

3 Sequence listing(OPA19164)

<110> CJ CheilJedang Corporation

<120> VARIANT PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE AND METHOD OF PREPARING PURINE NUCLEOTIDE USING THE SAME

<130> OPA19164

<150> KR 10-2019-0035683

<151> 2019-03-28

<160> 24

<170> KoPatentIn 3.0

<210> 1

<211> 1500

<212> DNA

<213> Unknown

<220>

<223> purF

<400> 1

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tactttggtc tgttcgcatt gcagcatcgt gggcaggaag ctgcaggtat cggcgtcggg	180
gatggagacc gcctcgttgt cttcaaagac atgggcttgg tctcgaatat tttcgatgag	240
tccattttta attccctcca tggctccgtg ggcgtggggc atacgcgcta ctcgactgcc	300
ggtggcaaag agtggtcgaa tgtccagccg atgtttaata ccacctcaaa tggggtagac	360
atcgctttgt gccacaacgg caacttggtg aactaccaag aactgcgcga tgaagcagta	420
gctctgggac tttaccgaga gaatgaaaaa tccctgtcgg attccatgat catgacagct	480
ttgctggcgc acggagtcgg ggaaggcaac tctgtctttg acgccgctaa gcaactgctg	540
ccaagcatca aaggcgcttt ttgcttgacc tttaccgatg gcaagacctt gtacgccgcg	600
cgtgacccgc acgggtgtacg ccccttggtc attggccgct tggcgcaagg ctgggttggt	660
gcttccgaaa cctgtgctgct ggatatcgtg ggcgcacagt ttatccgtga ggtagagccc	720
ggtgaactta tctctgtcaa tgaggcagga atccacagcg aaaaattcgc tgagccgaag	780
cgccagggct gcgtctttga atacgtctac ttggcacgtc cagacaccgt gatcaaaggc	840
cgcaacgttc acgcgacgcg cgtggatatt ggtcgcgcac ttgcgaaatc tcaccctgcg	900
ccagaagctg acatggtcat ccccggtgcca gaatccggaa acccggcagc tgttggctac	960
gcccgggaat cgggcctgac atttgcgcac ggcttggtca aaaacgccta cgtgggtcga	1020
accttcattc agcccacca gaccttgctc cagctgggta ttcgcctcaa gctcaacccc	1080
ctgcgcgagg tcatcgaggg caagtcactc gttgtttag atgactctat tgtccgcggc	1140
aacacccaac gcgcgctggt gcgcatgctg cgtgaagcag gcgctgctga agtgcacgtg	1200
cgcattgctt caccgccagt caaatggcct tgtttctacg gcattgactt cgcctcgcct	1260
ggtgaattga ttgctaatat caagccttct gatgatcctc aggtagtaac cgatgcagtg	1320

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tgccaagcta tcggagcaga ctctttaggg tttgtatctg tagatgagat ggttgaggca	1380
acgcaccaac ctatcaattc cttgtgtacc gcttgctttg atggcaacta cgaactcgga	1440
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 <213> Unknown

<220>
 <223> purF

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 Glu Gln Glu Pro Arg Glu Glu Cys Gly Val Phe Gly Val Trp Ala Pro
 20 25 30
 Gly Glu Asp Val Ala Thr Leu Thr Tyr Phe Gly Leu Phe Ala Leu Gln
 35 40 45
 His Arg Gly Gln Glu Ala Ala Gly Ile Gly Val Gly Asp Gly Asp Arg
 50 55 60
 Leu Val Val Phe Lys Asp Met Gly Leu Val Ser Asn Ile Phe Asp Glu
 65 70 75 80
 Ser Ile Leu Asn Ser Leu His Gly Ser Val Gly Val Gly His Thr Arg
 85 90 95
 Tyr Ser Thr Ala Gly Gly Lys Glu Trp Ser Asn Val Gln Pro Met Phe
 100 105 110
 Asn Thr Thr Ser Asn Gly Val Asp Ile Ala Leu Cys His Asn Gly Asn
 115 120 125
 Leu Val Asn Tyr Gln Glu Leu Arg Asp Glu Ala Val Ala Leu Gly Leu
 130 135 140
 Tyr Arg Glu Asn Glu Lys Ser Leu Ser Asp Ser Met Ile Met Thr Ala
 145 150 155 160
 Leu Leu Ala His Gly Val Gly Glu Gly Asn Ser Val Phe Asp Ala Ala
 165 170 175
 Lys Gln Leu Leu Pro Ser Ile Lys Gly Ala Phe Cys Leu Thr Phe Thr
 180 185 190
 Asp Gly Lys Thr Leu Tyr Ala Ala Arg Asp Pro His Gly Val Arg Pro
 195 200 205
 Leu Val Ile Gly Arg Leu Ala Gln Gly Trp Val Val Ala Ser Glu Thr
 210 215 220
 Cys Ala Leu Asp Ile Val Gly Ala Gln Phe Ile Arg Glu Val Glu Pro
 225 230 235 240
 Gly Glu Leu Ile Ser Val Asn Glu Ala Gly Ile His Ser Glu Lys Phe
 245 250 255
 Ala Glu Pro Lys Arg Gln Gly Cys Val Phe Glu Tyr Val Tyr Leu Ala

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260 265 270
 Arg Pro Asp Thr Val Ile Lys Gly Arg Asn Val His Ala Thr Arg Val
 275 280 285
 Asp Ile Gly Arg Ala Leu Ala Lys Ser His Pro Ala Pro Glu Ala Asp
 290 295 300
 Met Val Ile Pro Val Pro Glu Ser Gly Asn Pro Ala Ala Val Gly Tyr
 305 310 315 320
 Ala Arg Glu Ser Gly Leu Thr Phe Ala His Gly Leu Val Lys Asn Ala
 325 330 335
 Tyr Val Gly Arg Thr Phe Ile Gln Pro Thr Gln Thr Leu Arg Gln Leu
 340 345 350
 Gly Ile Arg Leu Lys Leu Asn Pro Leu Arg Glu Val Ile Glu Gly Lys
 355 360 365
 Ser Leu Val Val Val Asp Asp Ser Ile Val Arg Gly Asn Thr Gln Arg
 370 375 380
 Ala Leu Val Arg Met Leu Arg Glu Ala Gly Ala Ala Glu Val His Val
 385 390 395 400
 Arg Ile Ala Ser Pro Pro Val Lys Trp Pro Cys Phe Tyr Gly Ile Asp
 405 410 415
 Phe Ala Ser Pro Gly Glu Leu Ile Ala Asn Ile Lys Pro Ser Asp Asp
 420 425 430
 Pro Gln Val Val Thr Asp Ala Val Cys Glu Ala Ile Gly Ala Asp Ser
 435 440 445
 Leu Gly Phe Val Ser Val Asp Glu Met Val Glu Ala Thr His Gln Pro
 450 455 460
 Ile Asn Ser Leu Cys Thr Ala Cys Phe Asp Gly Asn Tyr Glu Leu Gly
 465 470 475 480
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 485 490 495
 Gln Lys Asn

<210> 3
 <211> 29
 <212> DNA
 <213> Artificial Sequence

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 <223> purA alt-1

<400> 3
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29

<210> 4
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<400> 4
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<212> DNA
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