SEQUENCE LISTING

<110> Genomatica
Li, Jingyi
Barton, Nelson R.
Warner, Joseph R.
Pharkya, Priti

<120> METHANOL DEHYDROGENASE FUSION PROTEINS

<130> GNO0027/WO

<150> US 62/249,032
<151> 2015-10-30

<150> US 62/260,189
<151> 2015-11-25

<160> 12

<170> PatentIn version 3.5

<210> 1
<211> 382
<212> PRT
<213> Bacillus methanolicus MGA3

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Ala Val Lys Glu Val Gly Thr Arg Leu Lys Gln Ile Gly Ala Lys Lys
20 25 30

Ala Leu Ile Val Thr Asp Ala Phe Leu His Ser Thr Gly Leu Ser Glu
35 40 45

Glu Val Ala Lys Asn Ile Arg Glu Ala Gly Val Asp Val Ala Ile Phe
50 55 60

Pro Lys Ala Gln Pro Asp Pro Ala Asp Thr Gln Val His Glu Gly Val
65 70 75 80

Asp Val Phe Lys Gln Glu Asn Cys Asp Ser Leu Val Ser Ile Gly Gly
85 90 95

Gly Ser Ser His Asp Thr Ala Lys Ala Ile Gly Leu Val Ala Ala Asn
100 105 110

Gly Gly Arg Ile Asn Asp Tyr Gln Gly Val Asn Ser Val Glu Lys Pro
115 120 125

Val Val Pro Val Val Ala Ile Thr Thr Thr Ala Gly Thr Gly Ser Glu
130 135 140

Thr Thr Ser Leu Ala Val Ile Thr Asp Ser Ala Arg Lys Val Lys Met
145 150 155 160

Pro Val Ile Asp Glu Lys Ile Thr Pro Thr Val Ala Ile Val Asp Pro
165 170 175

Glu Leu Met Val Lys Lys Pro Ala Gly Leu Thr Ile Ala Thr Gly Met
180 185 190

Asp Ala Leu Ser His Ala Ile Glu Ala Tyr Val Ala Lys Gly Ala Thr
195 200 205

Pro Val Thr Asp Ala Phe Ala Ile Gln Ala Met Lys Leu Ile Asn Glu
210 215 220

Tyr Leu Pro Lys Ala Val Ala Asn Gly Glu Asp Ile Glu Ala Arg Glu
225 230 235 240

Lys Met Ala Tyr Ala Gln Tyr Met Ala Gly Val Ala Phe Asn Asn Gly
245 250 255

Gly Leu Gly Leu Val His Ser Ile Ser His Gln Val Gly Gly Val Tyr
260 265 270

Lys Leu Gln His Gly Ile Cys Asn Ser Val Asn Met Pro His Val Cys
275 280 285

Ala Phe Asn Leu Ile Ala Lys Thr Glu Arg Phe Ala His Ile Ala Glu
290 295 300

Leu Leu Gly Glu Asn Val Ala Gly Leu Ser Thr Ala Ala Ala Ala Glu
305 310 315 320

Arg Ala Ile Val Ala Leu Glu Arg Ile Asn Lys Ser Phe Gly Ile Pro
325 330 335

Ser Gly Tyr Ala Glu Met Gly Val Lys Glu Glu Asp Ile Glu Leu Leu
340 345 350

Ala Lys Asn Ala Tyr Glu Asp Val Cys Thr Gln Ser Asn Pro Arg Val
355 360 365

Pro Thr Val Gln Asp Ile Ala Gln Ile Ile Lys Asn Ala Met
370 375 380

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<211> 1149
<212> DNA
<213> Bacillus methanolicus MGA3

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gtaggaacaa gacttaagca aattggagct aagaaagcgc ttatcgttac agatgcattc 120

cttcacagca caggtttatc tgaagaagtt gctaaaaaca ttcgtgaagc tggcgttgat 180

gttgcgattt tcccaaaagc tcaaccagat ccagcagata cacaagttca tgaaggtgta 240

gatgtattca aacaagaaaa ctgtgattca cttgtttcta tcggtggagg tagctctcac 300

gatacagcta aagcaatcgg tttagttgca gcaaacggcg gaagaatcaa tgactatcaa 360

ggtgtaaaca gcgtagaaaa accagtcgtt ccagtagttg caatcactac aacagctggt 420

actggtagtg aaacaacatc tcttgcggtt attacagact ctgcacgtaa agtaaaaatg 480

cctgttattg atgagaaaat tactccaact gtagcaattg ttgacccaga attaatggtg 540

aaaaaaccag ctggattaac aatcgcaact ggtatggatg cattgtccca tgcaattgaa 600

gcatatgttg caaaaggtgc tacaccagtt actgatgcat ttgctattca agcaatgaaa 660

cttatcaatg aatacttacc aaaagcggtt gcgaacggag aagacatcga agcacgtgaa 720

aaaatggctt atgcacaata catggcagga gtggcattta acaacggtgg tttaggacta 780

gttcactcta tttctcacca agtaggtgga gtttacaaat tacaacacgg aatctgtaac 840

tcagttaata tgccacacgt ttgcgcattc aacctaattg ctaaaactga gcgcttcgca 900

cacattgctg agcttttagg tgagaatgtt gctggcttaa gcactgcagc agctgctgag 960

agagcaattg tagctcttga aagaatcaac aaatccttcg gtatcccatc tggctatgca 1020

gaaatgggcg tgaaagaaga ggatatcgaa ttattagcga aaaacgcata cgaagacgta 1080

tgtactcaaa gcaacccacg cgttcctact gttcaagaca ttgcacaaat catcaaaaac 1140

gctatgtaa 1149

<210> 3
<211> 211
<212> PRT
<213> Bacillus methanolicus MGA3

<400> 3

Met Glu Leu Gln Leu Ala Leu Asp Leu Val Asn Ile Glu Glu Ala Lys
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Gln Val Val Ala Glu Val Gln Glu Tyr Val Asp Ile Val Glu Ile Gly
20 25 30

Thr Pro Val Ile Lys Ile Trp Gly Leu Gln Ala Val Lys Ala Val Lys
35 40 45

Asp Ala Phe Pro His Leu Gln Val Leu Ala Asp Met Lys Thr Met Asp
50 55 60

Ala Ala Ala Tyr Glu Val Ala Lys Ala Ala Glu His Gly Ala Asp Ile
65 70 75 80

Val Thr Ile Leu Ala Ala Ala Glu Asp Val Ser Ile Lys Gly Ala Val
85 90 95

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

100 105 110

Val Lys Asn Leu Glu Glu Arg Ala Lys Gln Val Asp Glu Met Gly Val
115 120 125

Asp Tyr Ile Cys Val His Ala Gly Tyr Asp Leu Gln Ala Val Gly Lys
130 135 140

Asn Pro Leu Asp Asp Leu Lys Arg Ile Lys Ala Val Val Lys Asn Ala
145 150 155 160

Lys Thr Ala Ile Ala Gly Gly Ile Lys Leu Glu Thr Leu Pro Glu Val
165 170 175

Ile Lys Ala Glu Pro Asp Leu Val Ile Val Gly Gly Gly Ile Ala Asn
180 185 190

Gln Thr Asp Lys Lys Ala Ala Ala Glu Lys Ile Asn Lys Leu Val Lys
195 200 205

Gln Gly Leu
210

<210> 4
<211> 184
<212> PRT
<213> Bacillus methanolicus MGA3

<400> 4

Met Leu Thr Thr Glu Phe Leu Ala Glu Ile Val Lys Glu Leu Asn Ser
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Ser Val Asn Gln Ile Ala Asp Glu Glu Ala Glu Ala Leu Val Asn Gly
20 25 30

Ile Leu Gln Ser Lys Lys Val Phe Val Ala Gly Ala Gly Arg Ser Gly
35 40 45

Phe Met Ala Lys Ser Phe Ala Met Arg Met Met His Met Gly Ile Asp
50 55 60

Ala Tyr Val Val Gly Glu Thr Val Thr Pro Asn Tyr Glu Lys Glu Asp
65 70 75 80

Ile Leu Ile Ile Gly Ser Gly Ser Gly Glu Thr Lys Ser Leu Val Ser
85 90 95

Met Ala Gln Lys Ala Lys Ser Ile Gly Gly Thr Ile Ala Ala Val Thr
100 105 110

Ile Asn Pro Glu Ser Thr Ile Gly Gln Leu Ala Asp Ile Val Ile Lys
115 120 125

Met Pro Gly Ser Pro Lys Asp Lys Ser Glu Ala Arg Glu Thr Ile Gln
130 135 140

Pro Met Gly Ser Leu Phe Glu Gln Thr Leu Leu Leu Phe Tyr Asp Ala
145 150 155 160

Val Ile Leu Arg Phe Met Glu Lys Lys Gly Leu Asp Thr Lys Thr Met
165 170 175

Tyr Gly Arg His Ala Asn Leu Glu
180

<210> 5
<211> 406
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein

<400> 5

Met Lys Leu Gln Val Ala Ile Asp Leu Leu Ser Thr Glu Ala Ala Leu
1 5 10 15

Glu Leu Ala Gly Lys Val Ala Glu Tyr Val Asp Ile Ile Glu Leu Gly
20 25 30

Thr Pro Leu Ile Lys Ala Glu Gly Leu Ser Val Ile Thr Ala Val Lys
35 40 45

Lys Ala His Pro Asp Lys Ile Val Phe Ala Asp Met Lys Thr Met Asp
50 55 60

Ala Gly Glu Leu Glu Ala Asp Ile Ala Phe Lys Ala Gly Ala Asp Leu
65 70 75 80

Val Thr Val Leu Gly Ser Ala Asp Asp Ser Thr Ile Ala Gly Ala Val
85 90 95

Lys Ala Ala Gln Ala His Asn Lys Gly Val Val Val Asp Leu Ile Gly
100 105 110

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

Lys Phe Val Glu Met His Ala Gly Leu Asp Glu Gln Ala Lys Pro Gly
130 135 140

Phe Asp Leu Asn Gly Leu Leu Ala Ala Gly Glu Lys Ala Arg Val Pro
145 150 155 160

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Phe Ser Val Ala Gly Gly Val Lys Val Ala Thr Ile Pro Ala Val Gln
                165                 170                 175

Lys Ala Gly Ala Glu Val Ala Val Ala Gly Gly Ala Ile Tyr Gly Ala
            180                 185                 190

Ala Asp Pro Ala Ala Ala Ala Lys Glu Leu Arg Ala Ala Ile Ala Met
        195                 200                 205

Thr Gln Ala Ala Glu Ala Asp Gly Ala Val Lys Val Val Gly Asp Asp
    210                 215                 220

Ile Thr Asn Asn Leu Ser Leu Val Arg Asp Glu Val Ala Asp Thr Ala
225                 230                 235                 240

Ala Lys Val Asp Pro Glu Gln Val Ala Val Leu Ala Arg Gln Ile Val
                245                 250                 255

Gln Pro Gly Arg Val Phe Val Ala Gly Ala Gly Arg Ser Gly Leu Val
            260                 265                 270

Leu Arg Met Ala Ala Met Arg Leu Met His Phe Gly Leu Thr Val His
        275                 280                 285

Val Ala Gly Asp Thr Thr Thr Pro Ala Ile Ser Ala Gly Asp Leu Leu
    290                 295                 300

Leu Val Ala Ser Gly Ser Gly Thr Thr Ser Gly Val Val Lys Ser Ala
305                 310                 315                 320

Glu Thr Ala Lys Lys Ala Gly Ala Arg Ile Ala Ala Phe Thr Thr Asn
                325                 330                 335

Pro Asp Ser Pro Leu Ala Gly Leu Ala Asp Ala Val Val Ile Ile Pro
            340                 345                 350

Ala Ala Gln Lys Thr Asp His Gly Ser His Ile Ser Arg Gln Tyr Ala
        355                 360                 365

Gly Ser Leu Phe Glu Gln Val Leu Phe Val Val Thr Glu Ala Val Phe
    370                 375                 380

Gln Ser Leu Trp Asp His Thr Glu Val Glu Ala Glu Glu Leu Trp Thr
385                 390                 395                 400

Arg His Ala Asn Leu Glu
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<210> 6
<211> 388
<212> PRT
<213> Desulfotomaculum reducens MI-1

<400> 6

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Leu Met Gly Val Gly Ala His Lys Glu Ile Pro Asp Gln Val Lys Val
            20                  25                  30

Leu Gly Gly Ser Asn Val Leu Ile Val Thr Asp Ala Phe Leu Gly Arg
        35                  40                  45

Pro Gly Gly Met Ala Asp Asp Ile Lys Gly Met Leu Glu Ala Glu Asn
    50                  55                  60

Ile Lys Val Thr Ile Tyr Ala Gly Ala Glu Pro Asn Pro Thr Asp Val
65                  70                  75                  80

Asn Val His Asp Gly Leu Lys Val Tyr Gln Glu Cys Gly Ala Asp Met
                85                  90                  95

Ile Leu Ser Leu Gly Gly Gly Ser Ser His Asp Cys Ala Lys Gly Ile
            100                 105                 110

Gly Ile Val Ala Thr Asn Gly Gly Asn Ile Arg Asp Tyr Glu Gly Ile
        115                 120                 125

Asn Lys Ser Ser Lys Ala Met Pro Pro Phe Ile Ala Val Asn Thr Thr
    130                 135                 140

Ala Gly Thr Ala Ser Glu Met Thr Arg Phe Cys Ile Ile Thr Asn Thr
145                 150                 155                 160

Ser Asn His Val Lys Met Ala Ile Val Asp Trp Arg Cys Thr Pro Asn
                165                 170                 175

Ile Ala Ile Asn Asp Pro Leu Leu Met Ala Gly Met Pro Pro Ala Leu
            180                 185                 190

Thr Ala Ala Thr Gly Met Asp Ala Leu Thr His Ala Ile Glu Ala Tyr
        195                 200                 205

Val Ser Val Ala Ala Thr Pro Val Thr Asp Ser Ala Ala Leu Met Ala
    210                 215                 220

Ile Lys Leu Ile Ser Gln Tyr Leu Arg Ala Ala Val Ala Asn Gly Glu
225                 230                 235                 240

Asn Met Glu Ala Arg Asp Lys Met Ala Tyr Ala Glu Phe Leu Gly Gly
                245                 250                 255

Met Ala Phe Asn Asn Ala Ser Leu Gly Tyr Val His Ala Met Ala His
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260 265 270

Gln Leu Gly Gly Phe Tyr Asn Leu Pro His Gly Val Cys Asn Ala Ile
275 280 285

Leu Leu Pro His Val Glu Ala Phe Asn Leu Ile Ala Cys Pro Glu Arg
290 295 300

Phe Val Asp Ile Ala Val Ala Met Gly Glu Asn Val Glu Gly Leu Ser
305 310 315 320

Val Arg Asp Ala Ala Asp Lys Ala Leu Ser Ala Ile Arg Lys Leu Ser
325 330 335

Ala Asp Val Gly Ile Pro Ala Gly Leu Thr Glu Leu Gly Val Lys Glu
340 345 350

Glu Asp Leu Lys Thr Met Ala Glu Asn Ala Met Lys Asp Ala Cys Ala
355 360 365

Leu Thr Asn Pro Arg Lys Ala Thr Leu Asn Asp Ile Val Gly Ile Tyr
370 375 380

Lys Thr Ala Leu
385

<210> 7
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> linker sequence

<400> 7

Gly Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly
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Ser Gly Gly Ser
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<210> 8
<211> 382
<212> PRT
<213> Artificial Sequence

<220>
<223> MeDH variant

<400> 8

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Ala Val Lys Glu Val Gly Thr Arg Leu Lys Gln Ile Gly Ala Lys Lys

20 25 30

Ala Leu Ile Val Thr Asp Ala Phe Leu His Ser Thr Gly Leu Ser Glu
35 40 45

Glu Val Ala Lys Asn Ile Arg Glu Ala Gly Val Asp Val Ala Ile Phe
50 55 60

Pro Lys Ala Gln Pro Asp Pro Ala Asp Thr Gln Val His Glu Gly Val
65 70 75 80

Asp Val Phe Lys Gln Glu Asn Cys Asp Ser Leu Val Ser Ile Gly Gly
85 90 95

Gly Ser Ser His Asp Thr Ala Lys Ala Ile Gly Leu Val Ala Ala Asn
100 105 110

Gly Gly Arg Ile Asn Asp Tyr Gln Gly Val Asn Ser Val Glu Lys Pro
115 120 125

Met Ile Pro Val Val Ala Ile Thr Thr Thr Ala Gly Thr Gly Ser Glu
130 135 140

Thr Thr Ser Leu Ala Val Ile Thr Asp Ser Ala Arg Lys Val Lys Met
145 150 155 160

Pro Val Ile Asp Glu Lys Ile Thr Pro Thr Val Ala Ile Val Asp Pro
165 170 175

Glu Leu Met Val Lys Lys Pro Ala Gly Leu Thr Ile Ala Thr Gly Met
180 185 190

Asp Ala Leu Ser His Ala Ile Glu Ala Tyr Val Ala Lys Gly Ala Thr
195 200 205

Pro Val Thr Asp Ala Phe Ala Ile Gln Ala Met Lys Leu Ile Asn Glu
210 215 220

Tyr Leu Pro Lys Ala Val Ala Asn Gly Glu Asp Ile Glu Ala Arg Glu
225 230 235 240

Lys Met Ala Tyr Ala Gln Tyr Met Ala Gly Val Ala Phe Asn Asn Gly
245 250 255

Gly Leu Gly Leu Val His Ser Ile Ser His Gln Val Gly Ser Val Tyr
260 265 270

Lys Leu Gln His Gly Ile Cys Asn Ser Val Asn Met Pro His Val Cys
275 280 285

Ala Phe Asn Leu Ile Ala Lys Thr Glu Arg Phe Ala His Ile Ala Glu

290 295 300

Leu Leu Gly Glu Asn Val Ala Gly Leu Ser Thr Ala Ala Ala Ala Glu
305 310 315 320

Arg Ala Ile Val Ala Leu Glu Arg Ile Asn Lys Ser Phe Gly Ile Pro
325 330 335

Ser Gly Tyr Ala Glu Met Gly Val Lys Glu Glu Asp Ile Glu Leu Leu
340 345 350

Ala Lys Asp Ala Tyr Glu Asp Val Cys Thr Gln Ser Asn Pro Arg Val
355 360 365

Pro Thr Val Gln Asp Ile Ala Gln Ile Ile Lys Asn Ala Met
370 375 380

<210> 9
<211> 1149
<212> DNA
<213> Artificial Sequence

<220>
<223> MeDH variant

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ctgcatagca ccggtttgag cgaagaagtg gcgaagaaca ttcgtgaagc gggcgtcgat 180

gtggcgattt tcccgaaagc ccagccggac cctgccgata cgcaagtcca cgaaggtgtt 240

gatgtcttta aacaggagaa ttgcgacagc ttggttagca tcggtggcgg ctcttcccat 300

gatacggcga aagcaattgg cctggtcgca gcaaatggtg gccgtatcaa tgactaccag 360

ggtgttaaca gcgtggagaa gccgatgatt ccggtggtcg cgatcacgac tacggcaggc 420

accggctccg aaaccaccag cttggcggtc atcacggata gcgcgcgtaa agtgaaaatg 480

ccggtgatcg atgagaaaat caccccgacc gtggcgattg tcgatccgga gctgatggtg 540

aagaagccgg ctggtttgac cattgcaacc ggtatggacg ccctgtctca cgccatcgaa 600

gcatacgtgg caaagggtgc gacgccggtg accgatgcgt tcgccattca ggcaatgaaa 660

ctgattaatg agtatctgcc gaaggctgtt gcgaatggcg aggacatcga ggcacgcgag 720

aaaatggcgt atgctcaata catggccggt gtcgcgttca acaatggtgg tctgggtctg 780

gtacacagca tcagccacca agtgggtagt gtgtacaaac tgcaacacgg catttgcaac 840

tccgtcaaca tgccgcacgt ttgtgcgttt aatctgattg ccaagaccga acgtttcgcc 900

catatcgctg agctgctggg tgagaacgtt gcaggcctga gcacggcggc tgcggcggag 960

cgcgcaattg tcgcgctgga acgcattaac aagagctttg gtatcccgag cggctatgcg 1020

gagatgggtg tgaaagaaga ggacattgaa ctgctggcta aggatgcgta cgaggacgtt 1080

tgtactcaga gcaacccgcg tgttccgacg gtccaggaca ttgcccagat tatcaagaac 1140

gcgatgtag 1149

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<211> 393
<212> PRT
<213> uncultured organism

<400> 10

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Phe Ile Pro Ser Val Thr Leu Val Gly Pro Gly Cys Val Lys Glu Val
20 25 30

Gly Pro Arg Ala Lys Met Leu Gly Ala Lys Arg Ala Leu Ile Val Thr
35 40 45

Asp Ala Gly Leu His Lys Met Gly Leu Ser Gln Glu Ile Ala Asp Leu
50 55 60

Leu Arg Ser Glu Gly Ile Asp Ser Val Ile Phe Ala Gly Ala Glu Pro
65 70 75 80

Asn Pro Thr Asp Ile Asn Val His Asp Gly Val Lys Val Tyr Gln Lys
85 90 95

Glu Lys Cys Asp Phe Ile Val Ser Leu Gly Gly Gly Ser Ser His Asp
100 105 110

Cys Ala Lys Gly Ile Gly Leu Val Thr Ala Gly Gly Gly His Ile Arg
115 120 125

Asp Tyr Glu Gly Val Asp Lys Ser Lys Val Pro Met Thr Pro Leu Ile
130 135 140

Ala Ile Asn Thr Thr Ala Gly Thr Ala Ser Glu Met Thr Arg Phe Cys
145 150 155 160

Ile Ile Thr Asn Thr Asp Thr His Val Lys Met Ala Ile Val Asp Trp
165 170 175

Arg Cys Thr Pro Leu Val Ala Ile Asp Asp Pro Arg Leu Met Val Lys
180 185 190

Met Pro Pro Ala Leu Thr Ala Ala Thr Gly Met Asp Ala Leu Thr His
195 200 205

Ala Val Glu Ala Tyr Val Ser Thr Ala Ala Thr Pro Ile Thr Asp Thr
210 215 220

Cys Ala Glu Lys Ala Ile Glu Leu Ile Gly Gln Trp Leu Pro Lys Ala
225 230 235 240

Val Ala Asn Gly Asp Trp Met Glu Ala Arg Ala Ala Met Cys Tyr Ala
245 250 255

Gln Tyr Leu Ala Gly Met Ala Phe Asn Asn Ala Ser Leu Gly Tyr Val
260 265 270

His Ala Met Ala His Gln Leu Gly Gly Phe Tyr Asn Leu Pro His Gly
275 280 285

Val Cys Asn Ala Ile Leu Leu Pro His Val Cys Gln Phe Asn Leu Ile
290 295 300

Ala Ala Thr Glu Arg Tyr Ala Arg Ile Ala Ala Leu Leu Gly Val Asp
305 310 315 320

Thr Ser Gly Met Glu Thr Arg Glu Ala Ala Leu Ala Ala Ile Ala Ala
325 330 335

Ile Lys Glu Leu Ser Ser Ser Ile Gly Ile Pro Arg Gly Leu Ser Glu
340 345 350

Leu Gly Val Lys Ala Ala Asp His Lys Val Met Ala Glu Asn Ala Gln
355 360 365

Lys Asp Ala Cys Met Leu Thr Asn Pro Arg Lys Ala Thr Leu Glu Gln
370 375 380

Val Ile Gly Ile Phe Glu Ala Ala Met
385 390

<210> 11
<211> 1182
<212> DNA
<213> uncultured organism

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gttaccctgg ttggtccggg ttgtgttaaa gaagttggtc ctcgcgcaaa aatgctgggt 120

gcaaaacgtg cactgattgt taccgatgca ggtctgcaca aaatgggtct gagccaagaa 180

attgccgatc tgctgcgtag cgaaggtatt gatagcgtta tttttgccgg tgcagaaccg 240

aatccgaccg atatcaatgt tcatgatggt gtgaaagtgt atcagaaaga gaaatgcgat 300

tttatcgtta gcctgggtgg tggtagcagc catgattgtg caaaaggtat tggtctggtt 360

accgcaggcg gtggtcatat tcgtgattat gaaggtgttg acaaaagcaa agttccgatg 420

acaccgctga ttgcaattaa taccaccgca ggcaccgcaa gcgaaatgac ccgtttttgt 480

attattacca acaccgatac ccatgtgaaa atggcaattg ttgattggcg ttgtactccg 540

ctggttgcca ttgatgatcc gcgtctgatg gttaaaatgc ctccggcact gaccgcagca 600

accggtatgg atgcactgac ccatgcagtt gaagcatatg tgagcaccgc agccaccccg 660

attaccgata cctgtgcaga aaaagcaatt gaactgattg gtcagtggct gccgaaagca 720

gttgcaaatg gtgattggat ggaagcacgt gcagcaatgt gttatgcaca gtatctggca 780

ggtatggcat tcaataatgc aagcctgggt tatgttcatg caatggcaca tcagctgggt 840

ggcttttata acctgccgca tggtgtttgt aatgcaattc tgctgcctca tgtttgccag 900

tttaatctga ttgcagccac cgaacgttat gcccgtattg cagcactgct gggtgttgat 960

accagcggta tggaaacccg tgaagcagca ctggcagcaa ttgccgcaat taaagaactg 1020

agcagcagca ttggtattcc gcgtggtctg agcgaactgg gtgttaaagc agccgatcat 1080

aaagttatgg cagaaaatgc acagaaagat gcatgtatgc tgacaaatcc gcgtaaagca 1140

accctggaac aggttattgg tatttttgaa gccgcaatgt ag 1182

<210> 12
<211> 185
<212> PRT
<213> Bacillus methanolicus

<400> 12

Met Gly Lys Leu Phe Glu Glu Lys Thr Ile Lys Thr Glu Gln Ile Phe
1 5 10 15

Ser Gly Arg Val Val Lys Leu Gln Val Asp Asp Val Glu Leu Pro Asn
20 25 30

Gly Gln Thr Ser Lys Arg Glu Ile Val Arg His Pro Gly Ala Val Ala
35 40 45

Val Ile Ala Ile Thr Asn Glu Asn Lys Ile Val Met Val Glu Gln Tyr
50 55 60

Arg Lys Pro Leu Glu Lys Ser Ile Val Glu Ile Pro Ala Gly Lys Leu
65 70 75 80

Glu Lys Gly Glu Asp Pro Arg Ile Thr Ala Leu Arg Glu Leu Glu Glu
85 90 95

Glu Thr Gly Tyr Glu Cys Glu Gln Met Glu Trp Leu Ile Ser Phe Ala
100 105 110

Thr Ser Pro Gly Phe Ala Asp Glu Ile Ile His Ile Tyr Val Ala Lys
115 120 125

Gly Leu Ser Lys Lys Glu Asn Ala Ala Gly Leu Asp Glu Asp Glu Phe
130 135 140

Val Asp Leu Ile Glu Leu Thr Leu Asp Glu Ala Leu Gln Tyr Ile Lys
145 150 155 160

Glu Gln Arg Ile Tyr Asp Ser Lys Thr Val Ile Ala Val Gln Tyr Leu
165 170 175

Gln Leu Gln Glu Ala Leu Lys Asn Lys
180 185