

Sequence listing(OPA18147)

<110> CJ CheilJedang Corporation

<120> Novel aspartokinase variant and method of producing L-amino acid using the same

<130> OPA18147

<150> 10-2017-0083437

<151> 2017-06-30

<160> 36

<170> KoPatentIn 3.0

<210> 1

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

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20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile

260 265 270

<210>	2
<211>	1266
<212>	DNA
<213>	Corynebacterium glutamicum

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cgcgcgatgg agatcttgaa gaagcttcag gttcagggca actggaccaa tgtgctttac 1020
gacgaccagg tcggcaaagt ctccctcgtg ggtgctggca tgaagtctca cccagggtgtt 1080
accgcagagt tcatggaagc tctgcgcgat gtcaacgtga acatcgaatt gatttccacc 1140
tctgagattc gtatttccgt gctgatccgt gaagatgata tggatgctgc tgcacgtgca 1200
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<210> 3
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<212> PRT
<213> Corynebacterium glutamicum

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

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245	250	255
Gly Val Ala Thr Asp Lys Ser Glu	Ala Lys Val Thr Val	Leu Gly Ile
260	265	270
Ser Asp Lys Pro Gly Glu Ala	Ala Lys Val Phe Arg	Ala Leu Ala Asp
275	280	285
Ala Glu Ile Asn Ile Asp Met	Val Leu Gln Asn Val	Ser Ser Val Glu
290	295	300
Asp Gly Thr Thr Asp Ile Thr	Phe Thr Cys Pro Arg	Ser Asp Gly Arg
305	310	315
Arg Ala Met Glu Ile Leu Lys	Lys Leu Gln Val Gln	Gly Asn Trp Thr
325	330	335
Asn Val Leu Tyr Asp Asp Gln	Val Gly Lys Val Ser	Leu Val Gly Ala
340	345	350
Gly Met Lys Ser His Pro Gly	Val Thr Ala Glu Phe	Met Glu Ala Leu
355	360	365
Arg Asp Val Asn Val Asn Ile	Glu Lys Ile Ser Thr	Ser Glu Ile Arg
370	375	380
Ile Ser Val Leu Ile Arg Glu	Asp Asp Leu Asp	Ala Ala Ala Arg
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Leu His Glu Gln Phe Gln	Leu Gly Gly Glu Asp	Glu Ala Val Val Tyr
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Ala Gly Thr Gly Arg		
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<210> 4
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 <213> Corynebacterium glutamicum

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aaggctggaa atgatgtcgt ggttgctctg	
tccgcaatgg gagacaccac ggaatgaactt	180
ctagaacttg cagcggcagt gaatcccgtt	
ccgccagctc gtgaaatgga tatgctcctg	240
actgctgggtg agcgtatitc taacgtctc	
gtcgccatgg ctattgagtc ccttggcgca	300
gaagcccaat ctttcacggg ctctcaggct	
gggtgtctca ccaccgagcg ccacggaaac	360
gcacgcattg ttgatgtcac tccaggctgt	
gtgcgtgaag cactcgatga gggcaagatc	420
tgcatgttg ctggtttcca ggggtttaat	
aaagaaacct gcgatgtcac cacgttgggt	480
cggtgtgggt ctgacaccac tgcagttgcg	
ttggcagctg ctttgaacgc tgatgtgtgt	540
gagatttact cggacgttga cgggtgtgtat	
accgctgacc cgcgcacgtg tcctaataca	600
cagaagctgg aaaagctcag cttcgaagaa	
atgctggaac ttgctgctgt tggctccaag	660
attttgggtc tgcgcagtgt tgaatacgct	
cgtgcattca atgtgccact tcgcgtacgc	720
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attgccggct ctatggagga tattcctgtg	780
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aaggttttcc gtgcgttggc tgaatgcagaa atcaacattg acatggttct gcagaacgtc	900
tcttctgtag aagacggcac caccgacatc accttcacct gccctcgttc cgacggccgc	960
cgcgcatgg agatcttgaa gaagcttcag gttcagggca actggaccaa tgtgctttac	1020
gacgaccagg tcggcaaagt ctccctcgtg ggtgctggca tgaagtctca cccaggtgtt	1080
accgcagagt tcatggaagc tctgcgcgat gtcaacgtga acatcgaaaa gatttccacc	1140
tctgagattc gtatttccgt gctgatccgt gaagatgac tggtatgctgc tgcacgtgca	1200
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 20 25 30
 Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
 35 40 45
 Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
 50 55 60
 Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80
 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 85 90 95
 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
 100 105 110
 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125
 Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
 130 135 140
 Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
 145 150 155 160
 Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
 165 170 175
 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
 180 185 190
 Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
 195 200 205
 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
 210 215 220
 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu

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225		230		235		240
Ile Ala Gly Ser	Met Glu Asp Ile Pro Val Glu Glu Ala Val	Leu Thr				
	245		250		255	
Gly Val Ala Thr	Asp Lys Ser Glu Ala Lys Val Thr Val	Leu Gly Ile				
	260		265		270	
Ser Asp Lys Pro	Gly Glu Ala Ala Lys Val Phe Arg Ala	Leu Ala Asp				
	275		280		285	
Ala Glu Ile Asn	Ile Asp Met Val Leu Gln Asn Val	Ser Ser Val Glu				
	290		295		300	
Asp Gly Thr Thr	Asp Ile Thr Phe Thr Cys Pro Arg Ser	Asp Gly Arg				
305		310		315		320
Arg Ala Met Glu	Ile Leu Lys Lys Leu Gln Val Gln Gly Asn	Trp Thr				
	325		330		335	
Asn Val Leu Tyr	Asp Asp Gln Val Gly Lys Val Ser	Leu Val Gly Ala				
	340		345		350	
Gly Met Lys Ser	His Pro Gly Val Thr Ala Glu Phe	Met Glu Ala Leu				
	355		360		365	
Arg Asp Val Asn	Val Asn Ile Glu Met Ile Ser Thr	Ser Glu Ile Arg				
	370		375		380	
Ile Ser Val Leu	Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala	Arg Ala				
385		390		395		400
Leu His Glu Gln	Phe Gln Leu Gly Gly Glu Asp Glu Ala Val	Val Tyr				
	405		410		415	
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<210> 6
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tccgcaatgg gagacaccac ggaatgaactt ctagaacttg cagcggcagt gaatccggtt	180
ccgccagctc gtgaaatgga tatgtctctg actgtctggg agcgtatttc taacgtcttc	240
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atgttggaac ttgtgtctgt tggctccaag attttgggtc tgcgcagttg tgaatacgct	660
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tcttctgtag aagacggcac caccgacatc accttcacct gccctcgttc cgacggccgc      960
cgcgcgatgg agatcttgaa gaagcttcag gttcagggca actggaccaa tgtgcattac     1020
gacgaccagg tcggcaaagt ctccctcgtg ggtgctggca tgaagtctca cccagggtgtt     1080
accgcagagt tcatggaagc tctgcgcgat gtcaacgtga acatcgaaat gatttcacc     1140
tctgagattc gtatttccgt gctgatccgt gaagatgata tggatgctgc tgcacgtgca     1200
tggcatgagc agttccagct gggcggcgaa gacgaagccg tcgtttatgc aggcaccgga     1260
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Sequence listing(OPA18147)

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Sequence listing(OPA18147)

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<400> 22
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<210> 23
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<400> 23
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Sequence listing(OPA18147)

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43

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<211> 24

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24

<210> 29

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<212> DNA

<213> Artificial Sequence

<220>

<223> primer 23

<400> 29

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28

<210> 30

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> primer 24

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Sequence listing(OPA18147)

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Sequence listing(OPA18147)

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