

OPA18596–sequence listing

<110> CJ CheilJedang Corporation
 <120> IMP–producing microorganism and method of producing IMP using the same
 <130> OPA18596
 <150> KR10–2017–0173504
 <151> 2017–12–15
 <160> 31
 <170> KoPatentIn 3.0
 <210> 1
 <211> 222
 <212> PRT
 <213> Unknown
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 <223> ImpE1

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

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Ala Met Glu Leu Val Lys Asn Tyr Thr Lys Gly Leu Glu Trp		
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<220>
 <223> ImpE2

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 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

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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
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 Val Leu Thr Thr Leu Ala Gly Thr Val Leu Gly Leu Ala Met Met Gly
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 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
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 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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 <213> Unknown

<220>
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 attccccgac gcacctttt taattattc agcacgaaag aaagcgccgt tattggcgcg 240
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 ctctgcagc tgatgggtga gcagatcaaa caacacttgg agtcttctca ccagagtcaa 360
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 gaatggtagc taaaaactcc accccaagca cggccggcca cgccagtgtc cacactgcgg 720
 aagaattccc agtggccaat gctgaaatgg caacgccttc agcaatcgac ccaaaccacg 780
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 ttgcggccat cgcaatcacg accagcacc caggtctgct caccacttgg ggcggaagcg 1440
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agaaccgcaa catggttttg accaccctcg ccggtactgt ttgggtctg gccatgatgg	1620
gctgctcgg ctacatgcca acctacctgc agatggtgca caccctgacg ccaactgaag	1680
caggcttgat gatgatcccg atgatggtcg gcatgatcgg tgtctccact ggtgttggt	1740
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agaatgagat ggctaccgct ttgctgatg cccttgcac gttgggcaag gaaggcgccg	2100
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cagagcttcc cgatgtctc cgtgacgcta tctaaattc ctacaatgac ggtctgacct	2220
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<220>
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ttggttgatg aatcgagctt tgacaaagta acaattgaag aaatttgca agccgcccgg	180
atttcccgac gcacctttt taattattc agcacgaaag aaagcgccgt tattggcgcg	240
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ctcctgcagc tgatggttga gcagatcaaa caacacttgg agtcttctca ccagagtcaa	360
gcgattcacg accgtcgtca gcgaatctt gcggatccgg atgtcgcggt acgtgcaatg	420
gcgtttcgca aggaacgctc acgggaaacc atggagctaa tcgctcaacg tcttcgggag	480
catcctgaag aacaacgcgc ccagaattg gatccggaaa cagaggcgat gctgctgagc	540
ggattcattc gcgaagccac ctggatggct atctcacgac ccgatcgtga ttgtgcactg	600
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669

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<212> DNA
<213> Unknown

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aaaaagaccg cggataacgt cggcattatc ttcgctgcct tgatgtcac catgtgatg 180
agctctttgg ggcagatgat ttccggttcc gctctgccaa ccatcgtcgg cgagctcggc 240
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cagattgggt cggcattggg tgcttccatc gtgggttcca tgttcattca caatatgcag 1380
aatgagatgg ctaccggtt gcctgatgcc ctgcatcgt tgggcaagga aggcgccgct 1440

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<210> 7
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<210> 8
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<223> impE1 kop-3

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<210> 9
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<400> 10
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<210> 11
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<400> 11
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<210> 12
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