

107345_00374_SEQLIST
SEQUENCE LISTING

<110> AMYRIS, INC.
GARDNER, Timothy Stevens
HAWKINS, Kristy Michelle
MEADOWS, Adam Leon
TSONG, Annie Ening
TSEGAYE, Yoseph

<120> PRODUCTION OF ACETYL-COENZYME A DERIVED ISOPRENOIDS

<130> 107345.00374

<150> US 61/557,893

<151> 2011-11-09

<160> 54

<170> PatentIn version 3.5

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<211> 1380

<212> DNA

<213> Dickeya zeae

<220>

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<222> (1)..(1380)

<223> Dickeya zeae eutE gene sequence

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gatataccga aagccgctcg cgcaatagta aagggcgctt cgtttgacaa caatattatt	780
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 35 40 45
 Gln Gln Val Ile Lys Ala Ile Arg Val Ala Gly Glu Arg Tyr Ala Gln
 50 55 60
 Val Leu Ala Glu Met Ala Val Ala Glu Thr Gly Met Gly Arg Val Val
 65 70 75 80
 Asp Lys Tyr Ile Lys Asn Val Ser Gln Ala Arg His Thr Pro Gly Ile
 85 90 95
 Glu Cys Leu Ser Ala Glu Val Leu Thr Gly Asp Asn Gly Leu Thr Leu
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 Ile Glu Asn Ala Pro Trp Gly Val Val Ala Ser Val Thr Pro Ser Thr
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 Asn Pro Ala Ala Thr Val Ile Asn Asn Ala Ile Ser Met Ile Ala Ala
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 Gly Asn Ser Val Val Phe Ala Pro His Pro Ser Ala Lys Asn Val Ser
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 Leu Arg Thr Ile Ser Leu Leu Asn Lys Ala Ile Val Ala Thr Gly Gly
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Gln Arg Leu Phe Arg Tyr Pro Gly Ile Gly Leu Leu Val Val Thr Gly
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Gly Glu Ala Val Val Glu Ala Ala Arg Lys His Thr Asp Lys Arg Leu
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Ile Ala Ala Gly Ala Gly Asn Pro Pro Val Val Val Asp Glu Thr Ala
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Asp Ile Pro Lys Ala Ala Arg Ala Ile Val Lys Gly Ala Ser Phe Asp
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Asn Asn Ile Ile Cys Ala Asp Glu Lys Val Leu Ile Val Val Asp Arg
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Val Ala Asp Ala Leu Leu Ala Glu Met Gln Arg Asn Asn Ala Val Leu
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Leu Thr Pro Glu Gln Thr Glu Arg Leu Leu Pro Ala Leu Leu Ser Asp
290 295 300

Ile Asp Glu Gln Gly Lys Gly Arg Val Asn Arg Asp Tyr Val Gly Arg
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Asp Ala Ala Lys Leu Ala Ala Ala Ile Gly Leu Glu Val Ser Glu His
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Thr Arg Leu Leu Leu Ala Glu Thr Asp Ala Asp His Pro Phe Ala Val
340 345 350

Thr Glu Leu Met Met Pro Val Leu Pro Val Ile Arg Val Lys Asn Val
355 360 365

Asp Asp Ala Ile Ala Leu Ala Val Lys Leu Glu Ser Gly Cys Arg His
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385 390 395 400

Asn Ala Ile Asn Thr Ser Ile Phe Val Lys Asn Gly Pro Cys Ile Ala
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Gln Gln Lys Lys Glu His Glu Tyr Glu His Leu Thr Ser Val Lys Ile
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Val Pro Gln Arg Pro Ile Ser Asp Arg Leu Gln Pro Ala Ile Ala Thr
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 Lys Glu Ser Ile Glu Asp Pro Ala Lys Phe Phe Gly Ser Lys Ala Thr
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 Gln Phe Leu Asn Trp Ser Lys Pro Phe Asp Lys Val Phe Ile Pro Asp
 100 105 110
 Ser Lys Thr Gly Arg Pro Ser Phe Gln Asn Asn Ala Trp Phe Leu Asn
 115 120 125
 Gly Gln Leu Asn Ala Cys Tyr Asn Cys Val Asp Arg His Ala Leu Lys
 130 135 140
 Thr Pro Asn Lys Lys Ala Ile Ile Phe Glu Gly Asp Glu Pro Gly Gln
 145 150 155 160
 Gly Tyr Ser Ile Thr Tyr Lys Glu Leu Leu Glu Glu Val Cys Gln Val
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 Ala Gln Val Leu Thr Tyr Ser Met Gly Val Arg Lys Gly Asp Thr Val
 180 185 190
 Ala Val Tyr Met Pro Met Val Pro Glu Ala Ile Ile Thr Leu Leu Ala
 195 200 205
 Ile Ser Arg Ile Gly Ala Ile His Ser Val Val Phe Ala Gly Phe Ser
 210 215 220
 Ser Asn Ser Leu Arg Asp Arg Ile Asn Asp Gly Asp Ser Lys Val Val
 225 230 235 240
 Ile Thr Thr Asp Glu Ser Asn Arg Gly Gly Lys Val Ile Glu Thr Lys
 245 250 255
 Arg Ile Val Asp Asp Ala Leu Arg Glu Thr Pro Gly Val Arg His Val
 260 265 270
 Leu Val Tyr Arg Lys Thr Asn Asn Pro Ser Val Ala Phe His Ala Pro
 275 280 285
 Arg Asp Leu Asp Trp Ala Thr Glu Lys Lys Lys Tyr Lys Thr Tyr Tyr
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 Pro Cys Thr Pro Val Asp Ser Glu Asp Pro Leu Phe Leu Leu Tyr Thr
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 435 440 445
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 Ala Ala Ile Ile Glu Asp Pro Ile Val Ala Glu Cys Ala Val Val Gly
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Ile Lys Lys His Leu Val Phe Thr Val Arg Lys Asp Ile Gly Pro Phe
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Ala Ala Pro Lys Leu Ile Ile Leu Val Asp Asp Leu Pro Lys Thr Arg
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Ser Gly Lys Ile Met Arg Arg Ile Leu Arg Lys Ile Leu Ala Gly Glu
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Tyr Val Phe Asp Ile His Pro Glu Asp Val Leu Phe Thr Ala Gly Asp
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Val Gly Trp Ile Thr Gly His Thr Tyr Ala Leu Tyr Gly Pro Leu Thr
325 330 335

Leu Gly Thr Ala Ser Ile Ile Phe Glu Ser Thr Pro Ala Tyr Pro Asp
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Tyr Gly Arg Tyr Trp Arg Ile Ile Gln Arg His Lys Ala Thr His Phe
355 360 365

Tyr Val Ala Pro Thr Ala Leu Arg Leu Ile Lys Arg Val Gly Glu Ala
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Phe Thr Gly Asp Gly Ala Gly Arg Asp His Asp Gly Tyr Tyr Trp Ile
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Leu Gln Val Arg Gly Glu Ile Gly Pro Phe Ala Ser Pro Lys Thr Ile
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Ile Leu Val Arg Asp Leu Pro Arg Thr Arg Ser Gly Lys Ile Met Arg
625 630 635 640

Arg Val Leu Arg Lys Val Ala Ser Asn Glu Ala Glu Gln Leu Gly Asp
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Ile Asn Asn Lys Phe Val Pro Ser Lys Gln Asn Lys Thr Phe Gln Val
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100 105 110

Tyr Arg Leu Ala Glu Leu Ile Glu Gln Asp Lys Asp Val Ile Ala Ser
115 120 125

Ile Glu Thr Leu Asp Asn Gly Lys Ala Ile Ser Ser Ser Arg Gly Asp
130 135 140

Val Asp Leu Val Ile Asn Tyr Leu Lys Ser Ser Ala Gly Phe Ala Asp
145 150 155 160

Lys Ile Asp Gly Arg Met Ile Asp Thr Gly Arg Thr His Phe Ser Tyr
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Thr Lys Arg Gln Pro Leu Gly Val Cys Gly Gln Ile Ile Pro Trp Asn
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Phe Pro Leu Leu Met Trp Ala Trp Lys Ile Ala Pro Ala Leu Val Thr
195 200 205

Gly Asn Thr Val Val Leu Lys Thr Ala Glu Ser Thr Pro Leu Ser Ala
210 215 220

Leu Tyr Val Ser Lys Tyr Ile Pro Gln Ala Gly Ile Pro Pro Gly Val
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Asn His Pro Lys Ile Lys Lys Val Ala Phe Thr Gly Ser Thr Ala Thr
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Gly Arg His Ile Tyr Gln Ser Ala Ala Ala Gly Leu Lys Lys Val Thr
275 280 285

Leu Glu Leu Gly Gly Lys Ser Pro Asn Ile Val Phe Ala Asp Ala Glu
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Leu Lys Lys Ala Val Gln Asn Ile Ile Leu Gly Ile Tyr Tyr Asn Ser
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Gly Glu Val Cys Cys Ala Gly Ser Arg Val Tyr Val Glu Glu Ser Ile
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Val Gly Asp Pro Phe Asp Glu Ser Thr Phe Gln Gly Ala Gln Thr Ser
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 370 375 380

Glu Gly Ala Thr Leu Ile Thr Gly Gly Glu Arg Leu Gly Ser Lys Gly
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Tyr Phe Ile Lys Pro Thr Val Phe Gly Asp Val Lys Glu Asp Met Arg
 405 410 415

Ile Val Lys Glu Glu Ile Phe Gly Pro Val Val Thr Val Thr Lys Phe
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Lys Ser Ala Asp Glu Val Ile Asn Met Ala Asn Asp Ser Glu Tyr Gly
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Ala Asp Arg Val Asn Ala Gly Thr Val Trp Ile Asn Thr Tyr Asn Asp
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Phe His His Ala Val Pro Phe Gly Gly Phe Asn Ala Ser Gly Leu Gly
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 (ALD6) nucleotide sequence

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Ser Thr Glu Asn Thr Val Cys Glu Val Ser Ser Ala Thr Thr Glu Asp	50	55	60	
Val Glu Tyr Ala Ile Glu Cys Ala Asp Arg Ala Phe His Asp Thr Glu	65	70	75	80
Trp Ala Thr Gln Asp Pro Arg Glu Arg Gly Arg Leu Leu Ser Lys Leu	85	90	95	
Ala Asp Glu Leu Glu Ser Gln Ile Asp Leu Val Ser Ser Ile Glu Ala	100	105	110	
Leu Asp Asn Gly Lys Thr Leu Ala Leu Ala Arg Gly Asp Val Thr Ile	115	120	125	
Ala Ile Asn Cys Leu Arg Asp Ala Ala Ala Tyr Ala Asp Lys Val Asn	130	135	140	

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 180 185 190

Cys Ile Leu Lys Pro Ala Ala Val Thr Pro Leu Asn Ala Leu Tyr Phe
 195 200 205

Ala Ser Leu Cys Lys Lys Val Gly Ile Pro Ala Gly Val Val Asn Ile
 210 215 220

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

Arg Ile Arg Lys Leu Ala Phe Thr Gly Ser Thr Glu Val Gly Lys Ser
 245 250 255

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

Leu Gly Gly Lys Ser Ala His Leu Val Phe Asp Asp Ala Asn Ile Lys
 275 280 285

Lys Thr Leu Pro Asn Leu Val Asn Gly Ile Phe Lys Asn Ala Gly Gln
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Ile Cys Ser Ser Gly Ser Arg Ile Tyr Val Gln Glu Gly Ile Tyr Asp
 305 310 315 320

Glu Leu Leu Ala Ala Phe Lys Ala Tyr Leu Glu Thr Glu Ile Lys Val
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Gly Asn Pro Phe Asp Lys Ala Asn Phe Gln Gly Ala Ile Thr Asn Arg
 340 345 350

Gln Gln Phe Asp Thr Ile Met Asn Tyr Ile Asp Ile Gly Lys Lys Glu
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Gly Ala Lys Ile Leu Thr Gly Gly Glu Lys Val Gly Asp Lys Gly Tyr
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Phe Ile Arg Pro Thr Val Phe Tyr Asp Val Asn Glu Asp Met Arg Ile
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Val Lys Glu Glu Ile Phe Gly Pro Val Val Thr Val Ala Lys Phe Lys
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Thr Leu Glu Glu Gly Val Glu Met Ala Asn Ser Ser Glu Phe Gly Leu
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450 455 460

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<223> Leuconostoc mesenteroides Phosphoketolase (PK) gene sequence

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<213> Leuconostoc mesenteroides

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<222> (1)..(813)

<223> Leuconostoc mesenteroides Phosphoketolase (PK) protein sequence

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Leu Tyr Ala His Ala Asn Arg Leu Ile Asn Lys Tyr Gly Leu Asn Met
 65 70 75 80

Phe Tyr Val Gly Gly Pro Gly His Gly Gly Gln Val Met Val Thr Asn
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Ala Tyr Leu Asp Gly Ala Tyr Thr Glu Asp Tyr Pro Glu Ile Thr Gln
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Asp Ile Glu Gly Met Ser His Leu Phe Lys Arg Phe Ser Phe Pro Gly
 115 120 125

Gly Ile Gly Ser His Met Thr Ala Gln Thr Pro Gly Ser Leu His Glu
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Gly Gly Glu Leu Gly Tyr Ser Leu Ser His Ala Phe Gly Ala Val Leu
 145 150 155 160

Asp Asn Pro Asp Gln Val Ala Phe Ala Val Val Gly Asp Gly Glu Ala
 165 170 175

Glu Thr Gly Pro Ser Met Ala Ser Trp His Ser Ile Lys Phe Leu Asn
 180 185 190

Ala Lys Asn Asp Gly Ala Val Leu Pro Val Leu Asp Leu Asn Gly Phe
 195 200 205

Lys Ile Ser Asn Pro Thr Ile Phe Ser Arg Met Ser Asp Glu Glu Ile
 210 215 220

Thr Lys Phe Phe Glu Gly Leu Gly Tyr Ser Pro Arg Phe Ile Glu Asn
 225 230 235 240

Asp Asp Ile His Asp Tyr Ala Thr Tyr His Gln Leu Ala Ala Asn Ile
 245 250 255

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 Gly Pro Asp Glu Thr Met Ser Asn Arg Leu Trp Gly Leu Phe Asn Val
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 465 470 475 480
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 485 490 495
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 Gln His Phe Lys Trp Leu Arg His Ala Ser Glu Gln Ala Trp Arg Asn
 515 520 525

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 Ala Glu Lys Lys Ser Asn Phe Ile Arg Glu Tyr Leu Pro Ala Asp Gly
 565 570 575
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 Ala Gly Thr Glu Pro Thr Ile Glu Thr Leu Ala Ala Leu Trp Leu Ile
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 Glu Leu Ser Ala Glu Glu Phe Asn Lys Tyr Phe Gln Ala Asp Thr Pro
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 Val Ile Phe Gly Phe His Ala Tyr Glu Asn Leu Ile Glu Ser Phe Phe
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 740 745 750
 Asp Arg Phe His Gln Ala Lys Glu Ala Ala Glu Ile Leu Ser Ala Asn
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 Gly Lys Ile Asp Gln Ala Ala Ala Asp Thr Phe Ile Ala Lys Met Asp
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gaatatggag aagatggatt ctgtgtattt gctgattgtg ctgtaaatgt atgtcctact      540
gctgaagaat tatcttcaat tgcaataact acagcagaaa ctgcaaaaaa tttgtgtaaa      600
atagaaccaa gagttgccat gctttcattt tctactatgg gaagtgctag tcatgaattg      660
gtagataaag ttacaaaagc aacaaaactt gctaaagaag ctagacctga tttggatata      720
gatggagaac ttcaattgga tgcttcccta gtaaaaaaag ttgcagactt aaaagctccg      780
ggcagtaaag tggcaggaaa agccaatgta cttatatattcc ctgatataca agcaggaaaat      840
ataggatata agttagttca aagatttgca aaagctgagg ctataggacc tatatgtcag      900
ggatttgcaa agcctataaa tgatttatca agaggctgca gcgttgatga tatagtaaag      960
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<210> 14
<211> 333
<212> PRT
<213> Clostridium kluyveri

<220>
<221> misc_feature
<222> (1)..(333)
<223> Clostridium kluyveri Phosphotransacetylase (PTA) protein sequence

<400> 14

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

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Lys Ile Val Leu Ala Glu Gly Glu Glu Glu Arg Asn Ile Arg Ala Ser
 20 25 30
 Glu Glu Ile Ile Arg Asp Gly Ile Ala Asp Ile Ile Leu Val Gly Ser
 35 40 45
 Glu Ser Val Ile Lys Glu Asn Ala Ala Lys Phe Gly Val Asn Leu Ala
 50 55 60
 Gly Val Glu Ile Val Asp Pro Glu Thr Ser Ser Lys Thr Ala Gly Tyr
 65 70 75 80
 Ala Asn Ala Phe Tyr Glu Ile Arg Lys Asn Lys Gly Val Thr Leu Glu
 85 90 95
 Lys Ala Asp Lys Ile Val Arg Asp Pro Ile Tyr Phe Ala Thr Met Met
 100 105 110
 Val Lys Leu Gly Asp Ala Asp Gly Leu Val Ser Gly Ala Ile His Thr
 115 120 125
 Thr Gly Asp Leu Leu Arg Pro Gly Leu Gln Ile Val Lys Thr Val Pro
 130 135 140
 Gly Ala Ser Val Val Ser Ser Val Phe Leu Met Ser Val Pro Asp Cys
 145 150 155 160
 Glu Tyr Gly Glu Asp Gly Phe Leu Leu Phe Ala Asp Cys Ala Val Asn
 165 170 175
 Val Cys Pro Thr Ala Glu Glu Leu Ser Ser Ile Ala Ile Thr Thr Ala
 180 185 190
 Glu Thr Ala Lys Asn Leu Cys Lys Ile Glu Pro Arg Val Ala Met Leu
 195 200 205
 Ser Phe Ser Thr Met Gly Ser Ala Ser His Glu Leu Val Asp Lys Val
 210 215 220
 Thr Lys Ala Thr Lys Leu Ala Lys Glu Ala Arg Pro Asp Leu Asp Ile
 225 230 235 240
 Asp Gly Glu Leu Gln Leu Asp Ala Ser Leu Val Lys Lys Val Ala Asp
 245 250 255
 Leu Lys Ala Pro Gly Ser Lys Val Ala Gly Lys Ala Asn Val Leu Ile
 260 265 270
 Phe Pro Asp Ile Gln Ala Gly Asn Ile Gly Tyr Lys Leu Val Gln Arg
 275 280 285

Phe Ala Lys Ala Glu Ala Ile Gly Pro Ile Cys Gln Gly Phe Ala Lys
290 295 300

Pro Ile Asn Asp Leu Ser Arg Gly Cys Ser Val Asp Asp Ile Val Lys
305 310 315 320

Val Val Ala Val Thr Ala Val Gln Ala Gln Ala Gln Gly
325 330

<210> 15
<211> 2137
<212> DNA
<213> Streptomyces sp. CL190

<220>
<221> misc-feature
<222> (1)..(2137)
<223> Streptomyces sp. CL190 nphT7 gene sequence

<400> 15

cctgcaggcc gtcgaggcgc cctggaagga ctacgcgagc caggaacggcc ggtcgcgtgga
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ggagtctcgcg ggttcgtctt accaccagcc gttaacggaag atggcctaca aggcgcacgc
120
ccacctgctg aacttcaacg gctacgacac cgaacaaggac gccatcgaag gcgcctcgcg
180
ccagacgacg gcgtacaaca acgtcatcgc caacagctac accgcgtcgc tgtacctggg
240
cctgcgcgcc ctgctcgacc aggcggacga cctgaacggc cgttccatcg gcttcctgag
300
ctacgcgtcg ggcagcgtcg ccgaattctt ctgcggcacg gtctgcgcg ggtaccgcga
360
gctctcgcg accgaggcga accaaggagc gatcgcccg cgaagagcg tcgaactacg
420
cactacccg gactcgacg agtacacgct ccgttcgaac ggcggcgacc accgcacccc
480
ggtgcagacc accgcccctt tcgcgctgac cgggatcaac gaccacaagc gcatctacga
540
ggcgcgctag cgacacccct cggcaacggg gtgcgccact gttcggcgca ccccgctcgc
600
ggcttctgca cagctattca cgaccattg aggggcgggc agccgcataga ccgaacgtcgc
660
atccgcatt atcgttaccg gtgcctacgt accggaacgg atcgtctcca acgatgaagt
720
cgcgcgcgcg gccggggtgg acgaacgact gatcacccgc aagaacggtta tcggcgacgc
780
tcgcctgggc gccgaacgacc aggccacctc ggacctggcc accgcgcgcg ggcgggcagc
840
gctgaagcgc gccggcatca cggcccgaca gctgaacgtg atcgcgcgtcg ccaacctcac
900
gccggaccgc ccgcagccgc ccaacggcgc ctatgttcag caccacctcg gtgcgacgcg
960
cactgcgcgc ttcgaacgtca acgcggtctg ctccggcacc gtgttcgcgc tgtcctcgtg
1020
ggcgggcacc ctctgttacc ggggcggtta cgcgcgtgtc atcgcgcgcg acctgtactc
1080
gcgcatctc aacccgcgcg accgcgaagc ggtcgtgtcg ttcggggacg gcgcctcga
1140
aatgtcttc gggccgaacct cgaacggcac gggccccatc gtccggcgcg tcgcccctga
1200
caaccttcgcg gccctcaacc acccttcacc accctgatccg ggcagccgcg
1260

1320 ggacacggat ggcttcgacg cgggactgca gtaattcgcg atggacgggc gtgaggtgcg
 1380 ccgttcgtc acgagacac tgcgcagct gataaggc ttcttgacg aggcggggt
 1440 cgacggccc gacatcagc acttcgtgc gcatcagcc aacgtgtca tgcctgcagca
 1500 ggtcttcgac gactgcatc tgcgcgggc gaccatgcac cggacggtcg agacctacgg
 1560 caacacggga gcggcctcca tccgatac catggacgcg gccgtgcgcg ccgttcct
 1620 ccggccgggc gactgttc tcttgccgc gttcggcgc ggcattggccg cgaacttcg
 1680 cctgaticgag tggtagtcgc ccgtaccac acagcgttc gccgcacact gttccctgcg
 1740 ccggccgcc ctcgggcct ttaggccca caccgccca gccgacgat tcagtgcgcg
 1800 catcactca gatctccgt ggcagcgcgt ccggagagc ccggcgagga tcgcgggcc
 1860 ccttcgttc gtcgccgcc cctccgcga gcaaccaacc cggcggagc ccgcgtct
 1920 ccgcatagc ccggcgag tgcagcgga gcagccgga ccggagagc ccccccagca
 1980 ccagcaccc gccactcc tgcgcgcga ggcagcgtc cgcgcgtcg acgtcgtga
 2040 gcagcaccc gactcctgc gccccgcgt agaggtcgc cagccggtcg tagcaggtcg
 2100 cgggcggccc cggcgcggt atcacaga tctgtccgc ccgtcgtcg ctgcgccccc
 2137 gacgcgtgac cagcggaatg tcccgccag ctccgga

<210> 16
 <211> 325
 <212> PRT
 <213> streptomyces sp. CL190

<220>
 <221> misc-feature
 <222> (1)..(325)
 <223> Streptomyces sp. CL190 acetyl-coa:malonyl-coa acyltransferase
 <400> 16

1 Arg phe Arg Ile Ile Gly Thr Gly Ala Tyr Val Pro Gln Arg Ile Val
 5
 10
 15

20 Ser Asn Asp Gln Val Gly Ala Pro Ala Gly Val Asp Asp Asp Trp Ile
 25
 30

35 Thr Arg Lys Thr Gly Ile Arg Gln Arg Arg Trp Ala Ala Asp Asp Gln
 40
 45

50 Ala Thr Ser Asp Leu Ala Thr Ala Gly Arg Ala Ala Leu Lys Ala
 55
 60

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

85 Thr Pro Asp Arg Pro Gln Pro Pro Thr Ala Ala Tyr Val Gln His His
 90
 95

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Leu Gly Ala Thr Gly Thr Ala Ala Phe Asp Val Asn Ala Val Cys Ser
 100 105 110

Gly Thr Val Phe Ala Leu Ser Ser Val Ala Gly Thr Leu Val Tyr Arg
 115 120 125

Gly Gly Tyr Ala Leu Val Ile Gly Ala Asp Leu Tyr Ser Arg Ile Leu
 130 135 140

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

Ala Met Val Leu Gly Pro Thr Ser Thr Gly Thr Gly Pro Ile Val Arg
 165 170 175

Arg Val Ala Leu His Thr Phe Gly Gly Leu Thr Asp Leu Ile Arg Val
 180 185 190

Pro Ala Gly Gly Ser Arg Gln Pro Leu Asp Thr Asp Gly Leu Asp Ala
 195 200 205

Gly Leu Gln Tyr Phe Ala Met Asp Gly Arg Glu Val Arg Arg Phe Val
 210 215 220

Thr Glu His Leu Pro Gln Leu Ile Lys Gly Phe Leu His Glu Ala Gly
 225 230 235 240

Val Asp Ala Ala Asp Ile Ser His Phe Val Pro His Gln Ala Asn Gly
 245 250 255

Val Met Leu Asp Glu Val Phe Gly Glu Leu His Leu Pro Arg Ala Thr
 260 265 270

Met His Arg Thr Val Glu Thr Tyr Gly Asn Thr Gly Ala Ala Ser Ile
 275 280 285

Pro Ile Thr Met Asp Ala Ala Val Arg Ala Gly Ser Phe Arg Pro Gly
 290 295 300

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

Ala Leu Ile Glu Trp
 325

<210> 17

<211> 1287

<212> DNA

<213> Pseudomonas mevalonii

<220>

<221> misc_feature
 <222> (1)..(1287)
 <223> Pseudomonas mevaloni HMG-CoA reductase (mvaA) gene sequence

<400> 17

60 atgagcctcg attccgcct gccgccttc cgtaacctgt cccctgcgc gcgcctggac

120 cacatcggcc agttgctcgg cctgagccac gacgatgtca gcttgctggc caacgcctgt

180 gccctggccga tggacatcgc caacggcatg atcgaaaaag tcatcggcac cttcgagctg

240 cctatgcccg tggccagcaa cttccagatc aatggcccgt atgtgctgtg gccgctgtgt

300 gtggaagagc cctgcatcgt cgcgctgtct tcgtacatgg ccaagctggc ccgtgccaac

360 ggcggttca ccactccag cagcgcccgc ctgatgcatg cccaagtaca gatcgtcggc

420 atacaggacc cgtccaatgc acgcctgagc ctgctgcgc gccaaagaga aatcattgaa

480 ctggccaacc gcaaggacca gttgctcaac agcctcggcg gccgctgcgc cgaatcgaa

540 gtgcacacct tcgcgcatc cccgctggc ccgatgtgg tggcgcaact gatcgtcgat

600 gtacgcatg ccatgggcgc caacaccgtc aataccatgg ccgaaggccgt tgcgcgcgtg

660 atggaagcca tcaccggggg ccaagtacgc ctgcgcattc tgtccaacct ggcggaacct

720 cgcctggcca gggcccaggt gccgatattc ccgcagcaac tggaaaacgc cgaattcagt

780 ggcgaaggcag tgatcgaagg catcctcgac gccctcgac tgcctgcggt cgaaccttac

840 cgcgcggcca cccaacaaa gggcatcatg aatggcatcg acccaactgat cgtcggcaact

900 ggcacagcat ggcgtgcatg ggaagccggc gcccatcgt atgcctgcgc cagtgttcac

960 tacgctcgc tgaccacctg ggaaaagac aacaacggcc attgtgcgc caccctggaa

1020 atgcccgatg ccgtaggcct ggtcggcgcc gccaccaaa cccatccgt ggcgcaactg

1080 tcgtcgcga tcctcgcgct gaaaacagcc caggcgcctc ctgagatgc cgtgcccgtc

1140 ggcctggcgc aaaacctcgc ggcctatgcgc gccctggcca ccgaagcat ccagcgcgcg

1200 cacatggccc tgcatgcgc caatatgcc gtgtgtgcgc gcccccgaag cgatgaggtg

1260 gactgggttg cccggcagtt ggtggaatac caggaagtc gccgccgacc cgcgtagca

1287 ctgctgaaac aaaagcgcgc ccaatga

<210> 18

<211> 428

<212> PRT

<213> Pseudomonas mevaloni

<220>

<221> misc_feature

<222> (1)..(428)

<223> Pseudomonas mevaloni hydroxymethylglutaryl-CoA reductase

protein sequence

<400> 18

Met Ser Leu Asp Ser Arg Leu Pro Ala Phe Arg Asn Leu Ser Pro Ala
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 10
 15

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Ala Arg Leu Asp His Ile Gly Gln Leu Leu Gly Leu Ser His Asp Asp
 20 25 30
 Val Ser Leu Leu Ala Asn Ala Gly Ala Leu Pro Met Asp Ile Ala Asn
 35 40 45
 Gly Met Ile Glu Asn Val Ile Gly Thr Phe Glu Leu Pro Tyr Ala Val
 50 55 60
 Ala Ser Asn Phe Gln Ile Asn Gly Arg Asp Val Leu Val Pro Leu Val
 65 70 75 80
 Val Glu Glu Pro Ser Ile Val Ala Ala Ala Ser Tyr Met Ala Lys Leu
 85 90 95
 Ala Arg Ala Asn Gly Gly Phe Thr Thr Ser Ser Ser Ala Pro Leu Met
 100 105 110
 His Ala Gln Val Gln Ile Val Gly Ile Gln Asp Pro Leu Asn Ala Arg
 115 120 125
 Leu Ser Leu Leu Arg Arg Lys Asp Glu Ile Ile Glu Leu Ala Asn Arg
 130 135 140
 Lys Asp Gln Leu Leu Asn Ser Leu Gly Gly Gly Cys Arg Asp Ile Glu
 145 150 155 160
 Val His Thr Phe Ala Asp Thr Pro Arg Gly Pro Met Leu Val Ala His
 165 170 175
 Leu Ile Val Asp Val Arg Asp Ala Met Gly Ala Asn Thr Val Asn Thr
 180 185 190
 Met Ala Glu Ala Val Ala Pro Leu Met Glu Ala Ile Thr Gly Gly Gln
 195 200 205
 Val Arg Leu Arg Ile Leu Ser Asn Leu Ala Asp Leu Arg Leu Ala Arg
 210 215 220
 Ala Gln Val Arg Ile Thr Pro Gln Gln Leu Glu Thr Ala Glu Phe Ser
 225 230 235 240
 Gly Glu Ala Val Ile Glu Gly Ile Leu Asp Ala Tyr Ala Phe Ala Ala
 245 250 255
 Val Asp Pro Tyr Arg Ala Ala Thr His Asn Lys Gly Ile Met Asn Gly
 260 265 270
 Ile Asp Pro Leu Ile Val Ala Thr Gly Asn Asp Trp Arg Ala Val Glu
 275 280 285

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Ala Gly Ala His Ala Tyr Ala Cys Arg Ser Gly His Tyr Gly Ser Leu
 290 295 300

Thr Thr Trp Glu Lys Asp Asn Asn Gly His Leu Val Gly Thr Leu Glu
 305 310 315 320

Met Pro Met Pro Val Gly Leu Val Gly Gly Ala Thr Lys Thr His Pro
 325 330 335

Leu Ala Gln Leu Ser Leu Arg Ile Leu Gly Val Lys Thr Ala Gln Ala
 340 345 350

Leu Ala Glu Ile Ala Val Ala Val Gly Leu Ala Gln Asn Leu Gly Ala
 355 360 365

Met Arg Ala Leu Ala Thr Glu Gly Ile Gln Arg Gly His Met Ala Leu
 370 375 380

His Ala Arg Asn Ile Ala Val Val Ala Gly Ala Arg Gly Asp Glu Val
 385 390 395 400

Asp Trp Val Ala Arg Gln Leu Val Glu Tyr His Asp Val Arg Ala Asp
 405 410 415

Arg Ala Val Ala Leu Leu Lys Gln Lys Arg Gly Gln
 420 425

<210> 19
 <211> 1302
 <212> DNA
 <213> *Silicibacter pomeroyi*

<220>
 <221> misc_feature
 <222> (1)..(1302)
 <223> *Silicibacter pomeroyi* hydroxymethylglutaryl-CoA reductase gene
 sequence

<400> 19
 atgacaggca agacgggtca catcgatggt ttgaactcgc gcattgaaaa gatgcgagat 60
 ctcgaccccc cacaacggct ggtgcgcggt gccgaggcgg cgggcctcga gcccgaggcg 120
 atcagcgcgc tggcgggtaa cggcgccctg cccctctcgc tggccaacgg gatgatcgag 180
 aacgtcatcg gcaaattcga actgccgctg ggcgtggcca cgaatttcac tgtgaacggc 240
 cgcgactatc tgatccccgat ggcggctcga gagccctcgg tggcggcggc cgcgtcctat 300
 atggcgcgta tcgcgcgcga gaatggcgga ttcaccgcgc atggcaccgc gcccttgatg 360
 cgcgcccaga tccaggtggt cgggttgggt gatccccagg gcgcccggca gcgtctcttc 420
 gccacaagg ccgcgttcat ggaggcggcg gacgctgtcg atccggtgct tgtcgggctg 480
 ggtggcggct gccgcgatat cgaggttcac gtgttccggg atacgccggt gggcgcgatg 540
 gtcgtcctgc acctgatcgt cgatgtgcgc gacgcgatgg gggccaatac ggtcaacacg 600

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atggccgaac ggctggcccc cgaggtcgag cggattgccg gtggcaccgt gcggctgcgc      660
atcctgtcga acctcgccga cctgcgattg gtccggggcgc ggggtggaact ggccccggaa      720
acactgacaa cgcaggggcta tgacggcgcc gacgtggcgc ggggcatggt cgaggcctgc      780
gcgcttgcca tcgtcgaccc ctatcgcgcg gcgacccata acaaggggat catgaacggc      840
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gcctatgccg cccgcacggg tcattatacc tcgtgaccc gctgggaact ggcgaatgac      960
gggcggttg tgggcacgat cgaactgccc ctggcgcttg gccttgtcgg cggcgcgacc     1020
aagacgcacc cgaccgcacg ggcggcgctg gccctgatgc aggtagagac tgcaaccgaa     1080
ctggcccagg tcaccggcgc cgtgggtctg gcgcagaaca tggccgcat ccgcgcgctg     1140
gcgaccgaag gcatccagcg cggtcacatg acccttcatg cgcgcaacat cgcgatcatg     1200
gccggcgcaa caggcgccga tatcgaccgc gtcacccggg tcattgtcga agcgggcgac     1260
gtcagcgtgg cccgtgcaaa acaggtgctg gaaaacacct ga                        1302

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<210> 20
 <211> 433
 <212> PRT
 <213> *Silicibacter pomeroyi*

<220>
 <221> misc_feature
 <222> (1)..(433)
 <223> *Silicibacter pomeroyi* hydroxymethylglutaryl-CoA reductase protein
 sequence

<400> 20

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Lys Met Arg Asp Leu Asp Pro Ala Gln Arg Leu Val Arg Val Ala Glu
 20 25 30

Ala Ala Gly Leu Glu Pro Glu Ala Ile Ser Ala Leu Ala Gly Asn Gly
 35 40 45

Ala Leu Pro Leu Ser Leu Ala Asn Gly Met Ile Glu Asn Val Ile Gly
 50 55 60

Lys Phe Glu Leu Pro Leu Gly Val Ala Thr Asn Phe Thr Val Asn Gly
 65 70 75 80

Arg Asp Tyr Leu Ile Pro Met Ala Val Glu Glu Pro Ser Val Val Ala
 85 90 95

Ala Ala Ser Tyr Met Ala Arg Ile Ala Arg Glu Asn Gly Gly Phe Thr
 100 105 110

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Ala His Gly Thr Ala Pro Leu Met Arg Ala Gln Ile Gln Val Val Gly
115 120 125

Leu Gly Asp Pro Glu Gly Ala Arg Gln Arg Leu Leu Ala His Lys Ala
130 135 140

Ala Phe Met Glu Ala Ala Asp Ala Val Asp Pro Val Leu Val Gly Leu
145 150 155 160

Gly Gly Gly Cys Arg Asp Ile Glu Val His Val Phe Arg Asp Thr Pro
165 170 175

Val Gly Ala Met Val Val Leu His Leu Ile Val Asp Val Arg Asp Ala
180 185 190

Met Gly Ala Asn Thr Val Asn Thr Met Ala Glu Arg Leu Ala Pro Glu
195 200 205

Val Glu Arg Ile Ala Gly Gly Thr Val Arg Leu Arg Ile Leu Ser Asn
210 215 220

Leu Ala Asp Leu Arg Leu Val Arg Ala Arg Val Glu Leu Ala Pro Glu
225 230 235 240

Thr Leu Thr Thr Gln Gly Tyr Asp Gly Ala Asp Val Ala Arg Gly Met
245 250 255

Val Glu Ala Cys Ala Leu Ala Ile Val Asp Pro Tyr Arg Ala Ala Thr
260 265 270

His Asn Lys Gly Ile Met Asn Gly Ile Asp Pro Val Val Val Ala Thr
275 280 285

Gly Asn Asp Trp Arg Ala Ile Glu Ala Gly Ala His Ala Tyr Ala Ala
290 295 300

Arg Thr Gly His Tyr Thr Ser Leu Thr Arg Trp Glu Leu Ala Asn Asp
305 310 315 320

Gly Arg Leu Val Gly Thr Ile Glu Leu Pro Leu Ala Leu Gly Leu Val
325 330 335

Gly Gly Ala Thr Lys Thr His Pro Thr Ala Arg Ala Ala Leu Ala Leu
340 345 350

Met Gln Val Glu Thr Ala Thr Glu Leu Ala Gln Val Thr Ala Ala Val
355 360 365

Gly Leu Ala Gln Asn Met Ala Ala Ile Arg Ala Leu Ala Thr Glu Gly
370 375 380

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Ile Gln Arg Gly His Met Thr Leu His Ala Arg Asn Ile Ala Ile Met
385
390
395
400

Ala Gly Ala Thr Gly Ala Asp Ile Asp Arg Val Thr Arg Val Ile Val
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410
415

Glu Ala Gly Asp Val Ser Val Ala Arg Ala Lys Gln Val Leu Gln Asn
420
425
430

Thr

<210> 21
<211> 1290
<212> DNA
<213> Delftia acidovorans

<220>
<221> misc_feature
<222> (1).(1290)
<223> Delftia acidovorans hydroxymethylglutaryl-CoA reductase
nucleotide sequence

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ttcctggcgc atgcctgcgc cctgtccgat gccgaagcgc cctgtctgc
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gccctgcgcc tggcgcctgc cgaagcctgc atcgaagaacg tgttcggcag cttcgagctg
180
ccgctggcgc tggccggcaa cttccgcgtc aacggccgcg acgtgtctgt gcccatggcg
240
gtggaagcgc cctcgttgtt ggccgcgcgc tcgtacatgg ccaagctggc gccgcgaagc
300
gggggcttc agaccctcaag cagctgcgcg ctgattgcgc cccaagttcca ggtgtctggc
360
gtgaaccgat cacacggcgc gcgcctggcc gtgtctgcag cgcgtgcgca gatcatcgag
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cgcgcccaaa ggtgtgtgat ggcttggcgc gcggtctgcaa ggaatcgag
480
gtccatgtct tccccgaac gccgcgcgcg cccatgtgg tggttccaac gatcgtggac
540
gtgcgcgcgc ccatggcgc caacaccgtc aacaccatgg ccgaatcgtt ggccgccctc
600
gtcgaagaag tcaagggcgc cagcgttcgc ctcgcgcattc tgtccaacct ggccgaacctg
660
cgcctggccc gccgcctcgt gcgctcgcgc ccgcaagacc tggccaacga ggaatcgagc
720
ggcgaagaga tcatcgaagc cgtgttgac gcttatact tcgcgcgcct cgaacccctac
780
cgcgcgcgcca cgcacaacaa gggaatcatg aacggcattc acccgcgtcat cgtggccaag
840
ggcaacgaat ggccgcgcgt cgaagccgcg gcccatgtct atgcgaagcgc cagcggcagc
900
taacacctgc tgaagcgcgt ggaaaaagat gccggcgcgc cctgtgtcgc cagcatcgag
960
ctgcccctgc cgttggcctc tgtcgcgcgc gccacaaga cccatcgcct ggcaagcctg
1020
gcgtgaaga tcatggacct gcagtccgc cagcagctgg gcgaagatgc cgcgcgcgtg
1080
ggccttggcgc agaaccttgg gcgcctgcgc gcccttggcca ccgaagycat tcagcgcgcg
1140
cacatggccc tgcacgcgcc caacatcgcc ctgttggcgc gcgcccaagc cgaagaggtc
1200

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gatgccgtgg cgcgccagct ggccgcccag cacgacgtgc gcaccgaccg cgcgctggaa 1260
gtgctggccg cgctgcgcgc cagggcctga 1290

<210> 22
<211> 429
<212> PRT
<213> Delftia acidovorans

<220>
<221> misc_feature
<222> (1)..(429)
<223> Delftia acidovorans hydroxymethylglutaryl-CoA reductase protein
sequence

<400> 22

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Gln Arg Arg Asp Phe Leu Ala Asp Ala Cys Gly Leu Ser Asp Ala Glu
20 25 30

Arg Ala Leu Leu Ala Ala Pro Gly Ala Leu Pro Leu Ala Leu Ala Asp
35 40 45

Gly Met Ile Glu Asn Val Phe Gly Ser Phe Glu Leu Pro Leu Gly Val
50 55 60

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

Val Glu Glu Pro Ser Val Val Ala Ala Ala Ser Tyr Met Ala Lys Leu
85 90 95

Ala Arg Glu Asp Gly Gly Phe Gln Thr Ser Ser Thr Leu Pro Leu Met
100 105 110

Arg Ala Gln Val Gln Val Leu Gly Val Thr Asp Pro His Gly Ala Arg
115 120 125

Leu Ala Val Leu Gln Ala Arg Ala Gln Ile Ile Glu Arg Ala Asn Ser
130 135 140

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

Val His Val Phe Pro Asp Thr Pro Arg Gly Pro Met Leu Val Val His
165 170 175

Leu Ile Val Asp Val Arg Asp Ala Met Gly Ala Asn Thr Val Asn Thr
180 185 190

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Met Ala Glu Ser Val Ala Pro Leu Val Glu Lys Ile Thr Gly Gly Ser
195 200 205

Val Arg Leu Arg Ile Leu Ser Asn Leu Ala Asp Leu Arg Leu Ala Arg
210 215 220

Ala Arg Val Arg Leu Thr Pro Gln Thr Leu Ala Thr Gln Asp Arg Ser
225 230 235 240

Gly Glu Glu Ile Ile Glu Gly Val Leu Asp Ala Tyr Thr Phe Ala Ala
245 250 255

Ile Asp Pro Tyr Arg Ala Ala Thr His Asn Lys Gly Ile Met Asn Gly
260 265 270

Ile Asp Pro Val Ile Val Ala Thr Gly Asn Asp Trp Arg Ala Val Glu
275 280 285

Ala Gly Ala His Ala Tyr Ala Ser Arg Ser Gly Ser Tyr Thr Ser Leu
290 295 300

Thr Arg Trp Glu Lys Asp Ala Gly Gly Ala Leu Val Gly Ser Ile Glu
305 310 315 320

Leu Pro Met Pro Val Gly Leu Val Gly Gly Ala Thr Lys Thr His Pro
325 330 335

Leu Ala Arg Leu Ala Leu Lys Ile Met Asp Leu Gln Ser Ala Gln Gln
340 345 350

Leu Gly Glu Ile Ala Ala Ala Val Gly Leu Ala Gln Asn Leu Gly Ala
355 360 365

Leu Arg Ala Leu Ala Thr Glu Gly Ile Gln Arg Gly His Met Ala Leu
370 375 380

His Ala Arg Asn Ile Ala Leu Val Ala Gly Ala Thr Gly Asp Glu Val
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<210> 44
 <211> 2738
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct: Kan A-ADH1 disruption construct

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 1260 gagtgttcc tgaacatgg caaagttagc gtggccaatg atgttacaga tgagatgtc
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<210> 45

<211> 3059

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct: t2235 integration construct

<400> 45

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 3059

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 <211> 8106
 <212> DNA
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<220>
 <223> Synthetic construct: 174804 integration construct

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2160

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<212> DNA

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<223> Synthetic construct: i73830 integration construct

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