

<110> CJ CheilJedang Corporation

<120> L-METHIONINE PRODUCING MICROORGANISM TO WHICH PROTEIN ENCODED BY FOREIGN metZ GENE IS INTRODUCED AND METHOD FOR PRODUCING L-METHIONINE USING SAME

<130> OPA20069

<150> KR 10-2019-0134797

<151> 2019-10-28

<160> 81

<170> KoPatentIn 3.0

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120

cgacccaac gtgtacgaaa tccacgacga cacccaactc atgctggatc ttctccgtgc	180
cgagaaaatc ctcatgggtc agggcactgg ctcaactgg ccacatcacg atcacttccg	240
agtggtcacc ctgccatggg catcccagtt ggaaaacgca attgagcgcc tgggtaactt	300
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gttgggggtg ccagcacagg tgtgtggggc ctacttcat ctgctccac caccatcatt	1140
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atcatttggg gtgtggttct cattgtggcg atgggagctt tcgcggcgtg gcgaggtgtg	3060
cgtgcgctgg ttggtttggt cgtcaccttg ggaattgttg gtattttctt gctgccagga	3120
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atttggtgac cgatggttca cggaatcaac tggaatcgg cagctgcgtt ggcgggcacg	3240
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<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 50

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<210> 51

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 51

caggtagca gtacttctca agtttctcgg cgggtg

35

<210> 52

<211> 35

<212> DNA

<213> Artificial Sequence

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<223> primer

<400> 52

aacttgagaa gtactgctaa cctgcagaaa ccttg

35

<210> 53

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 53

gcctgcaggt cgactctaga ctccgcagaa atcgtggggc

40

<210> 54

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 54

cgccgagaaa cttgagaagt ggcgctcat gtcaa

35

<210> 55

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 55

ctgcaggta gcagtttagt caaggccccg caaca

35

<210> 56

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 56

ctgcaggta gcagttcaca agctgttaag cgaag

35

<210> 57

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 57

ctgcaggta gcagtcaga tcaccgcgag cgcct

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<210> 58

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 58

ttctccgtgc cgagaaaatc

20

<210> 59
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<220>
<223> primer

<400> 59
gtagatgatac tcgccatttg 20

<210> 60
<211> 394
<212> PRT
<213> Chromobacterium violaceum

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1 5 10 15

Ile Arg Ala Gly Leu Glu Thr Ser Gln Phe Asn Glu His Ser Gln Gly
20 25 30

Leu Phe Leu Thr Ser Ser Phe Thr Tyr Glu Ser Ala Ala Gln Ala Ala
35 40 45

Ala Met Phe Leu Gly Glu Ile Asp Gly Tyr Thr Tyr Ser Arg Phe Thr

50

55

60

Asn Pro Thr Val Ala Ala Phe Gln His Arg Leu Ala Gln Met Glu Gly

65

70

75

80

Gly Glu Arg Ala Ile Ala Thr Ala Thr Gly Met Ala Ala Ile Gln Ala

85

90

95

Ile Met Met Thr Leu Leu Gln Ala Gly Asp His Ile Val Ser Ser Gln

100

105

110

Ser Leu Phe Gly Ser Thr Thr Asn Leu Phe Ala Asn Gln Leu Ala Lys

115

120

125

Phe Ala Val Ala Thr Asp Phe Val Asp Ala Arg Asp Leu Ser Ala Trp

130

135

140

Arg Glu Ala Leu Arg Pro Asn Thr Lys Leu Leu Phe Leu Glu Thr Pro

145

150

155

160

Ser Asn Pro Leu Thr Glu Val Ala Asp Ile Ala Ala Ile Ala Asp Ile

165

170

175

Ala His Ala His Gly Ala Leu Leu Val Val Asp Asn Ser Phe Cys Ser

180

185

190

Pro Ala Leu Gln Gln Pro Leu Lys Leu Gly Ala Asp Leu Val Met His

195	200	205	
Ser Ala Thr Lys Phe Ile Asp Gly His Gly Arg Val Met Gly Gly Ala			
210	215	220	
Val Val Gly Ser Asp Lys Leu Val Glu Gln Val Tyr Leu His Val Arg			
225	230	235	240
Ala Ala Gly Pro Ser Leu Ala Pro Phe Asn Ala Trp Thr Leu Leu Ser			
	245	250	255
Gly Leu Glu Thr Leu His Leu Arg Met Glu Lys His Ser Ala Asn Ala			
260	265	270	
Leu Glu Leu Ala Arg Trp Leu Glu Ala Gln Pro Asn Val Glu Arg Val			
275	280	285	
Tyr Tyr Pro Gly Leu Glu Ser His Pro Gln His Glu Leu Ala Leu Arg			
290	295	300	
Gln Gln Lys Ser Gly Gly Ala Val Val Ser Phe Val Val Lys Gly Gly			
305	310	315	320
Arg Lys Ala Ala Trp Lys Val Val Asp Ala Val Arg Val Ile Ser Arg			
	325	330	335
Thr Ala Asn Leu Gly Asp Val Lys Thr Thr Leu Thr His Pro Ala Ser			
340	345	350	

Thr Thr His Ala Arg Val Thr Gln Glu Ala Arg Glu Arg Ala Gly Ile

355

360

365

Val Glu Gly Leu Leu Arg Val Ser Val Gly Leu Glu Asn Val Arg Asp

370

375

380

Leu Gln Gln Asp Leu Leu Arg Gly Leu Asp

385

390

<210> 61

<211> 399

<212> PRT

<213> Unknown

<220>

<223> Hyphomonas neptunium

<400> 61

Met Ala Asp Ala Pro Gly Gly Asp Lys Lys Gly Trp Lys Pro Ala Thr

1

5

10

15

Gln Ala Val Arg Gly Gly Leu Met Arg Ser Gln His Gly Glu Ile Ser

20

25

30

Glu Ala Leu Tyr Leu Thr Ser Gly Tyr Ala Tyr Asp Ser Ala Glu Gln

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

Ala Thr Pro Val Leu Gln Arg Pro Leu Glu Met Gly Ala Asp Val Ile

195

200

205

Ala Tyr Ser Ala Thr Lys His Met Asp Gly Gln Gly Arg Val Leu Leu

210

215

220

Gly Ala Ile Leu Thr Asp Ala Lys Arg Met Ser Asp Val Tyr Asp Pro

225

230

235

240

Trp Leu Arg His Met Gly Pro Ala Ala Ser Pro Phe Asn Ala Trp Val

245

250

255

Val Leu Lys Gly Leu Glu Thr Met Gln Leu Arg Val Glu Ala Gln Ser

260

265

270

Arg Thr Ala Ala Arg Leu Ala Asp Val Leu Ala Asp His Pro Ala Val

275

280

285

Asn Ala Val Arg Tyr Pro His Arg Lys Asp His Pro His Tyr Glu Val

290

295

300

His Lys Arg Gln Met Lys Ser Gly Gly Thr Leu Leu Ala Leu Ser Leu

305

310

315

320

Lys Gly Gly Gln Asp Ala Ala Phe Arg Phe Leu Asn Gly Leu Gln Leu

325

330

335

Val Asp Ile Cys Asn Asn Leu Gly Asp Thr Lys Ser Leu Ala Cys His

340

345

350

Pro Ser Thr Thr Thr His Arg Ala Leu Ser Asp Glu Asp Gln Ala Ala

355

360

365

Met Gly Leu Asp Arg Ser Trp Val Arg Leu Ser Val Gly Leu Glu Asp

370

375

380

Ala Asp Asp Leu Glu Ala Asp Leu Leu Ala Ser Leu Asn Ser Leu

385

390

395

<210> 62

<211> 393

<212> PRT

<213> Rhodobacter sphaeroides

<400> 62

Met Thr Lys Asp Trp Lys Thr Arg Thr Gln Leu Val His Gly Gly Ser

1

5

10

15

Arg Arg Ser Gln Tyr Gly Glu Met Ala Glu Ala Ile Phe Leu Thr Gln

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30

Gly Phe Val Tyr Asp Ser Ala Glu Gln Ala Glu Ala Arg Phe Ile Glu

35

40

45

Thr Gly Ala Asp Glu Phe Ile Tyr Ala Arg Tyr Gly Asn Pro Thr Thr

50

55

60

Arg Met Phe Glu Glu Arg Ile Ala Ala Val Glu Gly Thr Glu Asp Ala

65

70

75

80

Phe Ala Thr Ala Ser Gly Met Ala Ala Ile His Gly Val Leu Thr Ser

85

90

95

Ile Val Arg Ala Gly Asp His Leu Val Ala Ala Arg Ala Leu Phe Gly

100

105

110

Ser Cys Ile Tyr Ile Leu Glu Glu Val Leu Gly Arg Phe Gly Val Glu

115

120

125

Val Thr Phe Val Asp Gly Thr Asp Leu Asp Gln Trp Arg Ala Ala Val

130

135

140

Arg Pro Gly Thr Lys Ala Val Phe Phe Glu Ser Val Ser Asn Pro Thr

145

150

155

160

Leu Glu Val Ala Asp Ile Gly Ala Ile Ala Glu Ile Ala His Ala Val

165

170

175

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

180

185

190

Thr Ala Val Arg Gln Gly Ala Asp Val Val Ile Tyr Ser Ala Thr Lys

195	200	205	
His Ile Asp Gly Gln Gly Arg Ala Leu Gly Gly Val Val Cys Ala Ser			
210	215	220	
Gln Ala Phe Ile Arg Lys Val Leu Glu Pro Phe Met Lys His Thr Gly			
225	230	235	240
Gly Ser Met Ser Pro Phe Asn Ala Trp Leu Met Leu Asn Gly Met Ala			
	245	250	255
Thr Leu Asp Leu Arg Cys Arg Ala Met Ala Asp Thr Ala Glu Lys Ile			
	260	265	270
Ala Arg Ala Leu Glu Gly His Pro Gln Leu Gly Arg Val Ile His Pro			
	275	280	285
Ala Leu Glu Ser His Pro Gln His Glu Met Ala Lys Ala Gln Met Glu			
	290	295	300
Arg Pro Gly Thr Met Ile Ala Leu Asp Leu Ala Gly Gly Lys Glu Ala			
305	310	315	320
Ala Phe Arg Phe Leu Asp Ala Leu Arg Ile Val Lys Ile Ser Asn Asn			
	325	330	335
Leu Gly Asp Ala Arg Ser Ile Ala Thr His Pro Ala Thr Thr Thr His			
	340	345	350

Gln Arg Leu Ser Asp Ala Gln Lys Ala His Leu Gly Ile Thr Pro Gly

355

360

365

Leu Val Arg Leu Ser Val Gly Leu Glu Asp Ala Asp Asp Leu Ile Ala

370

375

380

Asp Leu Lys Gln Ala Leu Ala Val Ile

385

390

<210> 63

<211> 1185

<212> DNA

<213> Chromobacterium violaceum

<400> 63

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cgcaaggccg cgtggaaagt ggtggacgcg gtcagggtga tctcgcgcac cgccaatctg	1020
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gaggcgcgcg agcgcgccg catcgtcgag gggctgttc gcgtcagcgt cggcctggaa	1140
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<210> 64
 <211> 1200
 <212> DNA
 <213> Unknown

<220>
 <223> Hyphomonas neptunium

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cattatgagg tgcacaagcg ccagatgaaa tcgggcggca cgctgctcgc gctgtcgtc	960
aaggcggggc aggacgcggc gttccgcttc ctcaacgggc tgcagctggt cgacatctgc	1020
aacaaccttg gcgatacgaa atcgctggcc tgcattccct ccaccacgac gcaccgcgcg	1080
ttgagtgatg aggatcaggc ggcgatgggg cttgaccgca gctgggtccg gctctctgtt	1140
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<210> 65

<211> 1182

<212> DNA

<213> Rhodobacter sphaeroides

<400> 65

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tatggcgaaa tggccgaggc gatcttctg acccagggt tcgttacga ctggccgaa 120

caggccgaag cgcgcttcat cgagaccgc gccgacgaat tcattatgc ccgtacggc 180

aacccacga cgcgcatgtt cgaagagcg atcgggccg tcgagggcac cgaggatgcg 240

ttgccaccg cctcgggcat ggccgcgac cacggcgtgc tcacctgat cgtcgggcg 300

ggcgatcac tggtagggc gcgcgctctg ttcggtcct gcattacat cctcaggag 360

gtgctggcc gattcggcgt cgaggtagc ttctcgacg gcaccgatct cgatcagtg 420

cgcgcggcg tgcggcccg cacgaaggc gtgttctcg agtcggtctc gaatccgacg 480

ctcaggttg ccgatatcg cgccatgcc gagatgccc atgccgtgg cgcgtcgtc 540

atcgtggaca atgtcttcg gacgccgct ttctcgacg cggcgcgca gggcgcgat 600

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gtctgcgct cgcaggcct catccgaag gtgtcgaac cttcatgaa gcacaccgc 720

ggctcgatga gccccttcaa cgctggctc atgctgaacg ggatggcgac gctcgacctg	780
cgctgccgcg cgatggccga cacggccgag aagatcgccc gcgcgctcga gggccatccg	840
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gcgcagatgg agcgtcccgg cacgatgac gcgctcgacc tcgccggggg caaggaggcg	960
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cgctcgatcg cgaccaccc ggcaacgacc acccaccagc gtctttccga cgcgcagaag	1080
gcccattcgc gcatcacgcc cgggctcgtg cggctgtcgg tggggctcga ggatcgggac	1140
gacctgatcg ccgatctgaa acaggcgctc gcggtgatct ga	1182

<210> 66

<211> 404

<212> PRT

<213> Artificial Sequence

<220>

<223> RspmetZ_long

<400> 66

Met Gly Ile Ala Phe Arg Glu Gly Arg Thr Gly Met Thr Lys Asp Trp
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Lys Thr Arg Thr Gln Leu Val His Gly Gly Ser Arg Arg Ser Gln Tyr
20 25 30

Gly Glu Met Ala Glu Ala Ile Phe Leu Thr Gln Gly Phe Val Tyr Asp
35 40 45

Ser Ala Glu Gln Ala Glu Ala Arg Phe Ile Glu Thr Gly Ala Asp Glu
50 55 60

Phe Ile Tyr Ala Arg Tyr Gly Asn Pro Thr Thr Arg Met Phe Glu Glu
65 70 75 80

Arg Ile Ala Ala Val Glu Gly Thr Glu Asp Ala Phe Ala Thr Ala Ser
85 90 95

Gly Met Ala Ala Ile His Gly Val Leu Thr Ser Ile Val Arg Ala Gly
100 105 110

Asp His Leu Val Ala Ala Arg Ala Leu Phe Gly Ser Cys Ile Tyr Ile
115 120 125

Leu Glu Glu Val Leu Gly Arg Phe Gly Val Glu Val Thr Phe Val Asp
130 135 140

Gly Thr Asp Leu Asp Gln Trp Arg Ala Ala Val Arg Pro Gly Thr Lys

145 150 155 160

Ala Val Phe Phe Glu Ser Val Ser Asn Pro Thr Leu Glu Val Ala Asp

165 170 175

Ile Gly Ala Ile Ala Glu Ile Ala His Ala Val Gly Ala Leu Val Ile

180 185 190

Val Asp Asn Val Phe Ala Thr Pro Val Phe Ser Thr Ala Val Arg Gln

195 200 205

Gly Ala Asp Val Val Ile Tyr Ser Ala Thr Lys His Ile Asp Gly Gln

210 215 220

Gly Arg Ala Leu Gly Gly Val Val Cys Ala Ser Gln Ala Phe Ile Arg

225 230 235 240

Lys Val Leu Glu Pro Phe Met Lys His Thr Gly Gly Ser Met Ser Pro

245 250 255

Phe Asn Ala Trp Leu Met Leu Asn Gly Met Ala Thr Leu Asp Leu Arg

260 265 270

Cys Arg Ala Met Ala Asp Thr Ala Glu Lys Ile Ala Arg Ala Leu Glu

275 280 285

Gly His Pro Gln Leu Gly Arg Val Ile His Pro Ala Leu Glu Ser His

290 295 300

Pro Gln His Glu Met Ala Lys Ala Gln Met Glu Arg Pro Gly Thr Met
305 310 315 320

Ile Ala Leu Asp Leu Ala Gly Gly Lys Glu Ala Ala Phe Arg Phe Leu
 325 330 335

Asp Ala Leu Arg Ile Val Lys Ile Ser Asn Asn Leu Gly Asp Ala Arg
 340 345 350

Ser Ile Ala Thr His Pro Ala Thr Thr Thr His Gln Arg Leu Ser Asp
 355 360 365

Ala Gln Lys Ala His Leu Gly Ile Thr Pro Gly Leu Val Arg Leu Ser
 370 375 380

Val Gly Leu Glu Asp Ala Asp Asp Leu Ile Ala Asp Leu Lys Gln Ala
385 390 395 400

Leu Ala Val Ile

<210> 67

<211> 404

<212> PRT

<213> Artificial Sequence

<220>

<223> RspmetZ_3

<400> 67

Met Gly Asn Ala Phe Arg Glu Gly Arg Thr Gly Met Thr Lys Asp Trp

1 5 10 15

Lys Thr Arg Thr Gln Leu Val His Gly Gly Ser Arg Arg Ser Gln Tyr

20 25 30

Gly Glu Met Ala Glu Ala Ile Phe Leu Thr Gln Gly Phe Val Tyr Asp

35 40 45

Ser Ala Glu Gln Ala Glu Ala Arg Phe Ile Glu Thr Gly Ala Asp Glu

50 55 60

Phe Ile Tyr Ala Arg Tyr Gly Asn Pro Thr Thr Arg Met Phe Glu Glu

65 70 75 80

Arg Ile Ala Ala Val Glu Gly Thr Glu Asp Ala Phe Ala Thr Ala Ser

85 90 95

Gly Met Ala Ala Ile His Gly Val Leu Thr Ser Ile Val Arg Ala Gly

100 105 110

Asp His Leu Val Ala Ala Arg Ala Leu Phe Gly Ser Cys Ile Tyr Ile

115 120 125

Leu Glu Glu Val Leu Gly Arg Phe Gly Val Glu Val Thr Phe Val Asp

130

135

140

Gly Thr Asp Leu Asp Gln Trp Arg Ala Ala Val Arg Pro Gly Thr Lys

145

150

155

160

Ala Val Phe Phe Glu Ser Val Ser Asn Pro Thr Leu Glu Val Ala Asp

165

170

175

Ile Gly Ala Ile Ala Glu Ile Ala His Ala Val Gly Ala Leu Val Ile

180

185

190

Val Asp Asn Val Phe Ala Thr Pro Val Phe Ser Thr Ala Val Arg Gln

195

200

205

Gly Ala Asp Val Val Ile Tyr Ser Ala Thr Lys His Ile Asp Gly Gln

210

215

220

Gly Arg Ala Leu Gly Gly Val Val Cys Ala Ser Gln Ala Phe Ile Arg

225

230

235

240

Lys Val Leu Glu Pro Phe Met Lys His Thr Gly Gly Ser Met Ser Pro

245

250

255

Phe Asn Ala Trp Leu Met Leu Asn Gly Met Ala Thr Leu Asp Leu Arg

260

265

270

Cys Arg Ala Met Ala Asp Thr Ala Glu Lys Ile Ala Arg Ala Leu Glu

275

280

285

Gly His Pro Gln Leu Gly Arg Val Ile His Pro Ala Leu Glu Ser His

290

295

300

Pro Gln His Glu Met Ala Lys Ala Gln Met Glu Arg Pro Gly Thr Met

305

310

315

320

Ile Ala Leu Asp Leu Ala Gly Gly Lys Glu Ala Ala Phe Arg Phe Leu

325

330

335

Asp Ala Leu Arg Ile Val Lys Ile Ser Asn Asn Leu Gly Asp Ala Arg

340

345

350

Ser Ile Ala Thr His Pro Ala Thr Thr Thr His Gln Arg Leu Ser Asp

355

360

365

Ala Gln Lys Ala His Leu Gly Ile Thr Pro Gly Leu Val Arg Leu Ser

370

375

380

Val Gly Leu Glu Asp Ala Asp Asp Leu Ile Ala Asp Leu Lys Gln Ala

385

390

395

400

Leu Ala Val Ile

<210> 68
<211> 404
<212> PRT
<213> Artificial Sequence

<220>
<223> RspmetZ_65

<400> 68
Met Gly Ile Ala Phe Arg Glu Gly Arg Thr Gly Met Thr Lys Asp Trp
1 5 10 15

Lys Thr Arg Thr Gln Leu Val His Gly Gly Ser Arg Arg Ser Gln Tyr
20 25 30

Gly Glu Met Ala Glu Ala Ile Phe Leu Thr Gln Gly Phe Val Tyr Asp
35 40 45

Ser Ala Glu Gln Ala Glu Ala Arg Phe Ile Glu Thr Gly Ala Asp Glu
50 55 60

Tyr Ile Tyr Ala Arg Tyr Gly Asn Pro Thr Thr Arg Met Phe Glu Glu
65 70 75 80

Arg Ile Ala Ala Val Glu Gly Thr Glu Asp Ala Phe Ala Thr Ala Ser
85 90 95

Gly Met Ala Ala Ile His Gly Val Leu Thr Ser Ile Val Arg Ala Gly

100

105

110

Asp His Leu Val Ala Ala Arg Ala Leu Phe Gly Ser Cys Ile Tyr Ile

115

120

125

Leu Glu Glu Val Leu Gly Arg Phe Gly Val Glu Val Thr Phe Val Asp

130

135

140

Gly Thr Asp Leu Asp Gln Trp Arg Ala Ala Val Arg Pro Gly Thr Lys

145

150

155

160

Ala Val Phe Phe Glu Ser Val Ser Asn Pro Thr Leu Glu Val Ala Asp

165

170

175

Ile Gly Ala Ile Ala Glu Ile Ala His Ala Val Gly Ala Leu Val Ile

180

185

190

Val Asp Asn Val Phe Ala Thr Pro Val Phe Ser Thr Ala Val Arg Gln

195

200

205

Gly Ala Asp Val Val Ile Tyr Ser Ala Thr Lys His Ile Asp Gly Gln

210

215

220

Gly Arg Ala Leu Gly Gly Val Val Cys Ala Ser Gln Ala Phe Ile Arg

225

230

235

240

Lys Val Leu Glu Pro Phe Met Lys His Thr Gly Gly Ser Met Ser Pro

	245	250	255
Phe Asn Ala Trp Leu Met Leu Asn Gly Met Ala Thr Leu Asp Leu Arg			
	260	265	270
Cys Arg Ala Met Ala Asp Thr Ala Glu Lys Ile Ala Arg Ala Leu Glu			
	275	280	285
Gly His Pro Gln Leu Gly Arg Val Ile His Pro Ala Leu Glu Ser His			
	290	295	300
Pro Gln His Glu Met Ala Lys Ala Gln Met Glu Arg Pro Gly Thr Met			
305	310	315	320
Ile Ala Leu Asp Leu Ala Gly Gly Lys Glu Ala Ala Phe Arg Phe Leu			
	325	330	335
Asp Ala Leu Arg Ile Val Lys Ile Ser Asn Asn Leu Gly Asp Ala Arg			
	340	345	350
Ser Ile Ala Thr His Pro Ala Thr Thr Thr His Gln Arg Leu Ser Asp			
	355	360	365
Ala Gln Lys Ala His Leu Gly Ile Thr Pro Gly Leu Val Arg Leu Ser			
	370	375	380
Val Gly Leu Glu Asp Ala Asp Asp Leu Ile Ala Asp Leu Lys Gln Ala			
385	390	395	400

Leu Ala Val Ile

<210> 69

<211> 404

<212> PRT

<213> Artificial Sequence

<220>

<223> RspmetZ_104

<400> 69

Met Gly Ile Ala Phe Arg Glu Gly Arg Thr Gly Met Thr Lys Asp Trp

1 5 10 15

Lys Thr Arg Thr Gln Leu Val His Gly Gly Ser Arg Arg Ser Gln Tyr

20 25 30

Gly Glu Met Ala Glu Ala Ile Phe Leu Thr Gln Gly Phe Val Tyr Asp

35 40 45

Ser Ala Glu Gln Ala Glu Ala Arg Phe Ile Glu Thr Gly Ala Asp Glu

50 55 60

Phe Ile Tyr Ala Arg Tyr Gly Asn Pro Thr Thr Arg Met Phe Glu Glu

65 70 75 80

Arg Ile Ala Ala Val Glu Gly Thr Glu Asp Ala Phe Ala Thr Ala Ser

85 90 95

Gly Met Ala Ala Ile His Gly Ala Leu Thr Ser Ile Val Arg Ala Gly

100 105 110

Asp His Leu Val Ala Ala Arg Ala Leu Phe Gly Ser Cys Ile Tyr Ile

115 120 125

Leu Glu Glu Val Leu Gly Arg Phe Gly Val Glu Val Thr Phe Val Asp

130 135 140

Gly Thr Asp Leu Asp Gln Trp Arg Ala Ala Val Arg Pro Gly Thr Lys

145 150 155 160

Ala Val Phe Phe Glu Ser Val Ser Asn Pro Thr Leu Glu Val Ala Asp

165 170 175

Ile Gly Ala Ile Ala Glu Ile Ala His Ala Val Gly Ala Leu Val Ile

180 185 190

Val Asp Asn Val Phe Ala Thr Pro Val Phe Ser Thr Ala Val Arg Gln

195 200 205

Gly Ala Asp Val Val Ile Tyr Ser Ala Thr Lys His Ile Asp Gly Gln

210 215 220

Gly Arg Ala Leu Gly Gly Val Val Cys Ala Ser Gln Ala Phe Ile Arg

225 230 235 240

Lys Val Leu Glu Pro Phe Met Lys His Thr Gly Gly Ser Met Ser Pro

245 250 255

Phe Asn Ala Trp Leu Met Leu Asn Gly Met Ala Thr Leu Asp Leu Arg

260 265 270

Cys Arg Ala Met Ala Asp Thr Ala Glu Lys Ile Ala Arg Ala Leu Glu

275 280 285

Gly His Pro Gln Leu Gly Arg Val Ile His Pro Ala Leu Glu Ser His

290 295 300

Pro Gln His Glu Met Ala Lys Ala Gln Met Glu Arg Pro Gly Thr Met

305 310 315 320

Ile Ala Leu Asp Leu Ala Gly Gly Lys Glu Ala Ala Phe Arg Phe Leu

325 330 335

Asp Ala Leu Arg Ile Val Lys Ile Ser Asn Asn Leu Gly Asp Ala Arg

340 345 350

Ser Ile Ala Thr His Pro Ala Thr Thr Thr His Gln Arg Leu Ser Asp

355 360 365

Ala Gln Lys Ala His Leu Gly Ile Thr Pro Gly Leu Val Arg Leu Ser

370

375

380

Val Gly Leu Glu Asp Ala Asp Asp Leu Ile Ala Asp Leu Lys Gln Ala

385

390

395

400

Leu Ala Val Ile

<210> 70

<211> 404

<212> PRT

<213> Artificial Sequence

<220>

<223> RspmetZ_196

<400> 70

Met Gly Ile Ala Phe Arg Glu Gly Arg Thr Gly Met Thr Lys Asp Trp

1

5

10

15

Lys Thr Arg Thr Gln Leu Val His Gly Gly Ser Arg Arg Ser Gln Tyr

20

25

30

Gly Glu Met Ala Glu Ala Ile Phe Leu Thr Gln Gly Phe Val Tyr Asp

35

40

45

Ser Ala Glu Gln Ala Glu Ala Arg Phe Ile Glu Thr Gly Ala Asp Glu

50

55

60

Phe Ile Tyr Ala Arg Tyr Gly Asn Pro Thr Thr Arg Met Phe Glu Glu

65

70

75

80

Arg Ile Ala Ala Val Glu Gly Thr Glu Asp Ala Phe Ala Thr Ala Ser

85

90

95

Gly Met Ala Ala Ile His Gly Val Leu Thr Ser Ile Val Arg Ala Gly

100

105

110

Asp His Leu Val Ala Ala Arg Ala Leu Phe Gly Ser Cys Ile Tyr Ile

115

120

125

Leu Glu Glu Val Leu Gly Arg Phe Gly Val Glu Val Thr Phe Val Asp

130

135

140

Gly Thr Asp Leu Asp Gln Trp Arg Ala Ala Val Arg Pro Gly Thr Lys

145

150

155

160

Ala Val Phe Phe Glu Ser Val Ser Asn Pro Thr Leu Glu Val Ala Asp

165

170

175

Ile Gly Ala Ile Ala Glu Ile Ala His Ala Val Gly Ala Leu Val Ile

180

185

190

Val Asp Asn Ile Phe Ala Thr Pro Val Phe Ser Thr Ala Val Arg Gln

195

200

205

Gly Ala Asp Val Val Ile Tyr Ser Ala Thr Lys His Ile Asp Gly Gln

210

215

220

Gly Arg Ala Leu Gly Gly Val Val Cys Ala Ser Gln Ala Phe Ile Arg

225

230

235

240

Lys Val Leu Glu Pro Phe Met Lys His Thr Gly Gly Ser Met Ser Pro

245

250

255

Phe Asn Ala Trp Leu Met Leu Asn Gly Met Ala Thr Leu Asp Leu Arg

260

265

270

Cys Arg Ala Met Ala Asp Thr Ala Glu Lys Ile Ala Arg Ala Leu Glu

275

280

285

Gly His Pro Gln Leu Gly Arg Val Ile His Pro Ala Leu Glu Ser His

290

295

300

Pro Gln His Glu Met Ala Lys Ala Gln Met Glu Arg Pro Gly Thr Met

305

310

315

320

Ile Ala Leu Asp Leu Ala Gly Gly Lys Glu Ala Ala Phe Arg Phe Leu

325

330

335

Asp Ala Leu Arg Ile Val Lys Ile Ser Asn Asn Leu Gly Asp Ala Arg

	340	345	350
Ser Ile Ala Thr His Pro Ala Thr Thr Thr His Gln Arg Leu Ser Asp			
	355	360	365
Ala Gln Lys Ala His Leu Gly Ile Thr Pro Gly Leu Val Arg Leu Ser			
	370	375	380
Val Gly Leu Glu Asp Ala Asp Asp Leu Ile Ala Asp Leu Lys Gln Ala			
385	390	395	400
Leu Ala Val Ile			

<210> 71

<211> 404

<212> PRT

<213> Artificial Sequence

<220>

<223> RspmetZ_3_65_104

<400> 71

Met Gly Asn Ala Phe Arg Glu Gly Arg Thr Gly Met Thr Lys Asp Trp

1	5	10	15
---	---	----	----

Lys Thr Arg Thr Gln Leu Val His Gly Gly Ser Arg Arg Ser Gln Tyr

20

25

30

Gly Glu Met Ala Glu Ala Ile Phe Leu Thr Gln Gly Phe Val Tyr Asp

35

40

45

Ser Ala Glu Gln Ala Glu Ala Arg Phe Ile Glu Thr Gly Ala Asp Glu

50

55

60

Tyr Ile Tyr Ala Arg Tyr Gly Asn Pro Thr Thr Arg Met Phe Glu Glu

65

70

75

80

Arg Ile Ala Ala Val Glu Gly Thr Glu Asp Ala Phe Ala Thr Ala Ser

85

90

95

Gly Met Ala Ala Ile His Gly Ala Leu Thr Ser Ile Val Arg Ala Gly

100

105

110

Asp His Leu Val Ala Ala Arg Ala Leu Phe Gly Ser Cys Ile Tyr Ile

115

120

125

Leu Glu Glu Val Leu Gly Arg Phe Gly Val Glu Val Thr Phe Val Asp

130

135

140

Gly Thr Asp Leu Asp Gln Trp Arg Ala Ala Val Arg Pro Gly Thr Lys

145

150

155

160

Ala Val Phe Phe Glu Ser Val Ser Asn Pro Thr Leu Glu Val Ala Asp

	165	170	175
Ile Gly Ala Ile Ala Glu Ile Ala His Ala Val Gly Ala Leu Val Ile			
	180	185	190
Val Asp Asn Val Phe Ala Thr Pro Val Phe Ser Thr Ala Val Arg Gln			
	195	200	205
Gly Ala Asp Val Val Ile Tyr Ser Ala Thr Lys His Ile Asp Gly Gln			
	210	215	220
Gly Arg Ala Leu Gly Gly Val Val Cys Ala Ser Gln Ala Phe Ile Arg			
225	230	235	240
Lys Val Leu Glu Pro Phe Met Lys His Thr Gly Gly Ser Met Ser Pro			
	245	250	255
Phe Asn Ala Trp Leu Met Leu Asn Gly Met Ala Thr Leu Asp Leu Arg			
	260	265	270
Cys Arg Ala Met Ala Asp Thr Ala Glu Lys Ile Ala Arg Ala Leu Glu			
	275	280	285
Gly His Pro Gln Leu Gly Arg Val Ile His Pro Ala Leu Glu Ser His			
	290	295	300
Pro Gln His Glu Met Ala Lys Ala Gln Met Glu Arg Pro Gly Thr Met			
305	310	315	320

Ile Ala Leu Asp Leu Ala Gly Gly Lys Glu Ala Ala Phe Arg Phe Leu

325

330

335

Asp Ala Leu Arg Ile Val Lys Ile Ser Asn Asn Leu Gly Asp Ala Arg

340

345

350

Ser Ile Ala Thr His Pro Ala Thr Thr Thr His Gln Arg Leu Ser Asp

355

360

365

Ala Gln Lys Ala His Leu Gly Ile Thr Pro Gly Leu Val Arg Leu Ser

370

375

380

Val Gly Leu Glu Asp Ala Asp Asp Leu Ile Ala Asp Leu Lys Gln Ala

385

390

395

400

Leu Ala Val Ile

<210> 72

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 72

atcaaaacag atatcatggg tatcgcgttt cgtga

35

<210> 73

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 73

ccttcacgaa acgcgttacc catgatatct g

31

<210> 74

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 74

cagatatcat gggtaacgcg ttctgtgaag g

31

<210> 75

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 75

tagcgggcat agatgtattc gtcgggcccg g

31

<210> 76

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 76

ccggcgccga cgaatacatc tatgcccgct a

31

<210> 77

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 77

acgatcgagg tgagcgcgcc gtggatcgcg g

31

<210> 78

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 78

ccgcgatcca cggcgcgctc acctcgatcg t

31

<210> 79

<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 79
cgggcgtcgc gaagatattg tccacgatga c

31

<210> 80
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 80
gtcatcgtgg acaatatctt cgcgacgccc g

31

<210> 81
<211> 5803
<212> DNA

<213> Artificial Sequence

<220>

<223> pDCM2

<400> 81

gttcgcttgc tgtccataaa accgcccagt ctgctatcg ccatgtaagc ccaactgcaag	60
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tcatccgggg tcagcacctg ttctgcggac tggcttcta cgtgttccgc ttccttagc	180
agcccttgcg ccctgagtgc ttgcggcagc gtgaagctag ctttatcgc cattcgccat	240
tcaggctgcg caactgttgg gaagggcgat cggtcggggc ctcttcgcta ttacgccagc	300
tggcgaaagg gggatgtgct gcaaggcgat taagtgggt aacgccaggg tttccagt	360
cacgacgttg taaaacgacg gccagtgaat tcgagctcg taccgggga tcctctagag	420
tcgacctgca ggcatgcaag ctggcgtaa tcatggcat agctgttcc tgttgaaat	480
tggtatccgc tcacaattcc acacaacata cgagccggaa gcataaagtg taaagcctgg	540
ggcgctaata gagtgagcta actcacatta attgcgttc gctcactgcc cgcttccag	600
tcgggaaacc tgcgtgcca gctgcattaa tgaatcgcc aacgcgcggg gagaggcgg	660

ttgcgtattg ggcgctcttc cgcttcctcg ctactgact cgctgcgctc ggctgttcgg	720
ctgcggcgag cggtatcagc tcactcaaag gcggaatac gggtatccac agaatacagg	780
gataacgcag gaaagaacat gtgagcaaaa ggccagcaaa aggccaggaa ccgtaaaaag	840
gccgcgttgc tggcgtttt ccataggctc cgccccctg acgagcatca caaaaatcga	900
cgctcaagtc agagggtggcg aaacccgaca ggactataaa gataccaggc gttccccct	960
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cgtaagga tttggcat gagattatca aaaaggatct tcacctagat cctttggg	1560
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acctcaaaaa caccatcata cactaaatca gtaagttggc agcatcacc gacgcacttt	1980
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ccagccctcc tgttgaaga tggcaagta gttacgcaca ataaaaaag acctaaaata 4500

tgtagggggt gacgccaaag tatacactt gccctttaca catttaggt ctgcctgct 4560

ttatcagtaa caaaccgcg cgatttact ttcgacctca ttctattaga ctctcgttg 4620

gattgcaact ggtctatTTT cctcttttgt ttgatagaaa atcataaaag gatttgcaga 4680

ctacgggcct aaagaactaa aaaatctatc tgttctttt cattctctgt atttttata 4740

gttctgttg catgggcata aagttgcctt ttaatcaca attcagaaaa tatcataata 4800

tctcatttca ctaaataata gtgaacggca ggtatatgtg atgggttaaa aaggatcacc 4860

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