

<110> CJ CheilJedang Corporation

<120> Variant of inner membrane protein and method for producing target product by using same

<130> OPA20205

<150> KR 10-2019-0172055

<151> 2019-12-20

<160> 37

<170> KoPatentIn 3.0

<210> 1

<211> 418

<212> PRT

<213> Unknown

<220>

<223> Escherichia coli YjeH

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

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

180

185

190

Met Phe Trp Cys Phe Val Gly Leu Glu Ala Phe Ala His Leu Ala Ser

195

200

205

Glu Phe Lys Asn Pro Glu Arg Asp Phe Pro Arg Ala Leu Met Ile Gly

210

215

220

Leu Leu Leu Ala Gly Leu Val Tyr Trp Gly Cys Thr Val Val Val Leu

225

230

235

240

His Phe Asp Ala Tyr Gly Glu Lys Met Ala Ala Ala Ala Ser Leu Pro

245

250

255

Lys Ile Val Val Gln Leu Phe Gly Val Gly Ala Leu Trp Ile Ala Cys

260

265

270

Val Ile Gly Tyr Leu Ala Cys Phe Ala Ser Leu Asn Ile Tyr Ile Gln

275

280

285

Ser Phe Ala Arg Leu Val Trp Ser Gln Ala Gln His Asn Pro Asp His

290

295

300

Tyr Leu Ala Arg Leu Ser Ser Arg His Ile Pro Asn Asn Ala Leu Asn

305

310

315

320

Ala Val Leu Gly Cys Cys Val Val Ser Thr Leu Val Ile His Ala Leu
325 330 335

Glu Ile Asn Leu Asp Ala Leu Ile Ile Tyr Ala Asn Gly Ile Phe Ile
340 345 350

Met Ile Tyr Leu Leu Cys Met Leu Ala Gly Cys Lys Leu Leu Gln Gly
355 360 365

Arg Tyr Arg Leu Leu Ala Val Val Gly Gly Leu Leu Cys Val Leu Leu
370 375 380

Leu Ala Met Val Gly Trp Lys Ser Leu Tyr Ala Leu Ile Met Leu Ala
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aaaaggcgca ctcaaagcca tcaccacgac ctggccgaca acgaaaatcc aacgctgcct		180
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<223> Tn_3 R

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<223> CJ7

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catcttcttt agcaacaagt tgaggggtag gtgcaaataa gaacgacata gaaatcgtct 180

cctttctgtt ttaatacaac atacaccacc acctaaaaat tccccgacca gcaagttcac 240

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tccaccacca agtacatcgg aggacactcc gacgttgtg gcggccttgt ggttaccac	660
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<223> metB_N_del R

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cccatccact aaacttaaac agatgtgac gcccggc

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<223> metY_N_del F

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<223> metY_N_del R

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<223> metY_C_del F

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120

tccgcaatgg gagacaccac ggatgaactt ctagaacttg cagcggcagt gaatcccgtt

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gaagccggag caatcattac aaacgctgaa atcgctatc accgctgggg tgaataccgc

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gtagataaag aaggacgcag caatgtcgtt ctcatcgaac acgccctcac tggagattcc

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300

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360

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<400> 35

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20 25 30

Ala Ala Leu Val Ala Gly Asn Asn Ser Leu Trp Ala Trp Pro Val Leu

35 40 45

Ile Ile Leu Val Phe Pro Ile Ala Ile Val Phe Ala Ile Leu Gly Arg

50 55 60

His Tyr Pro Ser Ala Gly Gly Val Ala His Phe Val Gly Met Ala Phe

65 70 75 80

Gly Ser Arg Leu Glu Arg Val Thr Gly Trp Leu Asn Leu Ser Val Ile

85 90 95

Pro Val Gly Leu Pro Ala Ala Leu Gln Ile Ala Ala Gly Phe Gly Gln

100 105 110

Ala Met Phe Gly Trp His Ser Trp Gln Leu Leu Leu Ala Glu Leu Gly

115 120 125

Thr Leu Ala Leu Val Trp Tyr Ile Gly Thr Arg Gly Ala Ser Ser Ser

130

135

140

Ala Asn Leu Gln Thr Val Ile Ala Gly Leu Ile Val Ala Leu Ile Val

145

150

155

160

Ala Ile Trp Trp Ala Gly Asp Ile Lys Pro Ala Asn Ile Pro Phe Pro

165

170

175

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

180

185

190

Met Phe Trp Cys Phe Val Gly Leu Glu Ala Phe Ala His Leu Ala Ser

195

200

205

Glu Phe Lys Asn Pro Glu Arg Asp Phe Pro Arg Ala Leu Met Ile Gly

210

215

220

Leu Leu Leu Ala Gly Leu Val Tyr Trp Gly Cys Thr Val Val Val Leu

225

230

235

240

His Phe Asp Ala Tyr Gly Glu Lys Met Ala Ala Ala Ala Ser Leu Pro

245

250

255

Lys Ile Val Val Gln Leu Phe Gly Val Gly Ala Leu Trp Ile Ala Cys

260

265

270

Val Ile Gly Tyr Leu Ala Cys Phe Ala Ser Leu Asn Ile Tyr Ile Gln

275

280

285

Ser Phe Ala Arg Leu Val Trp Ser Gln Ala Gln His Asn Pro Asp His

290

295

300

Tyr Leu Ala Arg Leu Ser Ser Arg His Ile Pro Asn Asn Ala Leu Asn

305

310

315

320

Ala Val Leu Gly Cys Cys Val Val Ser Thr Leu Val Ile His Ala Leu

325

330

335

Glu Ile Asn Leu Asp Ala Leu Ile Ile Tyr Ala Asn Gly Ile Phe Ile

340

345

350

Met Ile Tyr Leu Leu Cys Met Leu Ala Gly Cys Lys Leu Leu Gln Gly

355

360

365

Arg Tyr Arg Leu Leu Ala Val Val Gly Gly Leu Leu Cys Val Leu Leu

370

375

380

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400

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Thr Thr

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Ile Ile Leu Val Phe Pro Ile Ala Ile Val Phe Ala Ile Leu Gly Arg
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His Tyr Pro Ser Ala Gly Gly Val Ala His Phe Val Gly Met Ala Phe
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His Phe Asp Ala Tyr Gly Glu Lys Met Ala Ala Ala Ala Ser Leu Pro

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Val Ile Gly Tyr Leu Ala Cys Phe Ala Ser Leu Asn Ile Tyr Ile Gln

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Ser Phe Ala Arg Leu Val Trp Ser Gln Ala Gln His Asn Pro Asp His

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Tyr Leu Ala Arg Leu Ser Ser Arg His Ile Pro Asn Asn Ala Leu Asn

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Ala Val Leu Gly Cys Cys Val Val Ser Thr Leu Val Ile His Ala Leu

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Glu Ile Asn Leu Asp Ala Leu Ile Ile Tyr Ala Asn Gly Ile Leu Ile

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