtc ccagatgacc gttgagactt cattgaccgg tatcggagtt     1200
cgcttccttg tattcgggtg cggttgggc tttgtcatgc aggtactggg gctgattgtt     1260
caaaactcct tccctgtatc gcaggtcggg actgccacgg cggtcaataa ctcttccgc     1320
cagattgggt cggcattggg tgcttccatc gtgggttcga tgttcattca caatatgcag     1380
aatgagatgg ctaccggtt gcctgatgcc cttgcatcgt tgggcaagga aggcgccgct     1440
atttcgcagc agttccaagg tgcagatgcc gccaactcct tgactccgca cgcagtcgca     1500
gagcttcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc     1560
gtgattggca tgatgggtgcc actggccatt gttgcaatgc tgattttgtt cccactgcgc     1620
caagagcgct tgaaggaaac catcgaataa                                     1650
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<210> 80
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
 <223> impE2(I243V)

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<400> 80
atggtagcta 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
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OPA18598-seq list

ccactagccg gtcagctcgg tgaccgcatg ggccgcaagt ggggtctacat ctcaggtatc 360
tccattttcg ttattggctc gacgctcggg ggctttgcca atggcatggg catgctgac 420
accggacgtg caatccaggg ctccggtgcc ggcatcatga tgatttcctc gcagtcgatt 480
gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
tttgccgtct cctccgtact ggggtccagtt ctccggtggct gggtcaccga tgggtccggg 600
tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
ttcgtactga agctgcgcgt gggcgagcaa ggcttaagg gcttgactg gatgggttt 720
gcggtccgtc caatcacgac cagcacctg attctgtca ccactgggg cggaagcgaa 780
tacgagtga cttccccaac tttttgtcc atggctgcc tagtcatcgt cggcgcgctg 840
ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccgggtca gctatttaag 900
aaccgcaaca tggtttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
gtgctcggct acatgccaac ctacctgag atggtgcaca ccctgacgcc aactgaagca 1020
ggcttgatga tgatcccgat gatggtcggc atgacgggtg tctccactgg tgttggttc 1080
atcatcgcta agaccggcaa ctacaagta taccatcgc cgggcctggc catcacggcg 1140
ttgctttgt ggtggatgtc ccagatgacc gttgagact cattgaccgg tatcgagtt 1200
cgcttccttg tattcgggtg cggttgggc ttgtcatgc aggtactgg gctgattgt 1260
caaaactcct tccctgtatc gcaggtcggg actgccacgg cggctaataa ctcttcgc 1320
cagattggtt cggcattggg tgcttcatc gtgggttca tgttcattca caatatgcag 1380
aatgagatgg ctaccggtt gcctgatgcc ctgcatcgt tgggcaagga aggcgccgt 1440
atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcga 1500
gagctcccg atgtctccg tgacgtatc taaattcct acaatgacgg tctgaccccc 1560
tgattggca tgatgggtcc actggccatt gttgcaatgc tgattttgt cccactgcgc 1620
caagagcgct tgaaggaaac catcgaataa 1650

<210> 81
<211> 1650
<212> DNA
<213> Unknown

<220>
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OPA18598-seq list

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OPA18598-seq list

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 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
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OPA18598-seq list

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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 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
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
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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
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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
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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
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
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Gln Met Ile Phe Gly Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly		
65	70	75
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
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
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
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

OPA18598-seq list

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
 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> 100
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
 <223> impE2 CJI0323 64D

<400> 100
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 gaattcccag tggccaatgc tgaatggca acgccttcag caatcgaccc aaaccacggt 120
 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgctcg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

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 accggacgtg caatccaggg cttcgggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
 tttggcgtct cctccgtact ggggtccagtt ctcgggtggct gggtcaccga tgggtccggg 600
 tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttcgtactga agctgcgcgt gggcgagcaa ggctttaagg gctttgactg gatgggtttt 720
 gcggccatcg caatcacgac cagcaccctg attctgctca ccactgggg cggaagcgaa 780
 tacgagtggg cttccccaac tattttgtcc atggctgccg tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
 aaccgcaaca tggttttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgcag atgggtgcaca cctgacgcc aactgaagca 1020
 ggcttgatga tgatcccgat gatggtcggc atgatcgggtg tctccactgg tgttggcttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcgc cgggcctggc catcacggcg 1140
 tttgctttgt ggtggatgtc ccagatgacc gttgagactt cattgaccgg tatcggagtt 1200
 cgcttccttg tattcgggtg cggcttgggc ttgtcatgc aggtactggg gctgattgtt 1260
 caaaactcct tccctgtatc gcaggtcggg actgccacgg cggctaataa cttcttccgc 1320
 cagattgggt cggcattggg tgcttccatc gtgggttcga tgttcattca caatatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc cttgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagcttcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc 1560
 gtgattggca tgatgggtgcc actggccatt gttgcaatgc tgattttgtt cccactgcgc 1620
 caagagcgct tgaaggaaac catcgaataa 1650

<210> 101
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> impE2(S387T, M413T, N458K)

<400> 101
 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

OPA18598-seq list

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

OPA18598-seq list

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 Thr 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 Thr 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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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> 102
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
 <223> impE2(S387T, M413T, N458K)

<400> 102
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 gaattcccag tggccaatgc tgaaatggca acgccttcag caatcgaccc aaaccacggt 120
 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg ggcagatgat ttgcggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

ccactagccg gtcagctcgg tgaccgcatg ggccgcaagt gggctctacat ctcaggtatc 360
 tccattttcg ttattggctc gacgctcggg ggctttgccca atggcatggg catgctgac 420
 accggacgtg caatccaggg cttcgggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
 tttggcgtct cctccgtact ggggtccagtt ctcgggtggct gggtcaccga tgggtccggg 600
 tggcggtggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttcgtactga agctgcgcgt gggcgagcaa ggctttaagg gctttgactg gatgggtttt 720
 gcggccatcg caatcacgac cagcaccctg attctgtca ccactgggg cggaagcgaa 780
 tacgagtggg cttccccaac tttttgtcc atggctgccg tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
 aaccgcaaca tggttttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgcag atgggtgcaca cctgacgcc aactgaagca 1020
 ggcttgatga tgatcccgat gatggtcggc atgatcgggtg tctccactgg tgttggcttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcgc cgggcctggc catcacggcg 1140
 tttgctttgt ggtggatgac ccagatgacc gttgagactt cattgaccgg tatcggagtt 1200
 cgcttccttg tattcgggtg cggcttgggc ttgtcacgc aggtactggg gctgattgtt 1260
 caaaactcct tccctgtatc gcaggtcggg actgccacgg cggctaataa cttcttccgc 1320
 cagattgggt cggcattggg tgcttccatc gtgggttcga tgttcattca caaatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc cttgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagcttcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc 1560
 gtgattggca tgatgggtgcc actggccatt gttgcaatgc tgattttgtt cccactgcgc 1620
 caagagcgcgt tgaaggaaac catcgaataa 1650

<210> 103
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> impE2(G64D, S387T, M413T, N458K)

<400> 103
 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

OPA18598-seq list

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

OPA18598-seq list

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 Thr 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 Thr 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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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> 104
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
 <223> impE2(G64D, S387T, M413T, N458K)

<400> 104
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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgctcg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

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 tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttctactga agctgcgcgt gggcgagcaa ggctttaagg gctttgactg gatgggtttt 720
 gcggccatcg caatcacgac cagcaccctg attctgctca ccactgggg cggaagcgaa 780
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 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
 aaccgcaaca tggttttgac caccctcgcc ggtactgttt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgcag atgggtgcaca cctgacgcc aactgaagca 1020
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 cgcttccttg tattcgggtg cggcttgggc ttgtcacgc aggtactggg gctgattgtt 1260
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 cagattgggt cggcattggg tgcttccatc gtgggttcga tgttcattca caaatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc ctgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagcttcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc 1560
 gtgattggca tgatgggtgcc actggccatt gttgcaatgc tgattttgtt cccactgcgc 1620
 caagagcgct tgaaggaaac catcgaataa 1650

<210> 105
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> impE2(G64D, F123C)

<400> 105
 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

OPA18598-seq list

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
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 Cys 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
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
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
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

OPA18598-seq list

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
 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
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Lys Glu Thr Ile Glu
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 <212> DNA
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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
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OPA18598-seq list

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 aatgagatgg ctaccggtt gcctgatgcc cttgcatcgt tgggcaagga aggcgccgct 1440
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 gagcttcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc 1560
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His Thr Ala Glu Glu Phe Pro Val Ala Asn Ala Glu Met Ala Thr Pro

OPA18598-seq list

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			Lys
			Thr
			Ala
			Asp
			Asn
			Val
			Gly
Ile	Ile	Phe	Ala
50	55	60	
Ala	Leu	Met	Leu
			Thr
			Met
			Leu
			Met
			Ser
			Ser
			Leu
			Asp
Gln	Met	Ile	Phe
65	70	75	80
Gly	Ser	Ala	Leu
			Pro
			Thr
			Ile
			Val
			Gly
			Glu
			Leu
			Gly
Gly	Val	Asp	Gln
85	90	95	
Met	Ser	Trp	Val
			Ile
			Ser
			Ala
			Phe
			Met
			Val
			Thr
			Met
Thr	Ile	Ala	Met
100	105	110	
Pro	Leu	Ala	Gly
			Gln
			Leu
			Gly
			Asp
			Arg
			Met
			Gly
			Arg
Lys	Trp	Val	Tyr
115	120	125	
Ile	Ser	Gly	Ile
			Ser
			Ile
			Phe
			Val
			Ile
			Gly
			Ser
			Thr
Leu	Gly	Gly	Phe
130	135	140	
Ala	Asn	Gly	Met
			Gly
			Met
			Leu
			Ile
			Thr
			Gly
			Arg
			Ala
Ile	Gln	Gly	Phe
145	150	155	160
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			Ile
			Ser
			Ser
			Gln
			Ser
			Ile
Val	Ala	Glu	Val
165	170	175	
Val	Ser	Ala	Arg
			Glu
			Arg
			Gly
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			Phe
			Met
			Gly
			Ile
Met	Gly	Gly	Val
180	185	190	
Phe	Gly	Val	Ser
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			Val
			Leu
			Gly
			Pro
			Val
			Leu
			Gly
Gly	Trp	Phe	Thr
195	200	205	
Asp	Gly	Pro	Gly
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			Arg
			Trp
			Gly
			Leu
			Trp
			Ile
			Asn
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			Cys
			Ala
			Phe
			Val
			Leu
			Lys
Leu	Arg	Val	Gly
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Glu	Gln	Gly	Phe
			Lys
			Gly
			Phe
			Asp
			Trp
			Met
			Gly
			Phe
Ala	Ala	Val	Ala
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			Thr
			Leu
			Ile
			Leu
			Leu
			Thr
			Thr
			Trp
Gly	Gly	Ser	Glu
260	265	270	
Tyr	Glu	Trp	Thr
			Ser
			Pro
			Thr
			Ile
			Leu
			Ser
			Met
			Ala
Ala	Val	Val	Ile
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			Leu
			Thr
			Val
			Phe
			Ile
			Glu
			Ser
			Arg
Ala	Ser	Gln	Pro
290	295	300	
Leu	Ile	Pro	Val
			Gln
			Leu
			Phe
			Lys
			Asn
			Arg
			Asn
			Met
Val	Leu	Thr	Thr
305	310	315	320
Leu	Ala	Gly	Thr
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			Leu
			Gly
			Leu
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			Met
			Gly
Val	Leu	Gly	Tyr
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Met	Pro	Thr	Tyr
			Leu
			Gln
			Met
			Val
			His
			Thr
			Leu
			Thr
Pro	Thr	Glu	Ala
340	345	350	
Gly	Leu	Met	Met
			Ile
			Pro
			Met
			Met
			Val
			Gly
			Met
			Ile

OPA18598-seq list

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
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
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Lys Glu Thr Ile Glu
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agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
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OPA18598-seq list

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His Thr Ala Glu Glu Phe Pro Val Ala Asn Ala Glu Met Ala Thr Pro

OPA18598-seq list

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Asn	His	Gly	Lys
Lys	Thr	Ala	Asp
Asn	Val	Gly	
Ile	Ile	Phe	Ala
50	55	60	Leu
Met	Leu	Thr	Met
Leu	Met	Ser	Ser
Leu	Asp		
Gln	Met	Ile	Phe
65	70	75	80
Gly	Ser	Ala	Leu
Pro	Thr	Ile	Val
Gly	Glu	Leu	Gly
Gly	Val	Asp	Gln
85	90	95	Met
Ser	Trp	Val	Ile
Ser	Ala	Phe	Met
Val	Thr	Met	
Thr	Ile	Ala	Met
100	105	110	Pro
Leu	Ala	Gly	Gln
Leu	Gly	Asp	Arg
Met	Gly	Arg	
Lys	Trp	Val	Tyr
115	120	125	Ile
Ser	Gly	Ile	Ser
Ile	Phe	Val	Ile
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Leu	Gly	Gly	Phe
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Asn	Gly	Met	Gly
Met	Leu	Ile	Thr
Gly	Arg	Ala	
Ile	Gln	Gly	Phe
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Gly	Ala	Gly	Ile
Met	Met	Ile	Ser
Ser	Ser	Gln	Ser
Ile			
Val	Ala	Glu	Val
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Ser	Ala	Arg	Glu
Arg	Gly	Lys	Phe
Met	Gly	Ile	
Met	Gly	Gly	Val
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Gly	Val	Ser	Ser
Val	Leu	Gly	Pro
Val	Leu	Gly	
Gly	Trp	Phe	Thr
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Arg	Trp	Gly	Leu
Trp	Ile	Asn	
Ile	Pro	Leu	Gly
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Ala	Ile	Val	Cys
Ala	Phe	Val	Leu
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Leu	Arg	Val	Gly
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Glu	Gln	Gly	Phe
Lys	Gly	Phe	Asp
Trp	Met	Gly	Phe
Ala	Ala	Ile	Ala
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Thr	Thr	Ser	Thr
Leu	Ile	Leu	Leu
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Gly	Gly	Ser	Glu
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Glu	Trp	Thr	Ser
Pro	Thr	Ile	Leu
Ser	Met	Ala	
Ala	Val	Val	Ile
275	280	285	Val
Gly	Ala	Leu	Leu
Thr	Val	Phe	Ile
Glu	Ser	Arg	
Ala	Ser	Gln	Pro
290	295	300	Leu
Ile	Pro	Val	Gln
Leu	Phe	Lys	Asn
Arg	Asn	Met	
Val	Leu	Thr	Thr
305	310	315	320
Leu	Ala	Gly	Thr
Val	Leu	Gly	Leu
Ala	Met	Met	Gly
Val	Leu	Gly	Tyr
325	330	335	Met
Pro	Thr	Tyr	Leu
Gln	Met	Val	His
Thr	Leu	Thr	
Pro	Thr	Glu	Ala
340	345	350	Gly
Leu	Met	Met	Ile
Pro	Met	Met	Val
Gly	Met	Ile	

OPA18598-seq list

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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 Tyr 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
 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
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Ala Ile Val Ala Met Leu Ile Leu Phe Pro Leu Arg Gln Glu Arg Leu
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Lys Glu Thr Ile Glu
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OPA18598-seq list

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His Thr Ala Glu Glu Phe Pro Val Ala Asn Ala Glu Met Ala Thr Pro

OPA18598-seq list

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Asp	Asn	Val	Gly
Ile	Ile	Phe	Ala
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Leu	Met	Leu	Thr
Met	Leu	Met	Ser
Ser	Ser	Leu	Gly
Gln	Met	Ile	Phe
65	70	75	80
Gly	Ser	Ala	Leu
Pro	Thr	Ile	Val
Gly	Glu	Leu	Gly
Gly	Val	Asp	Gln
85	90	95	Met
Met	Ser	Trp	Val
Ile	Ser	Ala	Phe
Met	Val	Thr	Met
Thr	Ile	Ala	Met
100	105	110	Pro
Leu	Ala	Gly	Gln
Leu	Gly	Asp	Arg
Met	Gly	Arg	
Lys	Trp	Val	Tyr
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Ser	Gly	Ile	Ser
Ile	Ser	Ile	Cys
Val	Ile	Gly	Ser
Thr			
Leu	Gly	Gly	Phe
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Asn	Gly	Met	Gly
Met	Gly	Met	Leu
Ile	Thr	Gly	Arg
Ala			
Ile	Gln	Gly	Phe
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Gly	Ala	Gly	Ile
Met	Met	Ile	Ser
Ser	Ser	Gln	Ser
Ile			
Val	Ala	Glu	Val
165	170	175	Val
Ser	Ala	Arg	Glu
Arg	Gly	Lys	Phe
Met	Gly	Ile	
Met	Gly	Gly	Val
180	185	190	Phe
Gly	Val	Ser	Ser
Val	Leu	Gly	Pro
Val	Leu	Gly	
Gly	Trp	Phe	Thr
195	200	205	Asp
Gly	Pro	Gly	Trp
Arg	Trp	Gly	Leu
Trp	Ile	Asn	
Ile	Pro	Leu	Gly
210	215	220	Leu
Ala	Ile	Ile	Val
Cys	Ala	Phe	Val
Leu	Lys		
Leu	Arg	Val	Gly
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Glu	Gln	Gly	Phe
Lys	Gly	Phe	Asp
Trp	Met	Gly	Phe
Ala	Ala	Val	Ala
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Thr	Thr	Ser	Thr
Leu	Ile	Leu	Leu
Thr	Thr	Trp	
Gly	Gly	Ser	Glu
260	265	270	Tyr
Glu	Trp	Thr	Ser
Pro	Thr	Ile	Leu
Ser	Met	Ala	
Ala	Val	Val	Ile
275	280	285	Val
Gly	Ala	Leu	Leu
Thr	Val	Phe	Ile
Glu	Ser	Arg	
Ala	Ser	Gln	Pro
290	295	300	Leu
Ile	Pro	Val	Gln
Leu	Phe	Lys	Asn
Arg	Asn	Met	
Val	Leu	Thr	Thr
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Leu	Ala	Gly	Thr
Val	Leu	Gly	Leu
Ala	Met	Met	Gly
Val	Leu	Gly	Tyr
325	330	335	Met
Pro	Thr	Tyr	Leu
Gln	Met	Val	His
Thr	Leu	Thr	
Pro	Thr	Glu	Ala
340	345	350	Gly
Leu	Met	Met	Ile
Pro	Met	Met	Val
Gly	Met	Ile	

OPA18598-seq list

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

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

Arg Phe Leu Val Tyr Gly Val Gly Leu Gly Phe Val Thr 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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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
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Lys Glu Thr Ile Glu
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 <211> 1650
 <212> DNA
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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg ggcagatgat ttgcggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
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OPA18598-seq list

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 accggacgtg caatccaggg cttcgggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
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 cgcttccttg tatacgggtgt cggcttgggc tttgtcacgc aggtactggg gctgattgtt 1260
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 cagattgggt cggcattggg tgcttccatc gtgggttcga tgttcattca caaatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc cttgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagcttcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc 1560
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His Thr Ala Glu Glu Phe Pro Val Ala Asn Ala Glu Met Ala Thr Pro

OPA18598-seq list

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			Lys
			Thr
			Ala
			Asp
			Asn
			Val
			Gly
Ile	Ile	Phe	Ala
50	55	60	
Ala	Leu	Met	Leu
			Thr
			Met
			Leu
			Met
			Ser
			Ser
			Leu
			Asp
Gln	Met	Ile	Phe
65	70	75	80
Gly	Ser	Ala	Leu
			Pro
			Thr
			Ile
			Val
			Gly
			Glu
			Leu
			Gly
Gly	Val	Asp	Gln
	85		90
Met	Ser	Trp	Val
			Ile
			Ser
			Ala
			Phe
			Met
			Val
			Thr
			Met
Thr	Ile	Ala	Met
100	105	110	
Pro	Leu	Ala	Gly
			Gln
			Leu
			Gly
			Asp
			Arg
			Met
			Gly
			Arg
Lys	Trp	Val	Tyr
115	120	125	
Ile	Ser	Gly	Ile
			Ser
			Ile
			Phe
			Val
			Ile
			Gly
			Ser
			Thr
Leu	Gly	Gly	Phe
130	135	140	
Ala	Asn	Gly	Met
			Gly
			Met
			Leu
			Ile
			Thr
			Gly
			Arg
			Ala
Ile	Gln	Gly	Phe
145	150	155	160
Ala	Gly	Ile	Met
			Met
			Ile
			Ser
			Ser
			Gln
			Ser
			Ile
Val	Ala	Glu	Val
	165		170
Val	Ser	Ala	Arg
			Glu
			Arg
			Gly
			Lys
			Phe
			Met
			Gly
			Ile
Met	Gly	Gly	Val
180	185	190	
Phe	Gly	Val	Ser
			Ser
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			Arg
			Trp
			Gly
			Leu
			Trp
			Ile
			Asn
Ile	Pro	Leu	Gly
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			Ile
			Val
			Cys
			Ala
			Phe
			Val
			Leu
			Lys
Leu	Arg	Val	Gly
225	230	235	240
Glu	Gln	Gly	Phe
			Lys
			Gly
			Phe
			Asp
			Trp
			Met
			Gly
			Phe
Ala	Ala	Ile	Ala
	245		250
Ile	Thr	Thr	Ser
			Thr
			Leu
			Ile
			Leu
			Leu
			Thr
			Thr
			Trp
Gly	Gly	Ser	Glu
	260		265
Tyr	Glu	Trp	Thr
			Ser
			Pro
			Thr
			Ile
			Leu
			Ser
			Met
			Ala
Ala	Val	Val	Ile
	275		280
Val	Gly	Ala	Leu
			Leu
			Thr
			Val
			Phe
			Ile
			Glu
			Ser
			Arg
Ala	Ser	Gln	Pro
	290		295
Leu	Ile	Pro	Val
			Gln
			Leu
			Phe
			Lys
			Asn
			Arg
			Asn
			Met
Val	Leu	Thr	Thr
305	310	315	320
Leu	Ala	Gly	Thr
			Val
			Leu
			Gly
			Leu
			Ala
			Met
			Met
			Gly
Val	Leu	Gly	Tyr
	325		330
Met	Pro	Thr	Tyr
			Leu
			Gln
			Met
			Val
			His
			Thr
			Leu
			Thr
Pro	Thr	Glu	Ala
	340		345
Gly	Leu	Met	Met
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			Pro
			Met
			Met
			Val
			Gly
			Met
			Ile

OPA18598-seq list

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 Thr 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
 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
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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
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OPA18598-seq list

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 ttcgtactga agctgcgcgt gggcgagcaa ggctttaagg gctttgactg gatgggtttt 720
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His Thr Ala Glu Glu Phe Pro Val Ala Asn Ala Glu Met Ala Thr Pro

OPA18598-seq list

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

OPA18598-seq list

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 Thr 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
 500 505 510

Ser Tyr Asn Asp Gly Leu Thr Pro Val Ile Gly Met Met Val Pro Leu
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Lys Glu Thr Ile Glu
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OPA18598-seq list

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 aaccgcaaca tggttttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
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His Thr Ala Glu Glu Phe Pro Val Ala Asn Ala Glu Met Ala Thr Pro

OPA18598-seq list

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

OPA18598-seq list

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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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
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<210> 118
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
 <223> impE2(G64D, N458K)

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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat tticggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

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 accggacgtg caatccaggg cttcggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
 tttggcgtct cctccgtact ggggtccagtt ctcggtggct gggtcaccga tgggtccggg 600
 tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
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 gcggccatcg caatcacgac cagcaccctg attctgtca ccactgggg cggaagcgaa 780
 tacgagtggg cttccccaac tttttgtcc atggctgccg tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccgggtca gctatttaag 900
 aaccgcaaca tggttttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
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 ggcttgatga tgatcccgat gatggctggc atgatcgggtg tctccactgg tgttggcttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcg cgggcctggc catcacggcg 1140
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<210> 119
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> impE2(G64D, I243V, S387T, M413T, N458K)

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 Met Val 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

OPA18598-seq list

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
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
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
Ala Ala Val 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
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

OPA18598-seq list

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 Thr 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 Thr 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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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> 120
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
 <223> impE2(G64D, I243V, S387T, M413T, N458K)

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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

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 accggacgtg caatccaggg ctccggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
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 tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttcgtactga agctgcgcgt gggcgagcaa ggctttaagg gctttgactg gatgggtttt 720
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 tacgagtggg cttccccaac tttttgtcc atggctgccg tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
 aaccgcaaca tggttttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
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 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagcttcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc 1560
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<210> 121
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> impE2(G64D, S387T, F405Y, M413T, N458K)

<400> 121
 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

78 페이지

OPA18598-seq list

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

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

Arg Phe Leu Val Tyr Gly Val Gly Leu Gly Phe Val Thr 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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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> 122
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
 <223> impE2(G64D, S387T, F405Y, M413T, N458K)

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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat tticggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

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 accggacgtg caatccaggg ctccggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
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 tggcggtggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttctactga agctgcgcgt gggcgagcaa ggctttaagg gctttgactg gatgggtttt 720
 gcggccatcg caatcacgac cagcaccctg attctgtca ccactgggg cggaagcgaa 780
 tacgagtggg cttccccaac tttttgtcc atggctgccg tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
 aaccgcaaca tggttttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
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<210> 123
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> impE2(G64D, F123C, S387T, M413T, N458K)

<400> 123
 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

OPA18598-seq list

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

OPA18598-seq list

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 Thr 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 Thr 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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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> 124
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
 <223> impE2(G64D, F123C, S387T, M413T, N458K)

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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgctcg cgagctcggc 240
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OPA18598-seq list

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 gagctcccg atgtcctccg tgacgctatc taaattcct acaatgacgg tctgaccccc 1560
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 caagagcgcgt tgaaggaaac catcgaataa 1650

<210> 125
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> impE2(G64D, I243V, S387T, F405Y, M413T, N458K)

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 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

OPA18598-seq list

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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 Asp
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
Ala	Ala	Val	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	

OPA18598-seq list

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

Arg Phe Leu Val Tyr Gly Val Gly Leu Gly Phe Val Thr 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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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> 126
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaattca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

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 accggacgtg caatccaggg ctccggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
 tttggcgtct cctccgtact ggggtccagtt ctccggtggct gggtcaccga tgggtccggg 600
 tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttctgactga agctgcgcgt gggcgagcaa ggctttaagg gctttgactg gatgggtttt 720
 gcgggccgtc caatcacgac cagcaccctg attctgctca ccactgggg cggaagcgaa 780
 tacgagtggg cttccccaac tttttgtcc atggctgccg tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
 aaccgcaaca tggttttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
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 ggcttgatga tgatcccgat gatggtcggc atgatcgggtg tctccactgg tgttggcttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcgc cgggcctggc catcacggcg 1140
 tttgctttgt ggtggatgac ccagatgacc gttgagactt cattgaccgg tatcggagtt 1200
 cgcttccttg tatacgggtgt cggcttgggc ttgtcacgc aggtactggg gctgattgtt 1260
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 aatgagatgg ctaccggtt gcctgatgcc ctgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagcttcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc 1560
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<210> 127
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 <212> PRT
 <213> Unknown

<220>
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<400> 127
 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

OPA18598-seq list

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

OPA18598-seq list

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

Arg Phe Leu Val Tyr Gly Val Gly Leu Gly Phe Val Thr 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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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> 128
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
 <223> impE2(G64D, F123C, I243V, S387T, F405Y, M413T, N458K)

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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgctcg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

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 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
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 tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
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 tacgagtggg cttcccaac tttttgtcc atggctgccg tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
 aaccgcaaca tggtttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgcag atgggtgcaca cctgacgcc aactgaagca 1020
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 atcatcgcta agaccggcaa ctacaagtac taccatcgc cgggcctggc catcacggcg 1140
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 aatgagatgg ctaccggtt gcctgatgcc ctgcatcgt tgggcaagga aggcgccgct 1440
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His Thr Ala Glu Glu Phe Pro Val Ala Asn Ala Glu Met Ala Thr Pro

OPA18598-seq list

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

OPA18598-seq list

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 Thr 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 Thr 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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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> 130
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg ggcagatgat ttgcggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

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 tccattttcg ttattggctc gacgctcggg ggctttgccca atggcatggg catgctgac 420
 accggacgtg caatccaggg ctccggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
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 aaccgcaaca tggttttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgcag atgggtgcaca cctgacgcc aactgaagca 1020
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 cagattgggt cggcattggg tgcttccatc gtgggttcga tgttcattca caaatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc ctgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
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 <212> PRT
 <213> Unknown

<220>
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 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

OPA18598-seq list

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

OPA18598-seq list

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 Thr 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 Thr 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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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> 132
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
 <223> CJI0323 impE2(G64D, S387T, M413T, N458K)

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 gaattcccag tggccaatgc tgaatggca acgccttcag caatcgaccc aaaccacggt 120
 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgctcg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaattca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

ccactagccg gtcagctcgg tgaccgcatg ggccgcaagt gggctacat ctcaggtatc 360
 tccattttcg ttattggctc gacgctcggg ggctttgcc atggcatggg catgctgac 420
 accggacgtg caatccaggg ctccggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
 tttggcgtct cctccgtact ggggtccagtt ctccggtggct gggtcaccga tgggtccggg 600
 tggcggtggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttctactga agctgcgcgt gggcgagcaa ggctttaagg gcttgactg gatgggtttt 720
 gcggccatcg caatcacgac cagcaccctg attctgtca ccactgggg cggaagcgaa 780
 tacgagtggg cttcccaac tttttgtcc atggctgcc tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
 aaccgcaaca tggtttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgcag atgggtgcaca cctgacgcc aactgaagca 1020
 ggcttgatga tgatcccgat gatggtcggc atgatcgggtg tctccactgg tgttggttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcgc cgggcctggc catcacggcg 1140
 tttgctttgt ggtggatgac ccagatgacc gttgagactt cattgaccgg tatcggagtt 1200
 cgcttccttg tattcgggtg cggcttgggc ttgtcacgc aggtactggg gctgattgtt 1260
 caaaactcct tccctgtatc gcaggctcgg actgccacgg cggctaataa cttcttccgc 1320
 cagattgggt cggcattggg tgcttccatc gtgggttcga tgttcattca caaatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc ctgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagcttcccg atgtcctccg tgacgctatc taaattcct acaatgacgg tctgaccccc 1560
 gtgattggca tgatgggtgcc actggccatt gttgcaatgc tgattttgtt cccactgcgc 1620
 caagagcgt tgaaggaaac catcgaataa 1650

<210> 133
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> CJI0323 impE2(G64D, F123C)

<400> 133
 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

OPA18598-seq list

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

OPA18598-seq list

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
 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> 134
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
 <223> CJI0323 impE2(G64D, F123C)

<400> 134
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 gaattcccag tggccaatgc tgaaatggca acgccttcag caatcgaccc aaaccacggt 120
 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
 ggcgtaggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

ccactagccg gtcagctcgg tgaccgcatg ggccgcaagt gggctctacat ctcaggtatc 360
 tccatttgcg ttattggctc gacgctcggg ggctttgccca atggcatggg catgctgac 420
 accggacgtg caatccaggg cttcgggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
 tttggcgtct cctccgtact ggggtccagtt ctcgggtggct gggtcaccga tgggtccggg 600
 tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttcgtactga agctgcgcgt gggcgagcaa ggctttaagg gctttgactg gatgggtttt 720
 gcggccatcg caatcacgac cagcaccctg attctgctca ccactgggg cggaagcgaa 780
 tacgagtggg cttccccaac tatttgtcc atggctgccg tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
 aaccgcaaca tggttttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgcag atgggtgcaca cctgacgcc aactgaagca 1020
 ggcttgatga tgatcccgat gatggtcggc atgatcgggtg tctccactgg tgttggcttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcg cgggcctggc catcacggcg 1140
 tttgctttgt ggtggatgtc ccagatgacc gttgagactt cattgaccgg tatcgagatt 1200
 cgcttccttg tattcgggtg cggcttgggc ttgtcatgc aggtactggg gctgattgtt 1260
 caaaactcct tccctgtatc gcaggtcggg actgccacgg cggctaataa cttcttccgc 1320
 cagattgggt cggcattggg tgcttccatc gtgggttcga tgttcattca caatatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc cttgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagcttcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc 1560
 gtgattggca tgatgggtgcc actggccatt gttgcaatgc tgattttgtt cccactgcgc 1620
 caagagcgct tgaaggaaac catcgaataa 1650

<210> 135
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> CJI0323 impE2(G64D, I243V)

<400> 135
 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

OPA18598-seq list

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
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	Val	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	

OPA18598-seq list

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
 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> 136
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
 <223> CJI0323 impE2(G64D, I243V)

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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

ccactagccg gtcagctcgg tgaccgcatg ggccgcaagt gggctctacat ctcaggtatc 360
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 accggacgtg caatccaggg cttcgggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
 tttggcgtct cctccgtact ggggtccagtt ctcgggtggct gggtcaccga tgggtccggg 600
 tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttcgtactga agctgcgcgt gggcgagcaa ggctttaagg gctttgactg gatgggtttt 720
 gcggccgtcg caatcacgac cagcaccctg attctgtca ccactgggg cggaagcgaa 780
 tacgagtggg cttccccaac tatttgtcc atggctgccg tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
 aaccgcaaca tggttttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgcag atgggtgcaca cctgacgcc aactgaagca 1020
 ggcttgatga tgatcccgat gatggtcggc atgatcgggtg tctccactgg tgttggcttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcgc cgggcctggc catcacggcg 1140
 tttgctttgt ggtggatgtc ccagatgacc gttgagactt cattgaccgg tatcggagtt 1200
 cgcttccttg tattcgggtg cggcttgggc ttgtcatgc aggtactggg gctgattgtt 1260
 caaaactcct tccctgtatc gcaggtcggg actgccacgg cggctaataa cttcttccgc 1320
 cagattgggt cggcattggg tgcttccatc gtgggttcga tgttcattca caatatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc cttgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagcttcccg atgtcctccg tgacgctatc taaattcct acaatgacgg tctgaccccc 1560
 gtgattggca tgatgggtgcc actggccatt gttgcaatgc tgattttgtt cccactgcgc 1620
 caagagcgct tgaaggaaac catcgaataa 1650

<210> 137
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> CJI0323 impE2(G64D, F405Y)

<400> 137
 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

OPA18598-seq list

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

OPA18598-seq list

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 Tyr 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
 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
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Lys Glu Thr Ile Glu
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 <211> 1650
 <212> DNA
 <213> Unknown

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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
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OPA18598-seq list

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 accggacgtg caatccaggg cttcgggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
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 tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttcgtactga agctgcgcgt gggcgagcaa ggctttaagg gctttgactg gatgggtttt 720
 gcggccatcg caatcacgac cagcaccctg attctgtca ccactgggg cggaagcgaa 780
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 aaccgcaaca tggttttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgcag atgggtgcaca cctgacgcc aactgaagca 1020
 ggcttgatga tgatcccgat gatggtcggc atgatcgggtg tctccactgg tgttggcttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcg cgggcctggc catcacggcg 1140
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 aatgagatgg ctaccggtt gcctgatgcc cttgcatcgt tgggcaagga aggcgccgct 1440
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 gagcttcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc 1560
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 <212> PRT
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 His Thr Ala Glu Glu Phe Pro Val Ala Asn Ala Glu Met Ala Thr Pro

OPA18598-seq list

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

OPA18598-seq list

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

Arg Phe Leu Val Tyr Gly Val Gly Leu Gly Phe Val Thr 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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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> 140
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 <212> DNA
 <213> Unknown

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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
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OPA18598-seq list

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His Thr Ala Glu Glu Phe Pro Val Ala Asn Ala Glu Met Ala Thr Pro

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			Lys
			Thr
			Ala
			Asp
			Asn
			Val
			Gly
Ile	Ile	Phe	Ala
50	55	60	
Ala	Leu	Met	Leu
			Thr
			Met
			Leu
			Met
			Ser
			Ser
			Leu
			Asp
Gln	Met	Ile	Phe
65	70	75	80
Gly	Ser	Ala	Leu
			Pro
			Thr
			Ile
			Val
			Gly
			Glu
			Leu
			Gly
Gly	Val	Asp	Gln
	85		90
Met	Ser	Trp	Val
			Ile
			Ser
			Ala
			Phe
			Met
			Val
			Thr
			Met
Thr	Ile	Ala	Met
100	105	110	
Pro	Leu	Ala	Gly
			Gln
			Leu
			Gly
			Asp
			Arg
			Met
			Gly
			Arg
Lys	Trp	Val	Tyr
115	120	125	
Ile	Ser	Gly	Ile
			Ser
			Ile
			Phe
			Val
			Ile
			Gly
			Ser
			Thr
Leu	Gly	Gly	Phe
130	135	140	
Ala	Asn	Gly	Met
			Gly
			Met
			Leu
			Ile
			Thr
			Gly
			Arg
			Ala
Ile	Gln	Gly	Phe
145	150	155	160
Ala	Gly	Ile	Met
			Met
			Ile
			Ser
			Ser
			Gln
			Ser
			Ile
Val	Ala	Glu	Val
	165		170
Val	Ser	Ala	Arg
			Glu
			Arg
			Gly
			Lys
			Phe
			Met
			Gly
			Ile
Met	Gly	Gly	Val
180	185	190	
Phe	Gly	Val	Ser
			Ser
			Val
			Leu
			Gly
			Pro
			Val
			Leu
			Gly
Gly	Trp	Phe	Thr
195	200	205	
Asp	Gly	Pro	Gly
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			Arg
			Trp
			Gly
			Leu
			Trp
			Ile
			Asn
Ile	Pro	Leu	Gly
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			Ile
			Val
			Cys
			Ala
			Phe
			Val
			Leu
			Lys
Leu	Arg	Val	Gly
225	230	235	240
Glu	Gln	Gly	Phe
			Lys
			Gly
			Phe
			Asp
			Trp
			Met
			Gly
			Phe
Ala	Ala	Ile	Ala
	245		250
Ile	Thr	Thr	Ser
			Thr
			Leu
			Ile
			Leu
			Leu
			Thr
			Thr
			Trp
Gly	Gly	Ser	Glu
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Tyr	Glu	Trp	Thr
			Ser
			Pro
			Thr
			Ile
			Leu
			Ser
			Met
			Ala
Ala	Val	Val	Ile
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Val	Gly	Ala	Leu
			Leu
			Thr
			Val
			Phe
			Ile
			Glu
			Ser
			Arg
Ala	Ser	Gln	Pro
	290		295
Leu	Ile	Pro	Val
			Gln
			Leu
			Phe
			Lys
			Asn
			Arg
			Asn
			Met
Val	Leu	Thr	Thr
305	310	315	320
Leu	Ala	Gly	Thr
			Val
			Leu
			Gly
			Leu
			Ala
			Met
			Met
			Gly
Val	Leu	Gly	Tyr
	325		330
Met	Pro	Thr	Tyr
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			Gln
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			Val
			His
			Thr
			Leu
			Thr
Pro	Thr	Glu	Ala
	340		345
Gly	Leu	Met	Met
			Ile
			Pro
			Met
			Met
			Val
			Gly
			Met
			Ile

OPA18598-seq list

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 Thr 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
 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
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Lys Glu Thr Ile Glu
 545

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 <212> DNA
 <213> Unknown

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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgctcg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

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 gcggccatcg caatcacgac cagcaccctg attctgtca ccactgggg cggaagcgaa 780
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 aaccgcaaca tggttttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
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 cgcttccttg tattcgggtg cggcttgggc ttgtcatgc aggtactggg gctgattgtt 1260
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 aatgagatgg ctaccggtt gcctgatgcc ctgcatcgt tgggcaagga aggcgccgct 1440
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His Thr Ala Glu Glu Phe Pro Val Ala Asn Ala Glu Met Ala Thr Pro

OPA18598-seq list

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

OPA18598-seq list

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

<220>
 <223> CJI0323 impE2(G64D, M413T)

<400> 144
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 gaattcccag tggccaatgc tgaaatggca acgccttcag caatcgaccc aaaccacggt 120
 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgctcg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

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 tccattttcg ttattggctc gacgctcggg ggctttgccca atggcatggg catgctgac 420
 accggacgtg caatccaggg cttcgggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
 tttggcgtct cctccgtact ggggtccagtt ctcgggtggct gggtcaccga tgggtccggg 600
 tggcggtggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttcgtactga agctgcgcgt gggcgagcaa ggctttaagg gctttgactg gatgggtttt 720
 gcggccatcg caatcacgac cagcaccctg attctgtca ccactgggg cggaagcgaa 780
 tacgagtggg cttccccaac tatttgtcc atggctgccg tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
 aaccgcaaca tggttttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgcag atgggtgcaca cctgacgcc aactgaagca 1020
 ggcttgatga tgatcccgat gatggtcggc atgatcgggtg tctccactgg tgttggcttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcgc cgggcctggc catcacggcg 1140
 tttgctttgt ggtggatgtc ccagatgacc gttgagactt cattgaccgg taccggagtt 1200
 cgcttccttg tattcgggtg cggcttgggc ttgtcacgc aggtactggg gctgattgtt 1260
 caaaactcct tccctgtatc gcaggctcggg actgccacgg cggctaataa cttcttcgc 1320
 cagattgggt cggcattggg tgcttccatc gtgggttcga tgttcattca caatatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc cttgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagctcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc 1560
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<210> 145
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> CJI0323 impE2(G64D, N458K)

<400> 145
 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

OPA18598-seq list

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

OPA18598-seq list

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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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> 146
 <211> 1650
 <212> DNA
 <213> Unknown

<220>
 <223> CJI0323 impE2(G64D, N458K)

<400> 146
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 gaattcccag tggccaatgc tgaatggca acgccttcag caatcgaccc aaaccacggt 120
 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaattca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

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 tccatttctg ttattggctc gacgctcggg ggctttgcc atggcatggg catgctgac 420
 accggacgtg caatccaggg ctccggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
 tttggcgtct cctccgtact ggggtccagtt ctccggtggct gggtcaccga tgggtccggg 600
 tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
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 gcggccatcg caatcacgac cagcaccctg attctgctca ccactgggg cggaagcgaa 780
 tacgagtggg ctccccaac tttttgtcc atggctgcc tagtcatcgt cggcgcgctg 840
 ctaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
 aaccgcaaca tggtttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgag atgggtgcaca cctgacgcc aactgaagca 1020
 ggcttgatga tgatcccgat gatggtcggc atgatcgggtg tctccactgg tgttggcttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcgc cgggcctggc catcacggcg 1140
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 cagattgggt cggcattggg tgcttccatc gtgggttcca tgttcattca caaatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc ctgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagcttcccg atgtcctccg tgacgctatc taaattcct acaatgacgg tctgaccccc 1560
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<210> 147
 <211> 549
 <212> PRT
 <213> Unknown

<220>
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<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

OPA18598-seq list

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

OPA18598-seq list

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 Thr 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 Thr 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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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>
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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
 ggcgtaggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

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 accggacgtg caatccaggg cttcggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
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 tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttctactga agctgcgcgt gggcgagcaa ggctttaagg gctttgactg gatgggtttt 720
 gcggccgtcg caatcacgac cagcaccctg attctgtca ccactgggg cggaagcgaa 780
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 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccgggtca gctatttaag 900
 aaccgcaaca tggttttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgcag atgggtgcaca cctgacgcc aactgaagca 1020
 ggcttgatga tgatcccgat gatggtcggc atgatcgggtg tctccactgg tgttggcttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcgc cgggcctggc catcacggcg 1140
 tttgctttgt ggtggatgac ccagatgacc gttgagactt cattgaccgg tatcggagtt 1200
 cgcttccttg tattcgggtg cggcttgggc ttgtcacgc aggtactggg gctgattgtt 1260
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 cagattgggt cggcattggg tgcttccatc gtgggttcga tgttcattca caaatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc ctgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagcttcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc 1560
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 <212> PRT
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 His Thr Ala Glu Glu Phe Pro Val Ala Asn Ala Glu Met Ala Thr Pro

OPA18598-seq list

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

OPA18598-seq list

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

Arg Phe Leu Val Tyr Gly Val Gly Leu Gly Phe Val Thr 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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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> CJI0323 impE2(G64D, S387T, F405Y, M413T, N458K)

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 gaattcccag tggccaatgc tgaatggca acgccttcag caatcgaccc aaaccacggt 120
 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

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 tccattttcg ttattggctc gacgctcggg ggctttgccca atggcatggg catgctgac 420
 accggacgtg caatccaggg cttcgggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
 tttggcgtct cctccgtact ggggtccagtt ctcgggtggct gggtcaccga tgggtccggg 600
 tggcggtggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttcgtactga agctgcgcgt gggcgagcaa ggctttaagg gctttgactg gatgggtttt 720
 gcggccatcg caatcacgac cagcaccctg attctgctca ccactgggg cggaagcgaa 780
 tacgagtggg cttccccaac tttttgtcc atggctgccg tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccgggtca gctatttaag 900
 aaccgcaaca tggttttgac caccctcgcc ggtactgttt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgcag atgggtgcaca cctgacgcc aactgaagca 1020
 ggcttgatga tgatcccgat gatggtcggc atgatcgggtg tctccactgg tgttggcttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcatc cgggcctggc catcacggcg 1140
 tttgctttgt ggtggatgac ccagatgacc gttgagactt cattgaccgg tatcggagtt 1200
 cgcttccttg tatacgggtgt cggcttgggc tttgtcacgc aggtactggg gctgattgtt 1260
 caaaactcct tccctgtatc gcaggctcggg actgccacgg cggctaataa cttcttccgc 1320
 cagattgggt cggcattggg tgcttccatc gtgggttcga tgttcattca caaatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc cttgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagcttcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc 1560
 gtgattggca tgatgggtgcc actggccatt gttgcaatgc tgattttgtt cccactgcgc 1620
 caagagcgct tgaaggaaac catcgaataa 1650

<210> 151
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> CJI0323 impE2(G64D, F123C, S387T, M413T, N458K)

<400> 151
 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

OPA18598-seq list

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

OPA18598-seq list

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 Thr 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 Thr 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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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> Unknown

<220>
 <223> CJI0323 impE2(G64D, F123C, S387T, M413T, N458K)

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 aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
 ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

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 tccatttgcg ttattggctc gacgctcggg ggctttgccca atggcatggg catgctgac 420
 accggacgtg caatccaggg cttcgggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
 tttggcgtct cctccgtact ggggtccagtt ctcgggtggct gggtcaccga tgggtccggg 600
 tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttcgtactga agctgcgcgt gggcgagcaa ggctttaagg gctttgactg gatgggtttt 720
 gcggccatcg caatcacgac cagcaccctg attctgctca ccactgggg cggaagcgaa 780
 tacgagtggg cttccccaac tttttgtcc atggctgccg tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
 aaccgcaaca tggttttgac caccctcgcc ggtactgttt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgcag atgggtgcaca cctgacgcc aactgaagca 1020
 ggcttgatga tgatcccgat gatggtcggc atgatcgggtg tctccactgg tgttggcttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcgc cgggcctggc catcacggcg 1140
 tttgctttgt ggtggatgac ccagatgacc gttgagactt cattgaccgg tatcggagtt 1200
 cgcttccttg tattcgggtg cggcttgggc ttgtcacgc aggtactggg gctgattgtt 1260
 caaaactcct tccctgtatc gcaggtcggg actgccacgg cggctaataa cttcttccgc 1320
 cagattgggt cggcattggg tgcttccatc gtgggttcga tgttcattca caaatgcag 1380
 aatgagatgg ctaccggtt gcctgatgcc cttgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagcttcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc 1560
 gtgattggca tgatgggtgcc actggccatt gttgcaatgc tgattttgtt cccactgcgc 1620
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<210> 153
 <211> 549
 <212> PRT
 <213> Unknown

<220>
 <223> CJI0323 impE2(G64D, I243V, S387T, F405Y, M413T, N458K)

<400> 153
 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

OPA18598-seq list

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

OPA18598-seq list

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

Arg Phe Leu Val Tyr Gly Val Gly Leu Gly Phe Val Thr 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
435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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> 154
<211> 1650
<212> DNA
<213> Unknown

<220>
<223> CJI0323 impE2(G64D, I243V, S387T, F405Y, M413T, N458K)

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gaattcccag tggccaatgc tgaatggca acgccttcag caatcgaccc aaaccacggt 120
aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgctcac catgctgatg 180
agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgctcg cgagctcggc 240
ggcgtggacc agatgagctg ggtaatttca gcatttatgg tcaccatgac cattgctatg 300

OPA18598-seq list

ccactagccg gtcagctcgg tgaccgcatg ggccgcaagt gggctctacat ctcaggtatc 360
 tccattttcg ttattggctc gacgctcggg ggctttgccca atggcatggg catgctgac 420
 accggacgtg caatccaggg cttcgggtgcc ggcatcatga tgatttctc gcagtcgatt 480
 gtggctgagg ttgtctccgc acgtgagcgc ggcaagtca tgggtattat gggcggcgtc 540
 tttggcgtct cctccgtact ggggccagtt ctcgggtggct gggtcaccga tgggtccggg 600
 tggcgttggg gcctgtggat caacattcca ctgggtctgc tggcaattat tgtctgcgct 660
 ttcgtactga agctgcgcgt gggcgagcaa ggctttaagg gcttgactg gatgggtttt 720
 gcggccgtcg caatcacgac cagcaccctg attctgctca ccactgggg cggaagcgaa 780
 tacgagtggg cttccccaac tttttgtcc atggctgccg tagtcatcgt cggcgcgctg 840
 ctcaccgtgt tcattgagtc gcgtgcatcc cagccgctga tcccggttca gctatttaag 900
 aaccgcaaca tggttttgac caccctcgcc ggtactgtt tgggtctggc catgatgggc 960
 gtgctcggct acatgccaac ctacctgcag atgggtgcaca cctgacgcc aactgaagca 1020
 ggcttgatga tgatcccgat gatggtcggc atgatcgggtg tctccactgg tgttggcttc 1080
 atcatcgcta agaccggcaa ctacaagtac taccatcgc cgggcctggc catcacggcg 1140
 tttgctttgt ggtggatgac ccagatgacc gttgagactt cattgaccgg tatcggagtt 1200
 cgcttccttg tatacgggtgt cggcttgggc tttgtcacgc aggtactggg gctgattgtt 1260
 caaaactcct tccctgtatc gcaggctcgg actgccacgg cggctaataa cttcttccgc 1320
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 aatgagatgg ctaccggtt gcctgatgcc cttgcatcgt tgggcaagga aggcgccgct 1440
 atttcgcagc agttccaagg tgcagatgcc gccaaactcct tgactccgca cgcagtcgca 1500
 gagcttcccg atgtcctccg tgacgctatc ttaaattcct acaatgacgg tctgaccccc 1560
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<210> 155
 <211> 549
 <212> PRT
 <213> Unknown

<220>
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<400> 155
 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

OPA18598-seq list

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

OPA18598-seq list

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

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

Arg Phe Leu Val Tyr Gly Val Gly Leu Gly Phe Val Thr 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
 435 440 445

Ser Ile Val Gly Ser Met Phe Ile His Lys 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
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Lys Glu Thr Ile Glu
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 agctctttgg accagatgat ttccggttcc gctctgccaa ccatcgctcg cgagctcggc 240
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OPA18598-seq list

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