SEQUENCE LISTING

<110> ExxonMobil Research and Engineering Company
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<120> Cell systems and methods for improving fatty acid synthesis by expression of dehydrogenases

<130> 2012EM093-WO / 16244-000016/WO/OA

<150> US 13/453,235
<151> 2012-04-23

<160> 30

<170> PatentIn version 3.5

<210> 1
<211> 981
<212> DNA
<213> Unknown

<220>
<223> Aquatic organism screen of a metagenomic library containing DNA fragments from water samples taken from ponds at Pacific Aquafarms located north of the Salton Sea in California.

<400> 1
tccggcgcaa atctgaaagc gcaaggtgcc accgtcatga aacccgtcgt tcccttcatt 60

gcccggatgt ctgccgagga acgtgcggag tggatggcgc agtttgaaag gctgatgccg 120

cagatcgatg tgcgcccgct ggccaccatg gacgccgcag agcgcctgtc ggcacgcgtg 180

gccattgtcg ccaatccgga tccggcgcat ctgcatgagc tgccgggcct tgtctgggtg 240

cagagcctgt gggccggggt ggagcggttg ctgggcgagc tgatcgatac ggactttgcc 300

atcgtccgca tgaccgatcc gcagctggcg gaaaccatgg ccgaggcggt gctggccttt 360

tcgctttatc ttcaccggga cattccgctc tatctggcgc agcagcgcga gaagatctgg 420

gccgaagcct tgccgcgcct tgccgctgac cggcatatcg gcattctcgg gctggggaac 480

ctcggcaagg ctgcggcgcg gcgcctgctg gccaatggct ttccggtcag cggctggagc 540

cgcacgcctg ccgaagtgga gggggcggag tgtttcagcg gtgaggaggg gctgcagcgg 600

gtgctgtcgc gctcggatat cgttgtcgtc ttgctgccgc tgacgccgga tacgcgcggc 660

ctgctcaaca cggctcgtct tgccatgctg ccgcgcggtg ctggactcat caattttggc 720

cgggggccga ttgtggacca gcctgcgctg ctggctgccc ttgatgaggg gcatctgtcc 780

catgcggtgc tggatgtctt tgcgcaggag ccgctgccgg tggacaatcc ctgctggagc 840

catccgtcgg tcacagtgct gccgcacatc agcgccccga caacaccggc gacggctgca 900

cggatcgtgg cggccaatct gtcggcttat ttcgagcggg gagaaatacc gccggcggtg 960

gaccgccagc ggggctactg a 981

<210> 2

<211> 326
<212> PRT
<213> Unknown

<220>
<223> Aquatic organism screen of a metagenomic library containing DNA fragments from water samples taken from ponds at Pacific Aquafarms located north of the Salton Sea in California.

<400> 2

Ser Gly Ala Asn Leu Lys Ala Gln Gly Ala Thr Val Met Lys Pro Val
1 5 10 15

Val Pro Phe Ile Ala Arg Met Ser Ala Glu Glu Arg Ala Glu Trp Met
20 25 30

Ala Gln Phe Glu Arg Leu Met Pro Gln Ile Asp Val Arg Pro Leu Ala
35 40 45

Thr Met Asp Ala Ala Glu Arg Leu Ser Ala Arg Val Ala Ile Val Ala
50 55 60

Asn Pro Asp Pro Ala His Leu His Glu Leu Pro Gly Leu Val Trp Val
65 70 75 80

Gln Ser Leu Trp Ala Gly Val Glu Arg Leu Leu Gly Glu Leu Ile Asp
85 90 95

Thr Asp Phe Ala Ile Val Arg Met Thr Asp Pro Gln Leu Ala Glu Thr
100 105 110

Met Ala Glu Ala Val Leu Ala Phe Ser Leu Tyr Leu His Arg Asp Ile
115 120 125

Pro Leu Tyr Leu Ala Gln Gln Arg Glu Lys Ile Trp Ala Glu Ala Leu
130 135 140

Pro Arg Leu Ala Ala Asp Arg His Ile Gly Ile Leu Gly Leu Gly Asn
145 150 155 160

Leu Gly Lys Ala Ala Ala Arg Arg Leu Leu Ala Asn Gly Phe Pro Val
165 170 175

Ser Gly Trp Ser Arg Thr Pro Ala Glu Val Glu Gly Ala Glu Cys Phe
180 185 190

Ser Gly Glu Glu Gly Leu Gln Arg Val Leu Ser Arg Ser Asp Ile Val
195 200 205

Val Val Leu Leu Pro Leu Thr Pro Asp Thr Arg Gly Leu Leu Asn Thr
210 215 220

Ala Arg Leu Ala Met Leu Pro Arg Gly Ala Gly Leu Ile Asn Phe Gly

225 230 235 240

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

Gly His Leu Ser His Ala Val Leu Asp Val Phe Ala Gln Glu Pro Leu
260 265 270

Pro Val Asp Asn Pro Cys Trp Ser His Pro Ser Val Thr Val Leu Pro
275 280 285

His Ile Ser Ala Pro Thr Thr Pro Ala Thr Ala Ala Arg Ile Val Ala
290 295 300

Ala Asn Leu Ser Ala Tyr Phe Glu Arg Gly Glu Ile Pro Pro Ala Val
305 310 315 320

Asp Arg Gln Arg Gly Tyr
325

<210> 3
<211> 1086
<212> DNA
<213> Unknown

<220>
<223> Aquatic organism screen of a metagenomic library containing DNA fragments from an environmental sample removed from a shipping channel in Laguna Madre, Texas

<400> 3
tcaaaaggaa aagtagtgcc agagccgtat ggtgtgacgc ttattattgc accgtggaac 60

tatccttttc aattagcaat tgcaccactt gtaggagcac ttgcagctgg aaatacaatc 120

gttttaaagc cgtcagagtt aacgccaagc gtttcaaaag tgcttaagag aatgttaggt 180

gaattattcc cagaagagct tgtagcggta gtagaaggtg gcgttgaaga gagtacatct 240

ttgctgaggg aaccaattga ttatattttc tttactggta gtgttggcgt tggaaaagtt 300

gtaatggaag cagcagcgaa acagttgacg ccgcttacgt tagaacttgg cgggaaaagt 360

ccttgtattg tacataaaga tgcaaagata gagatgacag caagaagaat tgtttggggt 420

aagtttttaa atgcagggca gacatgtgta gcgcctgatt atatgtacgt gcattcttcc 480

gtgaaagaac agctagttga ggcactgcga catgaaatca cagagcagta tagtaaagaa 540

cctttgcaaa atgaaaatta tgtgcgtatt gtaagtgagc gtcattttga acgattatgt 600

ggatttttac aagatggtca agtcgtaatt ggtggaaact atgagaaaga tacattacat 660

attgaaccga cagtgctagc ggatattaca tggcaagatg ctgttatgga agatgaaatt 720

tttggtccga ttttaccaat catagagtac gacaatatag aagatgtaat tggcacaatc 780

cagcaacatc cgaagccgtt agcgttatat gtattttcgg aagataaaga agtacaaaag 840

aaagtgacga gtaatatttc atatggtgga ggctgtatta atgatgttgt ctaccatctt 900

gccacgccat atttaccttt tgggggtgtt ggaagtagtg gattaggggg ttatcatggg 960

gaagaaagtt ttcggacttt ttcacattat aaaagcattt tagcccaatc tacagcattc 1020

gacatgaaaa ttcgttactc ttctacaaaa agtgctttaa aattcatacg aaagttgtta 1080

aaatga 1086

<210> 4
<211> 361
<212> PRT
<213> Unknown

<220>
<223> Aquatic organism screen of a metagenomic library containing DNA fragments from an environmental sample removed from a shipping channel in Laguna Madre, Texas

<400> 4

Ser Lys Gly Lys Val Val Pro Glu Pro Tyr Gly Val Thr Leu Ile Ile
1 5 10 15

Ala Pro Trp Asn Tyr Pro Phe Gln Leu Ala Ile Ala Pro Leu Val Gly
20 25 30

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

Pro Ser Val Ser Lys Val Leu Lys Arg Met Leu Gly Glu Leu Phe Pro
50 55 60

Glu Glu Leu Val Ala Val Val Glu Gly Gly Val Glu Glu Ser Thr Ser
65 70 75 80

Leu Leu Arg Glu Pro Ile Asp Tyr Ile Phe Phe Thr Gly Ser Val Gly
85 90 95

Val Gly Lys Val Val Met Glu Ala Ala Ala Lys Gln Leu Thr Pro Leu
100 105 110

Thr Leu Glu Leu Gly Gly Lys Ser Pro Cys Ile Val His Lys Asp Ala
115 120 125

Lys Ile Glu Met Thr Ala Arg Arg Ile Val Trp Gly Lys Phe Leu Asn
130 135 140

Ala Gly Gln Thr Cys Val Ala Pro Asp Tyr Met Tyr Val His Ser Ser
145 150 155 160

Val Lys Glu Gln Leu Val Glu Ala Leu Arg His Glu Ile Thr Glu Gln
165 170 175

Tyr Ser Lys Glu Pro Leu Gln Asn Glu Asn Tyr Val Arg Ile Val Ser
180 185 190

Glu Arg His Phe Glu Arg Leu Cys Gly Phe Leu Gln Asp Gly Gln Val
195 200 205

Val Ile Gly Gly Asn Tyr Glu Lys Asp Thr Leu His Ile Glu Pro Thr
210 215 220

Val Leu Ala Asp Ile Thr Trp Gln Asp Ala Val Met Glu Asp Glu Ile
225 230 235 240

Phe Gly Pro Ile Leu Pro Ile Ile Glu Tyr Asp Asn Ile Glu Asp Val
245 250 255

Ile Gly Thr Ile Gln Gln His Pro Lys Pro Leu Ala Leu Tyr Val Phe
260 265 270

Ser Glu Asp Lys Glu Val Gln Lys Lys Val Thr Ser Asn Ile Ser Tyr
275 280 285

Gly Gly Gly Cys Ile Asn Asp Val Val Tyr His Leu Ala Thr Pro Tyr
290 295 300

Leu Pro Phe Gly Gly Val Gly Ser Ser Gly Leu Gly Gly Tyr His Gly
305 310 315 320

Glu Glu Ser Phe Arg Thr Phe Ser His Tyr Lys Ser Ile Leu Ala Gln
325 330 335

Ser Thr Ala Phe Asp Met Lys Ile Arg Tyr Ser Ser Thr Lys Ser Ala
340 345 350

Leu Lys Phe Ile Arg Lys Leu Leu Lys
355 360

<210> 5
<211> 783
<212> DNA
<213> Unknown

<220>
<223> Aquatic organism screen of a metagenomic library containing DNA fragments from an environmental sample removed from a shipping channel in Laguna Madre, Texas

<220>
<221> misc_feature
<222> (755)..(755)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (762)..(762)
<223> n is a, c, g, or t

<400> 5
ttggccgatt cattaatgca gagatcaaaa ggaaaagtag tgccagagcc gtatggtgtg 60

acgcttatta ttgcaccgtg gaactatcct tttcaattag caattgcacc acttgtagga 120

gcacttgcag ctggaaatac aatcgtttta aagccgtcag agttaacgcc aagcgtttca 180

aaagtgctta agagaatgtt aggtgaatta ttcccagaag agcttgtagc ggtagtagaa 240

ggtggcgttg aagagagtac atctttgctg agggaaccaa ttgattatat tttctttact 300

ggtagtgttg gcgttggaaa agttgtaatg gaagcagcag cgaaacagtt gacgccgctt 360

acgttagaac ttggcgggaa aagtccttgt attgtacata aagatgcaaa gatagagatg 420

acagcaagaa gaattgtttg gggtaagttt ttaaatgcag ggcagacatg tgtagcgcct 480

gattatatgt acgtgcattc ttccgtgaaa gaacagctag ttgaggcact gcgacatgaa 540

atcacagagc agtatagtaa agaacctttg caaaatgaaa attatgtgcg tattgtaagt 600

gagcgtcatt ttgaacgatt atgtggattt ttacaagatg gtcaagtcgt aattggtgga 660

aactatgaga aagatacatt acatattgaa ccgacagtgc tagcggatat tacatggcaa 720

gatgctgtta tggaagatga aatttttggt ccgantttac cnatcataga gtacgacaat 780

ata 783

<210> 6
<211> 261
<212> PRT
<213> Unknown

<220>
<223> Aquatic organism screen of a metagenomic library containing DNA fragments from an environmental sample removed from a shipping channel in Laguna Madre, Texas

<400> 6

Leu Ala Asp Ser Leu Met Gln Arg Ser Lys Gly Lys Val Val Pro Glu
1 5 10 15

Pro Tyr Gly Val Thr Leu Ile Ile Ala Pro Trp Asn Tyr Pro Phe Gln
20 25 30

Leu Ala Ile Ala Pro Leu Val Gly Ala Leu Ala Ala Gly Asn Thr Ile
35 40 45

Val Leu Lys Pro Ser Glu Leu Thr Pro Ser Val Ser Lys Val Leu Lys
50 55 60

Arg Met Leu Gly Glu Leu Phe Pro Glu Glu Leu Val Ala Val Val Glu
65 70 75 80

Gly Gly Val Glu Glu Ser Thr Ser Leu Leu Arg Glu Pro Ile Asp Tyr
85 90 95

Ile Phe Phe Thr Gly Ser Val Gly Val Gly Lys Val Val Met Glu Ala
100 105 110

Ala Ala Lys Gln Leu Thr Pro Leu Thr Leu Glu Leu Gly Gly Lys Ser
115 120 125

Pro Cys Ile Val His Lys Asp Ala Lys Ile Glu Met Thr Ala Arg Arg
130 135 140

Ile Val Trp Gly Lys Phe Leu Asn Ala Gly Gln Thr Cys Val Ala Pro
145 150 155 160

Asp Tyr Met Tyr Val His Ser Ser Val Lys Glu Gln Leu Val Glu Ala
165 170 175

Leu Arg His Glu Ile Thr Glu Gln Tyr Ser Lys Glu Pro Leu Gln Asn
180 185 190

Glu Asn Tyr Val Arg Ile Val Ser Glu Arg His Phe Glu Arg Leu Cys
195 200 205

Gly Phe Leu Gln Asp Gly Gln Val Val Ile Gly Gly Asn Tyr Glu Lys
210 215 220

Asp Thr Leu His Ile Glu Pro Thr Val Leu Ala Asp Ile Thr Trp Gln
225 230 235 240

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

Glu Tyr Asp Asn Ile
260

<210> 7
<211> 455
<212> PRT
<213> Bacillus thuringiensis

<400> 7

Met Ser Ile Thr Ser Ile Val Ser Arg Gln Lys Glu Tyr Phe Leu Lys
1 5 10 15

Gly Cys Thr Arg Ser Ile Glu Met Arg Lys Asn Asn Leu Lys Lys Leu
20 25 30

Tyr Glu Gly Ile Gln Arg Phe Glu Glu Glu Ile Phe Gln Ala Leu Lys
35 40 45

Leu Asp Leu Asn Lys Ser Val His Glu Ser Phe Thr Thr Glu Val Gly
50 55 60

Tyr Val Leu Lys Glu Ile Ser Phe Gln Leu Lys His Met Ser Ser Trp
65 70 75 80

Ser Lys Pro Lys Arg Val Arg Thr Ala Leu Thr His Phe Gly Ser Lys

85 90 95

Gly Lys Val Val Pro Glu Pro Tyr Gly Val Thr Leu Ile Ile Ala Pro
100 105 110

Trp Asn Tyr Pro Phe Gln Leu Ala Ile Ala Pro Leu Val Gly Ala Leu
115 120 125

Ala Ala Gly Asn Thr Ile Val Leu Lys Pro Ser Glu Leu Thr Pro Ser
130 135 140

Val Ser Lys Val Leu Lys Arg Met Leu Gly Glu Leu Phe Pro Glu Glu
145 150 155 160

Leu Val Ala Val Val Glu Gly Gly Val Glu Glu Ser Thr Ser Leu Leu
165 170 175

Arg Glu Pro Ile Asp Tyr Ile Phe Phe Thr Gly Ser Val Gly Val Gly
180 185 190

Lys Val Val Met Glu Ala Ala Ala Lys Gln Leu Thr Pro Leu Thr Leu
195 200 205

Glu Leu Gly Gly Lys Ser Pro Cys Ile Val His Lys Asp Ala Lys Ile
210 215 220

Glu Met Thr Ala Arg Arg Ile Val Trp Gly Lys Phe Leu Asn Ala Gly
225 230 235 240

Gln Thr Cys Val Ala Pro Asp Tyr Met Tyr Val His Ser Ser Val Lys
245 250 255

Glu Gln Leu Val Glu Ala Leu Arg His Glu Ile Thr Glu Gln Tyr Ser
260 265 270

Lys Glu Pro Leu Gln Asn Glu Asn Tyr Val Arg Ile Val Ser Glu Arg
275 280 285

His Phe Glu Arg Leu Cys Gly Phe Leu Gln Asp Gly Gln Val Val Ile
290 295 300

Gly Gly Asn Tyr Lys Lys Asp Thr Leu His Ile Glu Pro Thr Val Leu
305 310 315 320

Ala Asp Ile Thr Trp Gln Asp Ala Val Met Glu Asp Glu Ile Phe Gly
325 330 335

Pro Ile Leu Pro Ile Ile Glu Tyr Asp Asn Ile Glu Asp Val Ile Gly
340 345 350

Thr Ile Gln Gln His Pro Lys Pro Leu Ala Leu Tyr Val Phe Ser Glu

355 360 365

Asp Lys Glu Val Gln Lys Lys Val Thr Ser Asn Ile Ser Tyr Gly Gly
370 375 380

Gly Cys Ile Asn Asp Val Val Tyr His Leu Ala Thr Pro Tyr Leu Pro
385 390 395 400

Phe Gly Gly Val Gly Ser Ser Gly Leu Gly Gly Tyr His Gly Glu Glu
405 410 415

Ser Phe Arg Thr Phe Ser His Tyr Lys Ser Ile Leu Ala Gln Ser Thr
420 425 430

Ala Phe Asp Met Lys Ile Arg Tyr Ser Ser Thr Lys Ser Ala Leu Lys
435 440 445

Phe Ile Arg Lys Leu Leu Lys
450 455

<210> 8
<211> 1753
<212> DNA
<213> Unknown

<220>
<223> Aquatic organism screen of a metagenomic library containing DNA fragments from an environmental sample removed from a shipping channel in Laguna Madre, Texas

<400> 8
gatccgcttt aacgctggca tctgcagcca cggtttgccg taaaacagct agtaaatttg 60

tgacattgtt ttccgccacg gcatctcgtt ctactaaagc tgggatgatg gaaacaattg 120

tgtcgtgctg ttttgcagcg tctaaatcga tgttgttata cccaatgcca tggcgagaaa 180

tcagcaacaa ttcatcttta tgttcaaaaa attctttcgt gaaaaatggc gtcacgctag 240

caataataat cgtatatcct tgtaaacgtt ccgctaactc tttgccacca atttcactgt 300

cgactgtaaa atgcttcacg gtgcctattt tttctaagcg cgtcaagtgt tcaggaaaaa 360

tttgaccaaa actactggaa ttcactatgg caatttttg ttttttaac atgactaaac 420

tcctttactg acttttacg acttcatgcc cgccaaatcc ttgtcgcaaa gaagcgacca 480

ctttgtttga aaaatgattt gctagcatac tttcatttcg agtaaataag gacaacgccg 540

tagttgggac gggcatctcc aaacgcaatg cttcttcaat catccatttg gcttcgccat 600

ttgctgccac tttcccttct agattggcta acgtaggatt ttccgcaaaa cctctttcgc 660

taagcccatc aagcgagctt caataatcga gccgtgattc cacacatcgg ctactttctc 720

caacgcaaaa tcatattcgg cagcttctaa taaattgaat ccttcgccca tggcttgcat 780

catgacgtac tcaatcccgt tatgcaccat tttcaaatag tgaccagctc ctgatttccc 840

agcataaaga taccttgtt cacaagctaa atcttcaaaa aatggggtta acactttgac 900

agcttcaggc gcaccgccaa ccattaaaca cgctccttcc cgcgctcctt tgatgccacc 960

agaagtacca caatcaataa aataaattcc tttttcctta gcaaattgag cattcgcaac 1020

actatcatga aaatttgaat tgccactatc cacaatgata tcctctggtg ctaattgctc 1080

taccaattct gccactaatt gattggtaat ctgaccagcg ggggtactta aaaaaatcac 1140

cttccttttt ttaagcgctt tcaataattc tgacaacgaa tctacaacgg aaagcccctg 1200

ctctctagca gtcgctcttg cttcctttgt cacatcaaag ccaataatgg gccagccttg 1260

ttcgtgaaca tttaatgcca tgttcaaacc cattttccca agtccaataa agccaatgtc 1320

cattttctt tcacctgcct cttttgatac ttcaatcata aaggataaaa aaaataatgt 1380

aaacgattac actaattaaa aaatattttt tatttttag caaaaatctt gcctactcaa 1440

aaggtaaaac gtttttattt ttaaggagct ttcatacaaa aaacacaagt aaatctcttg 1500

gtatcacgtt ctttttactg gctactttct ttagttgaga gaagtctttt caagacccct 1560

tcatttttca gaaaaaagat tatttatttt tttggggctt tttttaaaga atttcttttt 1620

tgtggagaaa aagagaaatt gtatttgtcc tctttttcca ctataatcag tctataccaa 1680

caatgaaaag gcattcattt tatttttaaa aaaataagat tggaggaacg tgttaatgaa 1740

aaaccactat ttg 1753

<210> 9
<211> 900
<212> DNA
<213> Unknown

<220>
<223> Aquatic organism screen of a metagenomic library containing DNA fragments from an environmental sample removed from a shipping channel in Laguna Madre, Texas

<400> 9
ttactgactt tttacgactt catgcccgcc aaatccttgt cgcaaagaag cgaccacttt 60

gtttgaaaaa tgatttgcta gcatactttc atttcgagta ataaggaca acgccgtagt 120

tgggacgggc atctccaaac gcaatgcttc ttcaatcatc catttggctt cgccatttgc 180

tgccactttc ccttctagat tggctaacgt aggattttcc gcaaaaacct ctttcgctaa 240

gcccatcaag cgagcttcaa taatcgagcc gtgattccac acatcggcta ctttctccaa 300

cgcaaaatca tattcggcag cttctaataa attgaatcct tcgcccatgg cttgcatcat 360

gacgtactca atcccgttat gcaccatttt caaatagtga ccagctcctg atttcccagc 420

ataaagatac ccttgttcac aagctaaatc ttcaaaaaat ggggttaaca ctttgacagc 480

ttcaggcgca ccgccaacca ttaaacacgc tccttcccgc gctcctttga tgccaccaga 540

agtaccacaa tcaataaaat aaattccttt ttccttagca aattgagcat tcgcaacact 600

atcatgaaaa tttgaattgc cactatccac aatgatatcc tctggtgcta attgctctac 660

caattctgcc actaattgat tggtaatctg accagcgggg gtacttaaaa aaatcacctt 720

ccttttttta agcgctttca ataattctga caacgaatct acaacggaaa gcccctgctc 780

tctagcagtc gctcttgctt cctttgtcac atcaaagcca ataatgggcc agccttgttc 840

gtgaacattt aatgccatgt tcaaacccat tttcccaagt ccaataaagc caatgtccat 900

<210> 10
<211> 299
<212> PRT
<213> Unknown

<220>
<223> Aquatic organism screen of a metagenomic library containing DNA fragments from an environmental sample removed from a shipping channel in Laguna Madre, Texas

<400> 10

Met Asp Ile Gly Phe Ile Gly Leu Gly Lys Met Gly Leu Asn Met Ala
1 5 10 15

Leu Asn Val His Glu Gln Gly Trp Pro Ile Ile Gly Phe Asp Val Thr
20 25 30

Lys Glu Ala Arg Ala Thr Ala Arg Glu Gln Gly Leu Ser Val Val Asp
35 40 45

Ser Leu Ser Glu Leu Leu Lys Ala Leu Lys Lys Arg Lys Val Ile Phe
50 55 60

Leu Ser Thr Pro Ala Gly Gln Ile Thr Asn Gln Leu Val Ala Glu Leu
65 70 75 80

Val Glu Gln Leu Ala Pro Glu Asp Ile Ile Val Asp Ser Gly Asn Ser
85 90 95

Asn Phe His Asp Ser Val Ala Asn Ala Gln Phe Ala Lys Glu Lys Gly
100 105 110

Ile Tyr Phe Ile Asp Cys Gly Thr Ser Gly Gly Ile Lys Gly Ala Arg
115 120 125

Glu Gly Ala Cys Leu Met Val Gly Gly Ala Pro Glu Ala Val Lys Val
130 135 140

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

Ala Gly Lys Ser Gly Ala Gly His Tyr Leu Lys Met Val His Asn Gly
165 170 175

Ile Glu Tyr Val Met Met Gln Ala Met Gly Glu Gly Phe Asn Leu Leu
180 185 190

Glu Ala Ala Glu Tyr Asp Phe Ala Leu Glu Lys Val Ala Asp Val Trp
195 200 205

```
Asn His Gly Ser Ile Ile Glu Ala Arg Leu Met Gly Leu Ala Lys Glu
    210                 215                 220

Val Phe Ala Glu Asn Pro Thr Leu Ala Asn Leu Glu Gly Lys Val Ala
225                 230                 235                 240

Ala Asn Gly Glu Ala Lys Trp Met Ile Glu Glu Ala Leu Arg Leu Glu
                245                 250                 255

Met Pro Val Pro Thr Thr Ala Leu Ser Leu Phe Thr Arg Asn Glu Ser
            260                 265                 270

Met Leu Ala Asn His Phe Ser Asn Lys Val Val Ala Ser Leu Arg Gln
        275                 280                 285

Gly Phe Gly Gly His Glu Val Val Lys Ser Gln
    290                 295
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<210> 11
<211> 311
<212> PRT
<213> Enterococcus faecalis

<400> 11

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Met Ile Glu Val Ser Lys Glu Ala Gly Glu Arg Lys Met Asp Ile Gly
1               5                   10                  15

Phe Ile Gly Leu Gly Lys Met Gly Leu Asn Met Ala Leu Asn Val His
            20                  25                  30

Glu Gln Gly Trp Pro Ile Ile Gly Phe Asp Val Thr Lys Glu Ala Arg
        35                  40                  45

Ala Thr Ala Arg Glu Gln Gly Leu Ser Val Val Asp Ser Leu Ser Glu
    50                  55                  60

Leu Leu Lys Ala Leu Lys Lys Arg Lys Val Ile Phe Leu Ser Thr Pro
65                  70                  75                  80

Ala Gly Gln Ile Thr Asn Gln Leu Val Ala Glu Leu Val Glu Gln Leu
                85                  90                  95

Ala Pro Glu Asp Ile Ile Val Asp Ser Gly Asn Ser Asn Phe His Asp
            100                 105                 110

Ser Val Ala Asn Ala Gln Phe Ala Lys Glu Lys Gly Ile Tyr Phe Ile
        115                 120                 125

Asp Cys Gly Thr Ser Gly Gly Ile Lys Gly Ala Arg Glu Gly Ala Cys
    130                 135                 140
```

```
Leu Met Val Gly Gly Ala Pro Glu Ala Val Lys Val Leu Thr Pro Phe
145                 150                 155                 160

Phe Glu Asp Leu Ala Cys Glu Gln Gly Tyr Leu Tyr Ala Gly Lys Ser
                165                 170                 175

Gly Ala Gly His Tyr Leu Lys Met Val His Asn Gly Ile Glu Tyr Val
            180                 185                 190

Met Met Gln Ala Met Gly Glu Gly Phe Asn Leu Leu Glu Ala Ala Glu
        195                 200                 205

Tyr Asp Phe Ala Leu Glu Lys Val Ala Asp Val Trp Asn His Gly Ser
    210                 215                 220

Ile Ile Glu Ala Arg Leu Met Gly Leu Ala Lys Glu Val Phe Ala Glu
225                 230                 235                 240

Asn Pro Thr Leu Ala Asn Leu Glu Gly Lys Val Ala Ala Asn Gly Glu
                245                 250                 255

Ala Lys Trp Met Ile Glu Glu Ala Leu Arg Leu Glu Met Pro Val Pro
            260                 265                 270

Thr Thr Ala Leu Ser Leu Phe Thr Arg Asn Glu Ser Met Leu Ala Asn
        275                 280                 285

His Phe Ser Asn Lys Val Val Ala Ser Leu Arg Gln Gly Phe Gly Gly
    290                 295                 300

His Glu Val Val Lys Ser Gln
305                 310
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<210> 12
<211> 1449
<212> DNA
<213> Synechocystis PCC6803

<400> 12

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tcaatcaagc cattccgtgt ggaaaaattc tcccctcggc ttatcagtcc gttcataggt       60

gtgggcccca aagtaatccc gttgcgcttg agtcaggttt tggggaagca ccgcccgccg      120

gtaactgtca aagtaatcca acgaggaact aaaggccggc actgcaatgc ccatttcatt      180

ggccagcatc aacacttctc gccatggccc ctggcgatcc aaaatacttt gcttgaattc      240

cggagctaga agtaaattgg gcaactgggg attgtcttta aaagctttct tgatcttgtc      300

taaaaagcca gctcggataa tgcaaccccc tttccaaatg cgggcaattt ccggcaggtt      360

aacgtcgtag ccaaattcct gggaagcttt ggcaattagg gccatgccct gggcatagga      420

acacattttc gagcaataga gggcatcccg caccttagga atccaggctt ctacgtcccc      480

actaaaggtt ttactgggac ccgacagttg accggaagcg gccacccgtt cttctttgag      540
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ggaagacatt accctggcgt taacggcggc gtaaatagtg ggaatgggca ctcctaattc 600

caaaccactc atcaccgtcc agcgtcctgt gccctttggg ccggcggcat caaggatgta 660

gtcaattaaa tggcctccgg tttcgggatc ctttttagca aaaatgtcgg tgctgatttc 720

aatcaggaag gagtttaact catcggtttg attccattgg ccaaaaactt cgtggagttg 780

ttcgttgctc aagccgaggc catttttcaa gatgtcgtag gcttcagcga ttagttgcat 840

atcgccatac tcaatgccgt tgtggaccat tttgacgtaa tgtcctgctc cccctgggcc 900

aataaaagtc acacaggcgg gattatcggg gtcttccacc tgggcggcaa ttttagtcag 960

aatgggttcc aattctttgt aggcggccgg ggtaccaccg ggcatcaaac taggacccag 1020

taatgcgcct tcttcccctc cactgactcc catgccgaca aagcccaggc cggtggcttc 1080

caaatctttg gtgcgacgtt ccgtatcttc ataaagggag ttgccaccat caatgatcat 1140

gtccccttct tccaacaggg gcttcaactc attgatcact gcatccacgg gtcccccagc 1200

tttgaccatt acaaggattt tacgggggcg ttccaacagt tggacaaatt cttctacggt 1260

gtaggcggct ttgatatctt tgcccacagc ccgttcggcc atgaatttct cagttttgtt 1320

gggggaacgg ttaaacacgg cgatgggaaa gcctcgactt tccacgttga gggcaagatt 1380

ttcccccatt accgctagtc caattacccc aaaagttcgc ttagtcataa tagctacgtt 1440

aaattgcac 1449

<210> 13
<211> 482
<212> PRT
<213> Synechocystis PCC6803

<400> 13

Met Gln Phe Asn Val Ala Ile Met Thr Lys Arg Thr Phe Gly Val Ile
1 5 10 15

Gly Leu Ala Val Met Gly Glu Asn Leu Ala Leu Asn Val Glu Ser Arg
20 25 30

Gly Phe Pro Ile Ala Val Phe Asn Arg Ser Pro Asn Lys Thr Glu Lys
35 40 45

Phe Met Ala Glu Arg Ala Val Gly Lys Asp Ile Lys Ala Ala Tyr Thr
50 55 60

Val Glu Glu Phe Val Gln Leu Leu Glu Arg Pro Arg Lys Ile Leu Val
65 70 75 80

Met Val Lys Ala Gly Gly Pro Val Asp Ala Val Ile Asn Glu Leu Lys
85 90 95

Pro Leu Leu Glu Glu Gly Asp Met Ile Ile Asp Gly Gly Asn Ser Leu
100 105 110

```
Tyr Glu Asp Thr Glu Arg Arg Thr Lys Asp Leu Glu Ala Thr Gly Leu
        115                 120                 125

Gly Phe Val Gly Met Gly Val Ser Gly Gly Glu Glu Gly Ala Leu Leu
    130                 135                 140

Gly Pro Ser Leu Met Pro Gly Gly Thr Pro Ala Ala Tyr Lys Glu Leu
145                 150                 155                 160

Glu Pro Ile Leu Thr Lys Ile Ala Ala Gln Val Glu Asp Pro Asp Asn
                165                 170                 175

Pro Ala Cys Val Thr Phe Ile Gly Pro Gly Gly Ala Gly His Tyr Val
            180                 185                 190

Lys Met Val His Asn Gly Ile Glu Tyr Gly Asp Met Gln Leu Ile Ala
        195                 200                 205

Glu Ala Tyr Asp Ile Leu Lys Asn Gly Leu Gly Leu Ser Asn Glu Gln
    210                 215                 220

Leu His Glu Val Phe Gly Gln Trp Asn Gln Thr Asp Glu Leu Asn Ser
225                 230                 235                 240

Phe Leu Ile Glu Ile Ser Thr Asp Ile Phe Ala Lys Lys Asp Pro Glu
                245                 250                 255

Thr Gly Gly His Leu Ile Asp Tyr Ile Leu Asp Ala Ala Gly Gln Lys
            260                 265                 270

Gly Thr Gly Arg Trp Thr Val Met Ser Gly Leu Glu Leu Gly Val Pro
        275                 280                 285

Ile Pro Thr Ile Tyr Ala Ala Val Asn Ala Arg Val Met Ser Ser Leu
    290                 295                 300

Lys Glu Glu Arg Val Ala Ala Ser Gly Gln Leu Ser Gly Pro Ser Lys
305                 310                 315                 320

Thr Phe Ser Gly Asp Val Glu Ala Trp Ile Pro Lys Val Arg Asp Ala
                325                 330                 335

Leu Tyr Cys Ser Lys Met Cys Ser Tyr Ala Gln Gly Met Ala Leu Ile
            340                 345                 350

Ala Lys Ala Ser Gln Glu Phe Gly Tyr Asp Val Asn Leu Pro Glu Ile
        355                 360                 365

Ala Arg Ile Trp Lys Gly Gly Cys Ile Ile Arg Ala Gly Phe Leu Asp
    370                 375                 380
```

Lys Ile Lys Lys Ala Phe Lys Asp Asn Pro Gln Leu Pro Asn Leu Leu
385 390 395 400

Leu Ala Pro Glu Phe Lys Gln Ser Ile Leu Asp Arg Gln Gly Pro Trp
405 410 415

Arg Glu Val Leu Met Leu Ala Asn Glu Met Gly Ile Ala Val Pro Ala
420 425 430

Phe Ser Ser Ser Leu Asp Tyr Phe Asp Ser Tyr Arg Arg Ala Val Leu
435 440 445

Pro Gln Asn Leu Thr Gln Ala Gln Arg Asp Tyr Phe Gly Ala His Thr
450 455 460

Tyr Glu Arg Thr Asp Lys Pro Arg Gly Glu Phe Phe His Thr Glu Trp
465 470 475 480

Leu Asp

<210> 14
<211> 412
<212> DNA
<213> Unknown

<220>
<223> Aquatic organism screen of a metagenomic library containing DNA fragments from an environmental sample removed from a shipping channel in Laguna Madre, Texas

<400> 14
atgttaaaaa aacaaaaaat tgccatagtg aattccagta gttttggtca aatttttcct 60

gaacacttga cgcgcttaga aaaaataggc accgtgaagc attttacagt cgacagtgaa 120

attggtggca aagagttagc ggaacgttta caaggatata cgattattat tgctagcgtg 180

acgccatttt tcacgaaaga atttttgaa cataaagatg aattgttgct gatttctcgc 240

catggcattg ggtataacaa catcgattta gacgctgcaa aacagcacga cacaattgtt 300

tccatcatcc cagctttagt agaacgagat gccgtggcgg aaaacaatgt cacaaattta 360

ctagctgttt tacggcaaac cgtggctgca gatgccagcg ttaaagcgga tc 412

<210> 15
<211> 137
<212> PRT
<213> Unknown

<220>
<223> Aquatic organism screen of a metagenomic library containing DNA fragments from an environmental sample removed from a shipping channel in Laguna Madre, Texas

<400> 15

Met Leu Lys Lys Gln Lys Ile Ala Ile Val Asn Ser Ser Ser Phe Gly
1 5 10 15

Gln Ile Phe Pro Glu His Leu Thr Arg Leu Glu Lys Ile Gly Thr Val
20 25 30

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

Arg Leu Gln Gly Tyr Thr Ile Ile Ile Ala Ser Val Thr Pro Phe Phe
50 55 60

Thr Lys Glu Phe Phe Glu His Lys Asp Glu Leu Leu Leu Ile Ser Arg
65 70 75 80

His Gly Ile Gly Tyr Asn Asn Ile Asp Leu Asp Ala Ala Lys Gln His
85 90 95

Asp Thr Ile Val Ser Ile Ile Pro Ala Leu Val Glu Arg Asp Ala Val
100 105 110

Ala Glu Asn Asn Val Thr Asn Leu Leu Ala Val Leu Arg Gln Thr Val
115 120 125

Ala Ala Asp Ala Ser Val Lys Ala Asp
130 135

<210> 16
<211> 333
<212> PRT
<213> Enterococcus faecalis

<400> 16

Met Leu Lys Lys Gln Lys Ile Ala Ile Val Asn Ser Ser Ser Phe Gly
1 5 10 15

Gln Ile Phe Pro Glu His Leu Thr Arg Leu Glu Lys Ile Gly Thr Val
20 25 30

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

Arg Leu Gln Gly Tyr Thr Ile Ile Ile Ala Ser Val Thr Pro Phe Phe
50 55 60

Thr Lys Glu Phe Phe Glu His Lys Asp Glu Leu Leu Leu Ile Ser Arg
65 70 75 80

His Gly Ile Gly Tyr Asn Asn Ile Asp Leu Asp Ala Ala Lys Gln His
85 90 95

Asp Thr Ile Val Ser Ile Ile Pro Ala Leu Val Glu Arg Asp Ala Val
100 105 110

```
Ala Glu Asn Asn Val Thr Asn Leu Leu Ala Val Leu Arg Gln Thr Val
        115                 120                 125

Ala Ala Asp Ala Ser Val Lys Ala Asp Gln Trp Glu Lys Arg Ala Asn
    130                 135                 140

Phe Val Gly Arg Thr Leu Phe Asn Lys Thr Val Gly Val Ile Gly Val
145                 150                 155                 160

Gly Asn Thr Gly Ser Cys Val Val Glu Thr Leu Arg Asn Gly Phe Arg
                165                 170                 175

Cys Asp Val Leu Ala Tyr Asp Pro Tyr Lys Ser Ala Thr Tyr Leu Gln
            180                 185                 190

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

Asp Ile Ile Cys Leu Cys Ala Asn Leu Thr Glu Glu Ser Tyr His Met
    210                 215                 220

Ile Gly Ser Ala Glu Ile Ala Lys Met Lys Asp Gly Val Tyr Leu Ser
225                 230                 235                 240

Asn Ser Ala Arg Gly Ala Leu Ile Asp Glu Glu Ala Met Ile Ala Gly
                245                 250                 255

Leu Gln Ser Gly Lys Ile Ala Gly Leu Gly Thr Asp Val Leu Glu Glu
            260                 265                 270

Glu Pro Gly Arg Lys Asn His Pro Tyr Leu Ala Phe Glu Asn Val Val
        275                 280                 285

Met Thr Pro His Thr Ser Ala Tyr Thr Met Glu Cys Leu Gln Ala Met
    290                 295                 300

Gly Glu Lys Cys Val Gln Asp Val Glu Asp Val Val Gln Gly Ile Leu
305                 310                 315                 320

Pro Gln Arg Thr Val Gln Glu Val Ser Arg Tyr Val Ser
                325                 330
```

<210> 17
<211> 552
<212> DNA
<213> Unknown

<220>
<223> Aquatic organism screen of a metagenomic library containing DNA fragments from an environmental sample removed from a shipping channel in Laguna Madre, Texas

<400> 17

cggggtctgc cgaagggcgt cttcaatgtc gtgcacggcg cgcatgacgt cgtaaacggc 60

gttcttgaac atccggagat taaagccatc tcattcgtcg gttcaaaacc tgtcggcgag 120

tatgttttca aaaaaggcag cgaacatttg aaacgcgtgc aggcgttaac gggcgcgaaa 180

aaccatacga tcgtgttaaa tgacgcccac cttgaagata cggtgacaaa cattatcggc 240

gcggcattcg gttcggcagg agagcgctgc atggcatgcg cggttgtgac ggttgaagag 300

ggaatcgccg atgagtttat ggcgaaatta caggaaaagg tcgcagacat caagatcgga 360

aacggactgg atgacggcgt gttcttaggc ccggtcatcc gcgaggacaa caaaaaacgg 420

acgcacagct atattgaaaa aggcatcgaa gaaggagcga gacttctttg tgacgggcgt 480

gaaaacgcaa cggaagacgg ctatttcgtc ggaccgacaa tttttgacaa cgtgacgacg 540

gatatggcga tc 552

<210> 18
<211> 184
<212> PRT
<213> Unknown

<220>
<223> Methylmalonate semialdehyde dehydrogenase identified from a screen of a metagenomic library containing DNA fragments from an environmental sample removed from a shipping channel in Laguna Madre, Texas.

<400> 18

Arg Gly Leu Pro Lys Gly Val Phe Asn Val Val His Gly Ala His Asp
1 5 10 15

Val Val Asn Gly Val Leu Glu His Pro Glu Ile Lys Ala Ile Ser Phe
20 25 30

Val Gly Ser Lys Pro Val Gly Glu Tyr Val Phe Lys Lys Gly Ser Glu
35 40 45

His Leu Lys Arg Val Gln Ala Leu Thr Gly Ala Lys Asn His Thr Ile
50 55 60

Val Leu Asn Asp Ala His Leu Glu Asp Thr Val Thr Asn Ile Ile Gly
65 70 75 80

Ala Ala Phe Gly Ser Ala Gly Glu Arg Cys Met Ala Cys Ala Val Val
85 90 95

Thr Val Glu Glu Gly Ile Ala Asp Glu Phe Met Ala Lys Leu Gln Glu
100 105 110

Lys Val Ala Asp Ile Lys Ile Gly Asn Gly Leu Asp Asp Gly Val Phe
115 120 125

Leu Gly Pro Val Ile Arg Glu Asp Asn Lys Lys Arg Thr His Ser Tyr
130 135 140

```
Ile Glu Lys Gly Ile Glu Glu Gly Ala Arg Leu Leu Cys Asp Gly Arg
145                 150                 155                 160

Glu Asn Ala Thr Glu Asp Gly Tyr Phe Val Gly Pro Thr Ile Phe Asp
                165                 170                 175

Asn Val Thr Thr Asp Met Ala Ile
            180
```

<210> 19
<211> 487
<212> PRT
<213> Bacillus amyloliquefaciens

<400> 19

```
Met Ala Glu Ile Arg Lys Leu Lys Asn Tyr Ile Asn Gly Glu Trp Val
1               5                   10                  15

Glu Ser Lys Thr Asp Gln Tyr Glu Asp Val Val Asn Pro Ala Thr Lys
            20                  25                  30

Glu Val Met Cys Gln Val Pro Ile Ser Thr Arg Glu Asp Val Glu Tyr
        35                  40                  45

Ala Val Arg Ser Ala Ser Glu Ala Phe Lys Thr Trp Ser Lys Thr Ala
    50                  55                  60

Val Pro Arg Arg Ala Arg Ile Leu Phe Asn Tyr Gln Gln Leu Leu Gln
65                  70                  75                  80

Gln Asn Lys Glu Glu Leu Ala Arg Leu Ile Thr Leu Glu Asn Gly Lys
                85                  90                  95

Asn Thr Thr Glu Ala Leu Gly Glu Val Gly Arg Gly Ile Glu Asn Val
            100                 105                 110

Glu Phe Ala Ala Gly Ala Pro Ser Leu Met Met Gly Asp Ser Leu Ala
        115                 120                 125

Ser Ile Ala Thr Asp Val Glu Ala Ala Asn Tyr Arg Tyr Pro Ile Gly
    130                 135                 140

Val Val Gly Gly Ile Ala Pro Phe Asn Phe Pro Met Met Val Pro Cys
145                 150                 155                 160

Trp Met Phe Pro Met Ala Ile Ser Leu Gly Asn Thr Phe Ile Leu Lys
                165                 170                 175

Pro Ser Glu Arg Thr Pro Leu Leu Thr Glu Lys Leu Ala Glu Leu Phe
            180                 185                 190
```

```
Glu Gln Ala Gly Leu Pro Lys Gly Val Phe Asn Val Val His Gly Ala
        195                 200                 205

His Asp Val Val Asn Gly Ile Leu Glu His Pro Asp Ile Lys Ala Ile
    210                 215                 220

Ser Phe Val Gly Ser Lys Pro Val Gly Glu Tyr Val Phe Lys Lys Gly
225                 230                 235                 240

Ser Glu His Leu Lys Arg Val Gln Ala Leu Thr Gly Ala Lys Asn His
                245                 250                 255

Thr Ile Val Leu Asn Asp Ala His Leu Glu Asp Thr Val Thr Asn Ile
            260                 265                 270

Ile Gly Ala Ala Phe Gly Ser Ala Gly Glu Arg Cys Met Ala Cys Ala
        275                 280                 285

Val Val Thr Val Glu Glu Gly Ile Ala Asp Glu Phe Met Ala Lys Leu
    290                 295                 300

Gln Glu Lys Ala Ala Asp Ile Lys Leu Gly Asn Gly Leu Asp Asp Gly
305                 310                 315                 320

Val Phe Leu Gly Pro Val Ile Arg Glu Asp Asn Lys Lys Arg Thr His
                325                 330                 335

Ser Tyr Ile Glu Lys Gly Ile Glu Glu Gly Ala Arg Leu Leu Cys Asp
            340                 345                 350

Gly Arg Glu Asn Val Thr Glu Asp Gly Tyr Phe Val Gly Pro Thr Ile
        355                 360                 365

Phe Asp Asn Val Thr Thr Asp Met Thr Ile Trp Lys Asp Glu Ile Phe
    370                 375                 380

Ala Pro Val Leu Ser Val Ile Arg Val Lys Asn Leu Lys Glu Ala Val
385                 390                 395                 400

Asp Ile Ala Asn Gln Ser Glu Phe Ala Asn Gly Ala Cys Leu Phe Thr
                405                 410                 415

Ser Asn Ala Asn Ala Ile Arg Tyr Phe Arg Glu Asn Ile Asp Ala Gly
            420                 425                 430

Met Leu Gly Ile Asn Leu Gly Val Pro Ala Pro Met Ala Phe Phe Pro
        435                 440                 445

Phe Ser Gly Trp Lys Ser Ser Phe Phe Gly Thr Leu His Ala Asn Gly
    450                 455                 460
```

Lys Asp Ser Val Asp Phe Tyr Thr Arg Lys Lys Val Val Thr Ala Arg
465 470 475 480

Tyr Pro Ser Pro Asp Phe Asn
485

<210> 20
<211> 1089
<212> DNA
<213> Cuphea carthagenensis

<400> 20
atggcgaacg gtagcgctgt ctctctgaag agcggctcct tgaatacgca agaggacact 60

tcttcttccc caccgccacg cgcgttcatc aaccaattac ccgactggtc catgttattg 120

acggcgatta ccactgtctt tgttgccgca gagaaacagt ggactatgtt agaccgcaag 180

agcaagcgct ccgatatgtt agtggattct tttggcatgg aacgcattgt gcaggatggc 240

ttagtgtttc gtcaatcttt tagcattcgt tcttatgaaa tcggtgcaga tcgtcgtgca 300

tccattgaaa ccttaatgaa ccatctgcag gaaactagct tgaatcattg caaatccatt 360

cgcttgttga atgagggttt tggtcgcacc cccgagatgt gcaaacgtga cttgatctgg 420

gtggttaccc gcatgcacat catggtcaac cgctacccta cctggggtga taccgttgag 480

attaacactt gggtttccca aagcggcaag aatggtatgg gtcgtgattg gctgatttcc 540

gactgtaata ccggcgaaat cctgatccgc gcgacgtctg catgggcgat gatgaaccaa 600

aagacccgtc gtctgtctaa actgccttac gaagtcagcc aagagattgc tccgcacttc 660

gtcgacagcc ctcccgtgat cgaggacggc gaccgtaagt tacacaagtt cgatgtgaaa 720

accggcgaca gcatccgtaa aggtttgact ccgcgttgga atgacttaga tgttaatcag 780

cacgttaaca acgttaagta tatcggctgg atcttagaga gcatgccgac cgaggtcttg 840

gaaactcatg aactgtgttt cttaactctg gagtatcgtc gcgagtgcgg tcgcgatagc 900

gtgctggaat ctgtgaccgc gatggatcct tctaatgaag gtggtcgctc ccactaccag 960

catttactgc gcttggagga cggtactgac atcgttaagg gccgcactga gtggcgtcca 1020

aagaatgccc ggaatattgg tgccattagt accggtaaaa ccagtaatgg taatcccgcc 1080

agttaataa 1089

<210> 21
<211> 361
<212> PRT
<213> Cuphea carthagenensis

<400> 21

Met Ala Asn Gly Ser Ala Val Ser Leu Lys Ser Gly Ser Leu Asn Thr
1 5 10 15

Gln Glu Asp Thr Ser Ser Ser Pro Pro Pro Arg Ala Phe Ile Asn Gln
20 25 30

```
Leu Pro Asp Trp Ser Met Leu Leu Thr Ala Ile Thr Thr Val Phe Val
        35                  40                  45

Ala Ala Glu Lys Gln Trp Thr Met Leu Asp Arg Lys Ser Lys Arg Ser
    50                  55                  60

Asp Met Leu Val Asp Ser Phe Gly Met Glu Arg Ile Val Gln Asp Gly
65                  70                  75                  80

Leu Val Phe Arg Gln Ser Phe Ser Ile Arg Ser Tyr Glu Ile Gly Ala
                85                  90                  95

Asp Arg Arg Ala Ser Ile Glu Thr Leu Met Asn His Leu Gln Glu Thr
            100                 105                 110

Ser Leu Asn His Cys Lys Ser Ile Arg Leu Leu Asn Glu Gly Phe Gly
        115                 120                 125

Arg Thr Pro Glu Met Cys Lys Arg Asp Leu Ile Trp Val Val Thr Arg
    130                 135                 140

Met His Ile Met Val Asn Arg Tyr Pro Thr Trp Gly Asp Thr Val Glu
145                 150                 155                 160

Ile Asn Thr Trp Val Ser Gln Ser Gly Lys Asn Gly Met Gly Arg Asp
                165                 170                 175

Trp Leu Ile Ser Asp Cys Asn Thr Gly Glu Ile Leu Ile Arg Ala Thr
            180                 185                 190

Ser Ala Trp Ala Met Met Asn Gln Lys Thr Arg Arg Leu Ser Lys Leu
        195                 200                 205

Pro Tyr Glu Val Ser Gln Glu Ile Ala Pro His Phe Val Asp Ser Pro
    210                 215                 220

Pro Val Ile Glu Asp Gly Asp Arg Lys Leu His Lys Phe Asp Val Lys
225                 230                 235                 240

Thr Gly Asp Ser Ile Arg Lys Gly Leu Thr Pro Arg Trp Asn Asp Leu
                245                 250                 255

Asp Val Asn Gln His Val Asn Asn Val Lys Tyr Ile Gly Trp Ile Leu
            260                 265                 270

Glu Ser Met Pro Thr Glu Val Leu Glu Thr His Glu Leu Cys Phe Leu
        275                 280                 285

Thr Leu Glu Tyr Arg Arg Glu Cys Gly Arg Asp Ser Val Leu Glu Ser
    290                 295                 300
```

Val Thr Ala Met Asp Pro Ser Asn Glu Gly Gly Arg Ser His Tyr Gln
305 310 315 320

His Leu Leu Arg Leu Glu Asp Gly Thr Asp Ile Val Lys Gly Arg Thr
325 330 335

Glu Trp Arg Pro Lys Asn Ala Arg Asn Ile Gly Ala Ile Ser Thr Gly
340 345 350

Lys Thr Ser Asn Gly Asn Pro Ala Ser
355 360

<210> 22
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> trcY promoter

<400> 22
ctgaaatgag ctgttgacaa ttaatcatcc ggctcgtata atgtgtggaa ttgtgagcgg 60

ataacaattt cacactaagg aggaaaaaaa 90

<210> 23
<211> 8645
<212> DNA
<213> Artificial Sequence

<220>
<223> YC28 Integration Vector

<400> 23
gtctgacgct cagtggaacg aaaactcacg ttaagggatt ttggtcatga gattatcaaa 60

aaggatcttc acctagatcc ttttaaatta aaaatgaagt tttaaatcaa tctaaagtat 120

atatgagtaa acttggtctg acagttacca atgcttaatc agtgaggcac ctatctcagc 180

gatctgtcta tttcgttcat ccatagttgc ctgactcccc gtcgtgtaga taactacgat 240

acgggagggc ttaccatctg gccccagtgc tgcaatgata ccgcgagacc cacgctcacc 300

ggctccagat ttatcagcaa taaaccagcc agccggaagg gccgagcgca gaagtggtcc 360

tgcaacttta tccgcctcca tccagtctat taattgttgc cgggaagcta gagtaagtag 420

ttcgccagtt aatagtttgc gcaactgttg ggaagggcga tcggtgcggg cctcttcgct 480

attacgccag ctggcgaaag ggggatgtgc tgcaaggcga ttaagttggg taacgccagg 540

gttttcccag tcacgacgtt gtaaaacgac ggccagtgcc aagctattgc tgaagcggaa 600

tccctggtta atgccgccgc cgatgccaat tgcattctcc aagtggggca cattgaacgc 660

ttcaacccgg catttttaga gctaaccaaa attctcaaaa cggaagagtt attggcgatc 720

gaagcccatc gcatgagtcc ctattcccag cgggccaatg atgtctccgt ggtattggat 780

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ggcttctcct ccggcattgt ggccaccctc accgccagta aggtcaccca tcgtaaaatt 960

cgttccatcg ccgcccactg caaaaattcc ctcaccgaag cggattttct caataacgaa 1020

attttgatcc atcgccaaac caccgctgat tggagcgcgg actatggcca ggtattgtat 1080

cgccaggatg gtctaatcga aaaggtttac accagtaata ttgaacctct ccacgctgaa 1140

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gccctcaagg ccctgaagtt agccagttta attgaagaaa tggccctgga cagtcaggaa 1260

tggcatgggg gggaagttgt gacagaatat caagatgcca ccctggccct cagtgcgagt 1320

gtttaaatca acttaattaa tgcaattatt gcgagttcaa actcgataac tttgtgaaat 1380

attactgttg aattaatcta tgactattca atacaccccc ctagccgatc gcctgttggc 1440

ctacctcgcc gccgatcgcc taaatctcag cgccaagagt agttccctca acaccagtat 1500

tctgctcagc agtgacctat tcaatcagga agggggaatt gtaacagcca actatggctt 1560

tgatggttat atggtaccat atggtgcact ctcagtacaa tctgctctga tgccgcatag 1620

ttaagccagt atacactccg ctatcgctac gtgactgggt catggctgcg ccccgacacc 1680

cgccaacacc cgctgacgcg ccctgacggg cttgtctgct cccggcatcc gcttacagac 1740

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catcgaatgg tgcaaaacct ttcgcggtat ggcatgatag cgcccggaag agagtcaatt 1920

cagggtggtg aatgtgaaac cagtaacgtt atacgatgtc gcagagtatg ccggtgtctc 1980

ttatcagacc gtttcccgcg tggtgaacca ggccagccac gtttctgcga aaacgcggga 2040

aaaagtggaa gcggcgatgg cggagctgaa ttacattccc aaccgcgtgg cacaacaact 2100

ggcgggcaaa cagtcgttgc tgattggcgt tgccacctcc agtctggccc tgcacgcgcc 2160

gtcgcaaatt gtcgcggcga ttaaatctcg cgccgatcaa ctgggtgcca gcgtggtggt 2220

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gcaacgcgtc agtgggctga tcattaacta tccgctggat gaccaggatg ccattgctgt 2340

ggaagctgcc tgcactaatg ttccggcgtt atttcttgat gtctctgacc agacacccat 2400

caacagtatt attttctccc atgaagacgg tacgcgactg ggcgtggagc atctggtcgc 2460

attgggtcac cagcaaatcg cgctgttagc gggcccatta agttctgtct cggcgcgtct 2520

gcgtctggct ggctggcata aatatctcac tcgcaatcaa attcagccga tagcggaacg 2580

ggaaggcgac tggagtgcca tgtccggttt tcaacaaacc atgcaaatgc tgaatgaggg 2640

catcgttccc actgcgatgc tggttgccaa cgatcagatg gcgctgggcg caatgcgcgc 2700

cattaccgag tccgggctgc gcgttggtgc ggatatctcg gtagtgggat acgacgatac 2760

cgaagacagc tcatgttata tcccgccgtt aaccaccatc aaacaggatt ttcgcctgct 2820

ggggcaaacc agcgtggacc gcttgctgca actctctcag ggccaggcgg tgaagggcaa 2880

tcagctgttg cccgtctcac tggtgaaaag aaaaaccacc ctggcgccca atacgcaaac 2940

cgcctctccc cgcgcgttgg ccgattcatt aatgcagctg gcacgacagg tttcccgact 3000

ggaaagcggg cagtgagcgc aacgcaatta atgtaagtta gcgcgaattg atctggtttg 3060

acagcttatc atcgactgca cggtgcacca atgcttctgg cgtcaggcag ccatcggaag 3120

ctgtggtatg gctgtgcagg tcgtaaatca ctgcataatt cgtgtcgctc aaggcgcact 3180

cccgttctgg ataatgtttt ttgcgccgac atcataacgg ttctggcaaa tattctgaaa 3240

tgagctgttg acaattaatc atccggctcg tataatgtgt ggaattgtga gcggataaca 3300

atttcacaca ggaaacagcg ccgctgagaa aaagcgaagc ggcactgctc tttaacaatt 3360

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Pro Ala His Leu His Glu Leu Pro Gly Leu Val Trp Val Gln Ser Leu

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Trp Ala Gly Val Glu Arg Leu Leu Gly Glu Leu Ile Asp Thr Asp Phe
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Ala Ile Val Arg Met Thr Asp Pro Gln Leu Ala Glu Thr Met Ala Glu
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Glu Gly Leu Gln Arg Val Leu Ser Arg Ser Asp Ile Val Val Val Leu
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Leu Pro Leu Thr Pro Asp Thr Arg Gly Leu Leu Asn Thr Ala Arg Leu
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Ser His Ala Val Leu Asp Val Phe Ala Gln Glu Pro Leu Pro Val Asp
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