

SEQUENCE LISTING

<110> The Regents of the University of California
 Keasling, Jay D.
 d'Espaux, Leo
 Wong, Jeff
 Luo, Xiaozhou
 Reiter, Michael
 Denby, Charles
 Lechner, Anna

<120> MICROORGANISMS AND METHODS FOR PRODUCING CANNABINOID AND CANNABINOID DERIVATIVES

<130> DMT-001/00WO 326934-2003

<150> US 62/569,532
 <151> 2017-10-07

<150> US 62/491,114
 <151> 2017-04-27

<160> 225

<170> PatentIn version 3.5

<210> 1
 <211> 776
 <212> PRT
 <213> Cannabis sativa

<400> 1

Met	Ala	Leu	Glu	Leu	Pro	His	Leu	Leu	Pro	Tyr	Lys	Leu	Val	Lys	Gly
1				5					10					15	

Gln	Thr	Leu	Val	Ala	Gln	Ala	Ala	Arg	Ala	Glu	Leu	Ala	Ser	Ser	Ser
			20					25					30		

Ser	Ser	Ser	Val	Ile	Leu	Lys	Ser	Asn	Phe	Ile	Asn	Asn	Asn	Tyr	Ile
		35					40					45			

Asn	Tyr	Cys	Asn	Asn	Asn	Asn	Asn	Asn	Glu	Arg	Arg	Leu	Val	Val	Arg
	50					55					60				

Arg	Asp	Trp	Glu	Thr	Met	Ala	Ser	Ser	Pro	Ser	His	Ser	Arg	Asn	Asn
65					70					75				80	

Asn	Asp	Ile	Arg	Thr	Ile	Asn	His	Leu	Arg	His	Val	Asp	Ser	Met	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85

90

95

Thr Met Pro Ser Gly Ala Gly Lys Ile Pro Arg Leu Asn Ala Val Ile
 100 105 110

Leu Gly Glu Ala Leu Ala Thr Glu Glu Asn Asp Leu Val Phe Pro Thr
 115 120 125

Asp Glu Phe Ser Gln Gln Ala His Val Pro Ser Pro Gln Lys Tyr Leu
 130 135 140

Glu Met Tyr Lys Arg Ser Ile Glu Asp Pro Ala Gly Phe Trp Ser Glu
 145 150 155 160

Ile Ala Ser Gln Phe Tyr Trp Lys Gln Lys Trp Asp Asp Ser Val Tyr
 165 170 175

Ser Glu Asn Leu Asp Val Ser Lys Gly Arg Val Asn Ile Glu Trp Phe
 180 185 190

Lys Gly Gly Ile Thr Asn Ile Cys Tyr Asn Cys Leu Asp Lys Asn Val
 195 200 205

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

Thr Gly Phe Asp Asp Ser Leu Thr Tyr Ser Gln Leu Leu His Lys Val
 225 230 235 240

Cys Gln Leu Ala Asn Tyr Leu Lys Asp Met Gly Val Gln Lys Gly Asp
 245 250 255

Ala Val Val Ile Tyr Leu Pro Met Leu Leu Glu Leu Pro Ile Thr Met
 260 265 270

Leu Ala Cys Ala Arg Ile Gly Ala Val His Ser Val Val Phe Ala Gly
 275 280 285

Phe Ser Ala Glu Ser Leu Ser Gln Arg Ile Ile Asp Cys Lys Pro Lys
 290 295 300

Val Val Ile Thr Cys Asn Ala Val Lys Arg Gly Pro Lys Ile Ile His
305 310 315 320

Leu Lys Asp Ile Val Asp Ala Ala Leu Val Glu Ser Ala Lys Thr Gly
325 330 335

Val Pro Ile Asp Thr Cys Leu Val Tyr Glu Asn Gln Leu Ala Met Lys
340 345 350

Arg Asp Ile Thr Lys Trp Gln Asp Gly Arg Asp Ile Trp Trp Gln Asp
355 360 365

Val Ile Pro Lys Tyr Pro Thr Glu Cys Ala Val Glu Trp Val Asp Ala
370 375 380

Glu Asp Pro Leu Phe Leu Leu Tyr Thr Ser Gly Ser Thr Gly Lys Pro
385 390 395 400

Lys Gly Val Leu His Thr Thr Gly Gly Tyr Met Val Tyr Thr Ala Thr
405 410 415

Thr Phe Lys Tyr Ala Phe Asp Tyr Lys Pro Ser Asp Val Tyr Trp Cys
420 425 430

Thr Ala Asp Cys Gly Trp Ile Thr Gly His Ser Tyr Val Thr Tyr Gly
435 440 445

Pro Leu Leu Asn Gly Ala Ser Cys Ile Val Phe Glu Gly Ala Pro Asn
450 455 460

Tyr Pro Asp Ser Gly Arg Cys Trp Asp Ile Val Asp Lys Tyr Lys Val
465 470 475 480

Thr Ile Phe Tyr Thr Ala Pro Thr Leu Val Arg Ser Leu Met Arg Asp
485 490 495

Gly Asp Glu Tyr Val Thr Arg Tyr Ser Arg Lys Ser Leu Arg Ile Leu
500 505 510

Gly Ser Val Gly Glu Pro Ile Asn Pro Ser Ala Trp Arg Trp Phe Tyr

515

520

525

Asn Val Val Gly Asp Ser Arg Cys Pro Ile Ser Asp Thr Trp Trp Gln
 530 535 540

Thr Glu Thr Gly Gly Phe Met Ile Thr Pro Leu Pro Gly Ala Trp Pro
 545 550 555 560

Gln Lys Pro Gly Ser Ala Thr Phe Pro Phe Phe Gly Val Lys Pro Val
 565 570 575

Ile Val Asp Glu Lys Gly Val Glu Ile Glu Gly Glu Cys Ser Gly Tyr
 580 585 590

Leu Cys Val Lys Gly Ser Trp Pro Gly Ala Phe Arg Thr Leu Tyr Gly
 595 600 605

Asp Tyr Glu Arg Tyr Glu Thr Thr Tyr Phe Lys Pro Phe Thr Gly Tyr
 610 615 620

Tyr Phe Thr Gly Asp Gly Cys Ser Arg Asp Lys Asp Gly Tyr His Trp
 625 630 635 640

Leu Thr Gly Arg Val Asp Asp Val Ile Asn Val Ser Gly His Arg Ile
 645 650 655

Gly Thr Ala Glu Val Glu Ser Ala Leu Val Ser His Pro Lys Cys Ala
 660 665 670

Glu Ala Ala Val Val Gly Ile Glu His Glu Val Lys Gly Gln Ala Ile
 675 680 685

Tyr Ala Phe Val Thr Leu Val Glu Gly Glu Pro Tyr Ser Glu Glu Leu
 690 695 700

Arg Lys Ser Leu Ile Leu Ser Val Arg Lys Gln Ile Gly Ala Phe Ala
 705 710 715 720

Ala Pro Glu Arg Ile His Trp Ala Pro Gly Leu Pro Lys Thr Arg Ser
 725 730 735

Gly Lys Ile Met Arg Arg Ile Leu Arg Lys Ile Ala Ser Gly Gln Leu
740 745 750

Asp Glu Leu Gly Asp Thr Ser Thr Leu Ala Asp Pro Asn Val Val Glu
755 760 765

Gln Leu Ile Ser Leu Ser Asn Cys
770 775

<210> 2
<211> 579
<212> PRT
<213> Streptomyces sp.

<400> 2

Met Glu Leu Ala Leu Pro Ala Glu Leu Ala Pro Thr Leu Pro Glu Ala
1 5 10 15

Leu Arg Leu Arg Ser Glu Gln Gln Pro Asp Thr Val Ala Tyr Val Phe
20 25 30

Leu Arg Asp Gly Glu Thr Pro Glu Glu Thr Leu Thr Tyr Gly Arg Leu
35 40 45

Asp Arg Ala Ala Arg Ala Arg Ala Ala Ala Leu Glu Ala Ala Gly Leu
50 55 60

Ala Gly Gly Thr Ala Val Leu Leu Tyr Pro Ser Gly Leu Glu Phe Val
65 70 75 80

Ala Ala Leu Leu Gly Cys Met Tyr Ala Gly Thr Ala Gly Ala Pro Val
85 90 95

Gln Val Pro Thr Arg Arg Arg Gly Met Glu Arg Ala Arg Arg Ile Ala
100 105 110

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

Glu Val Glu Glu His Phe Ala Asp Leu Leu Thr Gly Leu Thr Val Ile
130 135 140

Asp Thr Glu Ser Leu Pro Asp Val Pro Asp Asp Ala Pro Ala Val Arg
145 150 155 160

Leu Pro Gly Pro Asp Asp Val Ala Leu Leu Gln Tyr Thr Ser Gly Ser
165 170 175

Thr Gly Asp Pro Lys Gly Val Glu Val Thr His Ala Asn Phe Arg Ala
180 185 190

Asn Val Ala Glu Thr Val Glu Leu Trp Pro Val Arg Ser Asp Gly Thr
195 200 205

Val Val Asn Trp Leu Pro Leu Phe His Asp Met Gly Leu Met Phe Gly
210 215 220

Val Val Met Pro Leu Phe Thr Gly Val Pro Ala Tyr Leu Met Ala Pro
225 230 235 240

Gln Ser Phe Ile Arg Arg Pro Ala Arg Trp Leu Glu Ala Ile Ser Arg
245 250 255

Phe Arg Gly Thr His Ala Ala Ala Pro Ser Phe Ala Tyr Glu Leu Cys
260 265 270

Val Arg Ser Val Ala Asp Thr Gly Leu Pro Ala Gly Leu Asp Leu Ser
275 280 285

Ser Trp Arg Val Ala Val Asn Gly Ala Glu Pro Val Arg Trp Thr Ala
290 295 300

Val Ala Asp Phe Thr Glu Ala Tyr Ala Pro Ala Gly Phe Arg Pro Gln
305 310 315 320

Ala Met Cys Pro Gly Tyr Gly Leu Ala Glu Asn Thr Leu Lys Leu Ser
325 330 335

Gly Ser Pro Glu Asp Arg Pro Pro Thr Leu Leu Arg Ala Asp Ala Ala
340 345 350

Ala Leu Gln Asp Gly Arg Val Val Pro Leu Thr Gly Pro Gly Thr Asp
355 360 365

Gly Val Arg Leu Val Gly Ser Gly Val Thr Val Pro Ser Ser Arg Val
370 375 380

Ala Val Val Asp Pro Gly Thr Gly Thr Glu Gln Pro Ala Gly Arg Val
385 390 395 400

Gly Glu Ile Trp Ile Asn Gly Pro Cys Val Ala Arg Gly Tyr His Gly
405 410 415

Arg Pro Ala Glu Ser Ala Glu Ser Phe Gly Ala Arg Ile Ala Gly Gln
420 425 430

Glu Ala Arg Gly Thr Trp Leu Arg Thr Gly Asp Leu Gly Phe Leu His
435 440 445

Asp Gly Glu Val Phe Val Ala Gly Arg Leu Lys Asp Val Val Ile His
450 455 460

Gln Gly Arg Asn Phe Tyr Pro Gln Asp Ile Glu Leu Ser Ala Glu Val
465 470 475 480

Ser Asp Arg Ala Leu His Pro Asn Cys Ala Ala Ala Phe Ala Leu Asp
485 490 495

Asp Gly Arg Thr Glu Arg Leu Val Leu Leu Val Glu Ala Asp Gly Arg
500 505 510

Ala Leu Arg Asn Gly Gly Ala Asp Ala Leu Arg Ala Arg Val His Asp
515 520 525

Ala Val Trp Asp Arg Gln Arg Leu Arg Ile Asp Glu Ile Val Leu Leu
530 535 540

Arg Arg Gly Ala Leu Pro Lys Thr Ser Ser Gly Lys Val Gln Arg Arg
545 550 555 560

Leu Ala Arg Ser Arg Tyr Leu Asp Gly Glu Phe Gly Pro Ala Pro Ala
565 570 575

Arg Glu Ala

<210> 3

<211> 1671

<212> PRT

<213> Aspergillus sp.

<400> 3

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

Ala Ser Ser Leu Asp Ala Lys Lys Leu Cys Tyr Glu Tyr Asp Glu Arg
20 25 30

Gln Ala Pro Gly Val Thr Gln Ile Thr Glu Glu Ala Pro Thr Glu Gln
35 40 45

Pro Pro Leu Ser Thr Pro Pro Ser Leu Pro Gln Thr Pro Asn Ile Ser
50 55 60

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

Val Gln Ile Val Gln Ala Leu Val Ala Arg Lys Leu Lys Thr Ala Ile
85 90 95

Ala Gln Leu Pro Thr Ser Lys Ser Ile Lys Glu Leu Ser Gly Gly Arg
100 105 110

Ser Ser Leu Gln Asn Glu Leu Val Gly Asp Ile His Asn Glu Phe Ser
115 120 125

Ser Ile Pro Asp Ala Pro Glu Gln Ile Leu Leu Arg Asp Phe Gly Asp
130 135 140

Ala Asn Pro Thr Val Gln Leu Gly Lys Thr Ser Ser Ala Ala Val Ala
145 150 155 160

Lys Leu Ile Ser Ser Lys Met Pro Ser Asp Phe Asn Ala Asn Ala Ile

165

170

175

Arg Ala His Leu Ala Asn Lys Trp Gly Leu Gly Pro Leu Arg Gln Thr
 180 185 190

Ala Val Leu Leu Tyr Ala Ile Ala Ser Glu Pro Pro Ser Arg Leu Ala
 195 200 205

Ser Ser Ser Ala Ala Glu Glu Tyr Trp Asp Asn Val Ser Ser Met Tyr
 210 215 220

Ala Glu Ser Cys Gly Ile Thr Leu Arg Pro Arg Gln Asp Thr Met Asn
 225 230 235 240

Glu Asp Ala Met Ala Ser Ser Ala Ile Asp Pro Ala Val Val Ala Glu
 245 250 255

Phe Ser Lys Gly His Arg Arg Leu Gly Val Gln Gln Phe Gln Ala Leu
 260 265 270

Ala Glu Tyr Leu Gln Ile Asp Leu Ser Gly Ser Gln Ala Ser Gln Ser
 275 280 285

Asp Ala Leu Val Ala Glu Leu Gln Gln Lys Val Asp Leu Trp Thr Ala
 290 295 300

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

Lys Lys Ser Arg Arg Tyr Gly Ser Trp Trp Asn Met Ala Arg Gln Asp
 325 330 335

Val Leu Ala Phe Tyr Arg Arg Pro Ser Tyr Ser Glu Phe Val Asp Asp
 340 345 350

Ala Leu Ala Phe Lys Val Phe Leu Asn Arg Leu Cys Asn Arg Ala Asp
 355 360 365

Glu Ala Leu Leu Asn Met Val Arg Ser Leu Ser Cys Asp Ala Tyr Phe
 370 375 380

Lys Gln Gly Ser Leu Pro Gly Tyr His Ala Ala Ser Arg Leu Leu Glu
385 390 395 400

Gln Ala Ile Thr Ser Thr Val Ala Asp Cys Pro Lys Ala Arg Leu Ile
405 410 415

Leu Pro Ala Val Gly Pro His Thr Thr Ile Thr Lys Asp Gly Thr Ile
420 425 430

Glu Tyr Ala Glu Ala Pro Arg Gln Gly Val Ser Gly Pro Thr Ala Tyr
435 440 445

Ile Gln Ser Leu Arg Gln Gly Ala Ser Phe Ile Gly Leu Lys Ser Ala
450 455 460

Asp Val Asp Thr Gln Ser Asn Leu Thr Asp Ala Leu Leu Asp Ala Met
465 470 475 480

Cys Leu Ala Leu His Asn Gly Ile Ser Phe Val Gly Lys Thr Phe Leu
485 490 495

Val Thr Gly Ala Gly Gln Gly Ser Ile Gly Ala Gly Val Val Arg Leu
500 505 510

Leu Leu Glu Gly Gly Ala Arg Val Leu Val Thr Thr Ser Arg Glu Pro
515 520 525

Ala Thr Thr Ser Arg Tyr Phe Gln Gln Met Tyr Asp Asn His Gly Ala
530 535 540

Lys Phe Ser Glu Leu Arg Val Val Pro Cys Asn Leu Ala Ser Ala Gln
545 550 555 560

Asp Cys Glu Gly Leu Ile Arg His Val Tyr Asp Pro Arg Gly Leu Asn
565 570 575

Trp Asp Leu Asp Ala Ile Leu Pro Phe Ala Ala Ala Ser Asp Tyr Ser
580 585 590

Thr Glu Met His Asp Ile Arg Gly Gln Ser Glu Leu Gly His Arg Leu

595

600

605

Met Leu Val Asn Val Phe Arg Val Leu Gly His Ile Val His Cys Lys
 610 615 620

Arg Asp Ala Gly Val Asp Cys His Pro Thr Gln Val Leu Leu Pro Leu
 625 630 635 640

Ser Pro Asn His Gly Ile Phe Gly Gly Asp Gly Met Tyr Pro Glu Ser
 645 650 655

Lys Leu Ala Leu Glu Ser Leu Phe His Arg Ile Arg Ser Glu Ser Trp
 660 665 670

Ser Asp Gln Leu Ser Ile Cys Gly Val Arg Ile Gly Trp Thr Arg Ser
 675 680 685

Thr Gly Leu Met Thr Ala His Asp Ile Ile Ala Glu Thr Val Glu Glu
 690 695 700

His Gly Ile Arg Thr Phe Ser Val Ala Glu Met Ala Leu Asn Ile Ala
 705 710 715 720

Met Leu Leu Thr Pro Asp Phe Val Ala His Cys Glu Asp Gly Pro Leu
 725 730 735

Asp Ala Asp Phe Thr Gly Ser Leu Gly Thr Leu Gly Ser Ile Pro Gly
 740 745 750

Phe Leu Ala Gln Leu His Gln Lys Val Gln Leu Ala Ala Glu Val Ile
 755 760 765

Arg Ala Val Gln Ala Glu Asp Glu His Glu Arg Phe Leu Ser Pro Gly
 770 775 780

Thr Lys Pro Thr Leu Gln Ala Pro Val Ala Pro Met His Pro Arg Ser
 785 790 795 800

Ser Leu Arg Val Gly Tyr Pro Arg Leu Pro Asp Tyr Glu Gln Glu Ile
 805 810 815

Arg Pro Leu Ser Pro Arg Leu Glu Arg Leu Gln Asp Pro Ala Asn Ala
820 825 830

Val Val Val Val Gly Tyr Ser Glu Leu Gly Pro Trp Gly Ser Ala Arg
835 840 845

Leu Arg Trp Glu Ile Glu Ser Gln Gly Gln Trp Thr Ser Ala Gly Tyr
850 855 860

Val Glu Leu Ala Trp Leu Met Asn Leu Ile Arg His Val Asn Asp Glu
865 870 875 880

Ser Tyr Val Gly Trp Val Asp Thr Gln Thr Gly Lys Pro Val Arg Asp
885 890 895

Gly Glu Ile Gln Ala Leu Tyr Gly Asp His Ile Asp Asn His Thr Gly
900 905 910

Ile Arg Pro Ile Gln Ser Thr Ser Tyr Asn Pro Glu Arg Met Glu Val
915 920 925

Leu Gln Glu Val Ala Val Glu Glu Asp Leu Pro Glu Phe Glu Val Ser
930 935 940

Gln Leu Thr Ala Asp Ala Met Arg Leu Arg His Gly Ala Asn Val Ser
945 950 955 960

Ile Arg Pro Ser Gly Asn Pro Asp Ala Cys His Val Lys Leu Lys Arg
965 970 975

Gly Ala Val Ile Leu Val Pro Lys Thr Val Pro Phe Val Trp Gly Ser
980 985 990

Cys Ala Gly Glu Leu Pro Lys Gly Trp Thr Pro Ala Lys Tyr Gly Ile
995 1000 1005

Pro Glu Asn Leu Ile His Gln Val Asp Pro Val Thr Leu Tyr Thr
1010 1015 1020

Ile Cys Cys Val Ala Glu Ala Phe Tyr Ser Ala Gly Ile Thr His

1025						1030						1035			
Pro	Leu	Glu	Val	Phe	Arg	His	Ile	His	Leu	Ser	Glu	Leu	Gly	Asn	
1040						1045					1050				
Phe	Ile	Gly	Ser	Ser	Met	Gly	Gly	Pro	Thr	Lys	Thr	Arg	Gln	Leu	
1055						1060					1065				
Tyr	Arg	Asp	Val	Tyr	Phe	Asp	His	Glu	Ile	Pro	Ser	Asp	Val	Leu	
1070						1075					1080				
Gln	Asp	Thr	Tyr	Leu	Asn	Thr	Pro	Ala	Ala	Trp	Val	Asn	Met	Leu	
1085						1090					1095				
Leu	Leu	Gly	Cys	Thr	Gly	Pro	Ile	Lys	Thr	Pro	Val	Gly	Ala	Cys	
1100						1105					1110				
Ala	Thr	Gly	Val	Glu	Ser	Ile	Asp	Ser	Gly	Tyr	Glu	Ser	Ile	Met	
1115						1120					1125				
Ala	Gly	Lys	Thr	Lys	Met	Cys	Leu	Val	Gly	Gly	Tyr	Asp	Asp	Leu	
1130						1135					1140				
Gln	Glu	Glu	Ala	Ser	Tyr	Gly	Phe	Ala	Gln	Leu	Lys	Ala	Thr	Val	
1145						1150					1155				
Asn	Val	Glu	Glu	Glu	Ile	Ala	Cys	Gly	Arg	Gln	Pro	Ser	Glu	Met	
1160						1165					1170				
Ser	Arg	Pro	Met	Ala	Glu	Ser	Arg	Ala	Gly	Phe	Val	Glu	Ala	His	
1175						1180					1185				
Gly	Cys	Gly	Val	Gln	Leu	Leu	Cys	Arg	Gly	Asp	Ile	Ala	Leu	Gln	
1190						1195					1200				
Met	Gly	Leu	Pro	Ile	Tyr	Ala	Val	Ile	Ala	Ser	Ser	Ala	Met	Ala	
1205						1210					1215				
Ala	Asp	Lys	Ile	Gly	Ser	Ser	Val	Pro	Ala	Pro	Gly	Gln	Gly	Ile	
1220						1225					1230				

Leu Ser Phe Ser Arg Glu Arg Ala Arg Ser Ser Met Ile Ser Val
1235 1240 1245

Thr Ser Arg Pro Ser Ser Arg Ser Ser Thr Ser Ser Glu Val Ser
1250 1255 1260

Asp Lys Ser Ser Leu Thr Ser Ile Thr Ser Ile Ser Asn Pro Ala
1265 1270 1275

Pro Arg Ala Gln Arg Ala Arg Ser Thr Thr Asp Met Ala Pro Leu
1280 1285 1290

Arg Ala Ala Leu Ala Thr Trp Gly Leu Thr Ile Asp Asp Leu Asp
1295 1300 1305

Val Ala Ser Leu His Gly Thr Ser Thr Arg Gly Asn Asp Leu Asn
1310 1315 1320

Glu Pro Glu Val Ile Glu Thr Gln Met Arg His Leu Gly Arg Thr
1325 1330 1335

Pro Gly Arg Pro Leu Trp Ala Ile Cys Gln Lys Ser Val Thr Gly
1340 1345 1350

His Pro Lys Ala Pro Ala Ala Ala Trp Met Leu Asn Gly Cys Leu
1355 1360 1365

Gln Val Leu Asp Ser Gly Leu Val Pro Gly Asn Arg Asn Leu Asp
1370 1375 1380

Thr Leu Asp Glu Ala Leu Arg Ser Ala Ser His Leu Cys Phe Pro
1385 1390 1395

Thr Arg Thr Val Gln Leu Arg Glu Val Lys Ala Phe Leu Leu Thr
1400 1405 1410

Ser Phe Gly Phe Gly Gln Lys Gly Gly Gln Val Val Gly Val Ala
1415 1420 1425

Pro Lys Tyr Phe Phe Ala Thr Leu Pro Arg Pro Glu Val Glu Gly

1430						1435						1440			
Tyr	Tyr	Arg	Lys	Val	Arg	Val	Arg	Thr	Glu	Ala	Gly	Asp	Arg	Ala	
1445						1450					1455				
Tyr	Ala	Ala	Ala	Val	Met	Ser	Gln	Ala	Val	Val	Lys	Ile	Gln	Thr	
1460						1465					1470				
Gln	Asn	Pro	Tyr	Asp	Glu	Pro	Asp	Ala	Pro	Arg	Ile	Phe	Leu	Asp	
1475						1480					1485				
Pro	Leu	Ala	Arg	Ile	Ser	Gln	Asp	Pro	Ser	Thr	Gly	Gln	Tyr	Arg	
1490						1495					1500				
Phe	Arg	Ser	Asp	Ala	Thr	Pro	Ala	Leu	Asp	Asp	Asp	Ala	Leu	Pro	
1505						1510					1515				
Pro	Pro	Gly	Glu	Pro	Thr	Glu	Leu	Val	Lys	Gly	Ile	Ser	Ser	Ala	
1520						1525					1530				
Trp	Ile	Glu	Glu	Lys	Val	Arg	Pro	His	Met	Ser	Pro	Gly	Gly	Thr	
1535						1540					1545				
Val	Gly	Val	Asp	Leu	Val	Pro	Leu	Ala	Ser	Phe	Asp	Ala	Tyr	Lys	
1550						1555					1560				
Asn	Ala	Ile	Phe	Val	Glu	Arg	Asn	Tyr	Thr	Val	Arg	Glu	Arg	Asp	
1565						1570					1575				
Trp	Ala	Glu	Lys	Ser	Ala	Asp	Val	Arg	Ala	Ala	Tyr	Ala	Ser	Arg	
1580						1585					1590				
Trp	Cys	Ala	Lys	Glu	Ala	Val	Phe	Lys	Cys	Leu	Gln	Thr	His	Ser	
1595						1600					1605				
Gln	Gly	Ala	Gly	Ala	Ala	Met	Lys	Glu	Ile	Glu	Ile	Glu	His	Gly	
1610						1615					1620				
Gly	Asn	Gly	Ala	Pro	Lys	Val	Lys	Leu	Arg	Gly	Ala	Ala	Gln	Thr	
1625						1630					1635				

Ala Ala Arg Gln Arg Gly Leu Glu Gly Val Gln Leu Ser Ile Ser
1640 1645 1650

Tyr Gly Asp Asp Ala Val Ile Ala Val Ala Leu Gly Leu Met Ser
1655 1660 1665

Gly Ala Ser
1670

<210> 4
<211> 1888
<212> PRT
<213> Aspergillus sp.

<400> 4

Met Gly Ser Val Ser Arg Glu His Glu Ser Ile Pro Ile Gln Ala Ala
1 5 10 15

Gln Arg Gly Ala Ala Arg Ile Cys Ala Ala Phe Gly Gly Gln Gly Ser
20 25 30

Asn Asn Leu Asp Val Leu Lys Gly Leu Leu Glu Leu Tyr Lys Arg Tyr
35 40 45

Gly Pro Asp Leu Asp Glu Leu Leu Asp Val Ala Ser Asn Thr Leu Ser
50 55 60

Gln Leu Ala Ser Ser Pro Ala Ala Ile Asp Val His Glu Pro Trp Gly
65 70 75 80

Phe Asp Leu Arg Gln Trp Leu Thr Thr Pro Glu Val Ala Pro Ser Lys
85 90 95

Glu Ile Leu Ala Leu Pro Pro Arg Ser Phe Pro Leu Asn Thr Leu Leu
100 105 110

Ser Leu Ala Leu Tyr Cys Ala Thr Cys Arg Glu Leu Glu Leu Asp Pro
115 120 125

Gly Gln Phe Arg Ser Leu Leu His Ser Ser Thr Gly His Ser Gln Gly
130 135 140

Ile Leu Ala Ala Val Ala Ile Thr Gln Ala Glu Ser Trp Pro Thr Phe
145 150 155 160

Tyr Asp Ala Cys Arg Thr Val Leu Gln Ile Ser Phe Trp Ile Gly Leu
165 170 175

Glu Ala Tyr Leu Phe Thr Pro Ser Ser Ala Ala Ser Asp Ala Met Ile
180 185 190

Gln Asp Cys Ile Glu His Gly Glu Gly Leu Leu Ser Ser Met Leu Ser
195 200 205

Val Ser Gly Leu Ser Arg Ser Gln Val Glu Arg Val Ile Glu His Val
210 215 220

Asn Lys Gly Leu Gly Glu Cys Asn Arg Trp Val His Leu Ala Leu Val
225 230 235 240

Asn Ser His Glu Lys Phe Val Leu Ala Gly Pro Pro Gln Ser Leu Trp
245 250 255

Ala Val Cys Leu His Val Arg Arg Ile Arg Ala Asp Asn Asp Leu Asp
260 265 270

Gln Ser Arg Ile Leu Phe Arg Asn Arg Lys Pro Ile Val Asp Ile Leu
275 280 285

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

Gln Asp Arg Val Ile Glu Ala Leu Ser Ser Ala Ser Leu Ala Leu His
305 310 315 320

Ser Ile Lys Ile Pro Leu Tyr His Thr Gly Thr Gly Ser Asn Leu Gln
325 330 335

Glu Leu Gln Pro His Gln Leu Ile Pro Thr Leu Ile Arg Ala Ile Thr
340 345 350

Val Asp Gln Leu Asp Trp Pro Leu Val Cys Arg Gly Leu Asn Ala Thr
355 360 365

His Val Leu Asp Phe Gly Pro Gly Gln Thr Cys Ser Leu Ile Gln Glu
370 375 380

Leu Thr Gln Gly Thr Gly Val Ser Val Ile Gln Leu Thr Thr Gln Ser
385 390 395 400

Gly Pro Lys Pro Val Gly Gly His Leu Ala Ala Val Asn Trp Glu Ala
405 410 415

Glu Phe Gly Leu Arg Leu His Ala Asn Val His Gly Ala Ala Lys Leu
420 425 430

His Asn Arg Met Thr Thr Leu Leu Gly Lys Pro Pro Val Met Val Ala
435 440 445

Gly Met Thr Pro Thr Thr Val Arg Trp Asp Phe Val Ala Ala Val Ala
450 455 460

Gln Ala Gly Tyr His Val Glu Leu Ala Gly Gly Gly Tyr His Ala Glu
465 470 475 480

Arg Gln Phe Glu Ala Glu Ile Arg Arg Leu Ala Thr Ala Ile Pro Ala
485 490 495

Asp His Gly Ile Thr Cys Asn Leu Leu Tyr Ala Lys Pro Thr Thr Phe
500 505 510

Ser Trp Gln Ile Ser Val Ile Lys Asp Leu Val Arg Gln Gly Val Pro
515 520 525

Val Glu Gly Ile Thr Ile Gly Ala Gly Ile Pro Ser Pro Glu Val Val
530 535 540

Gln Glu Cys Val Gln Ser Ile Gly Leu Lys His Ile Ser Phe Lys Pro
545 550 555 560

Gly Ser Phe Glu Ala Ile His Gln Val Ile Gln Ile Ala Arg Thr His
565 570 575

Pro Asn Phe Leu Ile Gly Leu Gln Trp Thr Ala Gly Arg Gly Gly Gly
580 585 590

His His Ser Trp Glu Asp Phe His Gly Pro Ile Leu Ala Thr Tyr Ala
595 600 605

Gln Ile Arg Ser Cys Pro Asn Ile Leu Leu Val Val Gly Ser Gly Phe
610 615 620

Gly Gly Gly Pro Asp Thr Phe Pro Tyr Leu Thr Gly Gln Trp Ala Gln
625 630 635 640

Ala Phe Gly Tyr Pro Cys Met Pro Phe Asp Gly Val Leu Leu Gly Ser
645 650 655

Arg Met Met Val Ala Arg Glu Ala His Thr Ser Ala Gln Ala Lys Arg
660 665 670

Leu Ile Ile Asp Ala Gln Gly Val Gly Asp Ala Asp Trp His Lys Ser
675 680 685

Phe Asp Glu Pro Thr Gly Gly Val Val Thr Val Asn Ser Glu Phe Gly
690 695 700

Gln Pro Ile His Val Leu Ala Thr Arg Gly Val Met Leu Trp Lys Glu
705 710 715 720

Leu Asp Asn Arg Val Phe Ser Ile Lys Asp Thr Ser Lys Arg Leu Glu
725 730 735

Tyr Leu Arg Asn His Arg Gln Glu Ile Val Ser Arg Leu Asn Ala Asp
740 745 750

Phe Ala Arg Pro Trp Phe Ala Val Asp Gly His Gly Gln Asn Val Glu
755 760 765

Leu Glu Asp Met Thr Tyr Leu Glu Val Leu Arg Arg Leu Cys Asp Leu
770 775 780

Thr Tyr Val Ser His Gln Lys Arg Trp Val Asp Pro Ser Tyr Arg Ile
785 790 795 800

Leu Leu Leu Asp Phe Val His Leu Leu Arg Glu Arg Phe Gln Cys Ala
805 810 815

Ile Asp Asn Pro Gly Glu Tyr Pro Leu Asp Ile Ile Val Arg Val Glu
820 825 830

Glu Ser Leu Lys Asp Lys Ala Tyr Arg Thr Leu Tyr Pro Glu Asp Val
835 840 845

Ser Leu Leu Met His Leu Phe Ser Arg Arg Asp Ile Lys Pro Val Pro
850 855 860

Phe Ile Pro Arg Leu Asp Glu Arg Phe Glu Thr Trp Phe Lys Lys Asp
865 870 875 880

Ser Leu Trp Gln Ser Glu Asp Val Glu Ala Val Ile Gly Gln Asp Val
885 890 895

Gln Arg Ile Phe Ile Ile Gln Gly Pro Met Ala Val Gln Tyr Ser Ile
900 905 910

Ser Asp Asp Glu Ser Val Lys Asp Ile Leu His Asn Ile Cys Asn His
915 920 925

Tyr Val Glu Ala Leu Gln Ala Asp Ser Arg Glu Thr Ser Ile Gly Asp
930 935 940

Val His Ser Ile Thr Gln Lys Pro Leu Ser Ala Phe Pro Gly Leu Lys
945 950 955 960

Val Thr Thr Asn Arg Val Gln Gly Leu Tyr Lys Phe Glu Lys Val Gly
965 970 975

Ala Val Pro Glu Met Asp Val Leu Phe Glu His Ile Val Gly Leu Ser
980 985 990

Lys Ser Trp Ala Arg Thr Cys Leu Met Ser Lys Ser Val Phe Arg Asp
995 1000 1005

Gly Ser Arg Leu His Asn Pro Ile Arg Ala Ala Leu Gln Leu Gln
1010 1015 1020

Arg Gly Asp Thr Ile Glu Val Leu Leu Thr Ala Asp Ser Glu Ile
1025 1030 1035

Arg Lys Ile Arg Leu Ile Ser Pro Thr Gly Asp Gly Gly Ser Thr
1040 1045 1050

Ser Lys Val Val Leu Glu Ile Val Ser Asn Asp Gly Gln Arg Val
1055 1060 1065

Phe Ala Thr Leu Ala Pro Asn Ile Pro Leu Ser Pro Glu Pro Ser
1070 1075 1080

Val Val Phe Cys Phe Lys Val Asp Gln Lys Pro Asn Glu Trp Thr
1085 1090 1095

Leu Glu Glu Asp Ala Ser Gly Arg Ala Glu Arg Ile Lys Ala Leu
1100 1105 1110

Tyr Met Ser Leu Trp Asn Leu Gly Phe Pro Asn Lys Ala Ser Val
1115 1120 1125

Leu Gly Leu Asn Ser Gln Phe Thr Gly Glu Glu Leu Met Ile Thr
1130 1135 1140

Thr Asp Lys Ile Arg Asp Phe Glu Arg Val Leu Arg Gln Thr Ser
1145 1150 1155

Pro Leu Gln Leu Gln Ser Trp Asn Pro Gln Gly Cys Val Pro Ile
1160 1165 1170

Asp Tyr Cys Val Val Ile Ala Trp Ser Ala Leu Thr Lys Pro Leu
1175 1180 1185

Met Val Ser Ser Leu Lys Cys Asp Leu Leu Asp Leu Leu His Ser
1190 1195 1200

Ala	Ile	Ser	Phe	His	Tyr	Ala	Pro	Ser	Val	Lys	Pro	Leu	Arg	Val
1205						1210					1215			
Gly	Asp	Ile	Val	Lys	Thr	Ser	Ser	Arg	Ile	Leu	Ala	Val	Ser	Val
1220						1225					1230			
Arg	Pro	Arg	Gly	Thr	Met	Leu	Thr	Val	Ser	Ala	Asp	Ile	Gln	Arg
1235						1240					1245			
Gln	Gly	Gln	His	Val	Val	Thr	Val	Lys	Ser	Asp	Phe	Phe	Leu	Gly
1250						1255					1260			
Gly	Pro	Val	Leu	Ala	Cys	Glu	Thr	Pro	Phe	Glu	Leu	Thr	Glu	Glu
1265						1270					1275			
Pro	Glu	Met	Val	Val	His	Val	Asp	Ser	Glu	Val	Arg	Arg	Ala	Ile
1280						1285					1290			
Leu	His	Ser	Arg	Lys	Trp	Leu	Met	Arg	Glu	Asp	Arg	Ala	Leu	Asp
1295						1300					1305			
Leu	Leu	Gly	Arg	Gln	Leu	Leu	Phe	Arg	Leu	Lys	Ser	Glu	Lys	Leu
1310						1315					1320			
Phe	Arg	Pro	Asp	Gly	Gln	Leu	Ala	Leu	Leu	Gln	Val	Thr	Gly	Ser
1325						1330					1335			
Val	Phe	Ser	Tyr	Ser	Pro	Asp	Gly	Ser	Thr	Thr	Ala	Phe	Gly	Arg
1340						1345					1350			
Val	Tyr	Phe	Glu	Ser	Glu	Ser	Cys	Thr	Gly	Asn	Val	Val	Met	Asp
1355						1360					1365			
Phe	Leu	His	Arg	Tyr	Gly	Ala	Pro	Arg	Ala	Gln	Leu	Leu	Glu	Leu
1370						1375					1380			
Gln	His	Pro	Gly	Trp	Thr	Gly	Thr	Ser	Thr	Val	Ala	Val	Arg	Gly
1385						1390					1395			
Pro	Arg	Arg	Ser	Gln	Ser	Tyr	Ala	Arg	Val	Ser	Leu	Asp	His	Asn
1400						1405					1410			

Pro Ile His Val Cys Pro Ala Phe Ala Arg Tyr Ala Gly Leu Ser
1415 1420 1425

Gly Pro Ile Val His Gly Met Glu Thr Ser Ala Met Met Arg Arg
1430 1435 1440

Ile Ala Glu Trp Ala Ile Gly Asp Ala Asp Arg Ser Arg Phe Arg
1445 1450 1455

Ser Trp His Ile Thr Leu Gln Ala Pro Val His Pro Asn Asp Pro
1460 1465 1470

Leu Arg Val Glu Leu Gln His Lys Ala Met Glu Asp Gly Glu Met
1475 1480 1485

Val Leu Lys Val Gln Ala Phe Asn Glu Arg Thr Glu Glu Arg Val
1490 1495 1500

Ala Glu Ala Asp Ala His Val Glu Gln Glu Thr Thr Ala Tyr Val
1505 1510 1515

Phe Cys Gly Gln Gly Ser Gln Arg Gln Gly Met Gly Met Asp Leu
1520 1525 1530

Tyr Val Asn Cys Pro Glu Ala Lys Ala Leu Trp Ala Arg Ala Asp
1535 1540 1545

Lys His Leu Trp Glu Lys Tyr Gly Phe Ser Ile Leu His Ile Val
1550 1555 1560

Gln Asn Asn Pro Pro Ala Leu Thr Val His Phe Gly Ser Gln Arg
1565 1570 1575

Gly Arg Arg Ile Arg Ala Asn Tyr Leu Arg Met Met Gly Gln Pro
1580 1585 1590

Pro Ile Asp Gly Arg His Pro Pro Ile Leu Lys Gly Leu Thr Arg
1595 1600 1605

Asn	Ser	Thr	Ser	Tyr	Thr	Phe	Ser	Tyr	Ser	Gln	Gly	Leu	Leu	Met
1610						1615					1620			
Ser	Thr	Gln	Phe	Ala	Gln	Pro	Ala	Leu	Ala	Leu	Met	Glu	Met	Ala
1625						1630					1635			
Gln	Phe	Glu	Trp	Leu	Lys	Ala	Gln	Gly	Val	Val	Gln	Lys	Gly	Ala
1640						1645					1650			
Arg	Phe	Ala	Gly	His	Ser	Leu	Gly	Glu	Tyr	Ala	Ala	Leu	Gly	Ala
1655						1660					1665			
Cys	Ala	Ser	Phe	Leu	Ser	Phe	Glu	Asp	Leu	Ile	Ser	Leu	Ile	Phe
1670						1675					1680			
Tyr	Arg	Gly	Leu	Lys	Met	Gln	Asn	Ala	Leu	Pro	Arg	Asp	Ala	Asn
1685						1690					1695			
Gly	His	Thr	Asp	Tyr	Gly	Met	Leu	Ala	Ala	Asp	Pro	Ser	Arg	Ile
1700						1705					1710			
Gly	Lys	Gly	Phe	Glu	Glu	Ala	Ser	Leu	Lys	Cys	Leu	Val	His	Ile
1715						1720					1725			
Ile	Gln	Gln	Glu	Thr	Gly	Trp	Phe	Val	Glu	Val	Val	Asn	Tyr	Asn
1730						1735					1740			
Ile	Asn	Ser	Gln	Gln	Tyr	Val	Cys	Ala	Gly	His	Phe	Arg	Ala	Leu
1745						1750					1755			
Trp	Met	Leu	Gly	Lys	Ile	Cys	Asp	Asp	Leu	Ser	Cys	His	Pro	Gln
1760						1765					1770			
Pro	Glu	Thr	Val	Glu	Gly	Gln	Glu	Leu	Arg	Ala	Met	Val	Trp	Lys
1775						1780					1785			
His	Val	Pro	Thr	Val	Glu	Gln	Val	Pro	Arg	Glu	Asp	Arg	Met	Glu
1790						1795					1800			
Arg	Gly	Arg	Ala	Thr	Ile	Pro	Leu	Pro	Gly	Ile	Asp	Ile	Pro	Tyr
1805						1810					1815			

His Ser Thr Met Leu Arg Gly Glu Ile Glu Pro Tyr Arg Glu Tyr
1820 1825 1830

Leu Ser Glu Arg Ile Lys Val Gly Asp Val Lys Pro Cys Glu Leu
1835 1840 1845

Val Gly Arg Trp Ile Pro Asn Val Val Gly Gln Pro Phe Ser Val
1850 1855 1860

Asp Lys Ser Tyr Val Gln Leu Val His Gly Ile Thr Gly Ser Pro
1865 1870 1875

Arg Leu His Ser Leu Leu Gln Gln Met Ala
1880 1885

<210> 5
<211> 377
<212> PRT
<213> Mentha x piperita

<400> 5

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

Val Lys Asp Val His Gly Gly Arg Arg Arg Arg Ser Arg Ser Thr Leu
20 25 30

Phe Gln Ser His Pro Leu Arg Thr Glu Met Pro Phe Ser Leu Tyr Phe
35 40 45

Ser Ser Pro Leu Lys Ala Pro Ala Thr Phe Ser Val Ser Ala Val Tyr
50 55 60

Thr Lys Glu Gly Ser Glu Ile Arg Asp Lys Asp Pro Ala Pro Ser Thr
65 70 75 80

Ser Pro Ala Phe Asp Phe Asp Gly Tyr Met Leu Arg Lys Ala Lys Ser
85 90 95

Val Asn Lys Ala Leu Glu Ala Ala Val Gln Met Lys Glu Pro Leu Lys

	100		105		110														
Ile	His	Glu	Ser	Met	Arg	Tyr	Ser	Leu	Leu	Ala	Gly	Gly	Lys	Arg	Val				
	115						120					125							
Arg	Pro	Met	Leu	Cys	Ile	Ala	Ala	Cys	Glu	Leu	Val	Gly	Gly	Asp	Glu				
	130					135					140								
Ser	Thr	Ala	Met	Pro	Ala	Ala	Cys	Ala	Val	Glu	Met	Ile	His	Thr	Met				
145					150					155					160				
Ser	Leu	Met	His	Asp	Asp	Leu	Pro	Cys	Met	Asp	Asn	Asp	Asp	Leu	Arg				
				165					170					175					
Arg	Gly	Lys	Pro	Thr	Asn	His	Met	Ala	Phe	Gly	Glu	Ser	Val	Ala	Val				
			180					185					190						
Leu	Ala	Gly	Asp	Ala	Leu	Leu	Ser	Phe	Ala	Phe	Glu	His	Val	Ala	Ala				
	195						200					205							
Ala	Thr	Lys	Gly	Ala	Pro	Pro	Glu	Arg	Ile	Val	Arg	Val	Leu	Gly	Glu				
	210					215					220								
Leu	Ala	Val	Ser	Ile	Gly	Ser	Glu	Gly	Leu	Val	Ala	Gly	Gln	Val	Val				
225					230					235					240				
Asp	Val	Cys	Ser	Glu	Gly	Met	Ala	Glu	Val	Gly	Leu	Asp	His	Leu	Glu				
				245					250					255					
Phe	Ile	His	His	His	Lys	Thr	Ala	Ala	Leu	Leu	Gln	Gly	Ser	Val	Val				
			260					265					270						
Leu	Gly	Ala	Ile	Leu	Gly	Gly	Gly	Lys	Glu	Glu	Glu	Val	Ala	Lys	Leu				
	275					280						285							
Arg	Lys	Phe	Ala	Asn	Cys	Ile	Gly	Leu	Leu	Phe	Gln	Val	Val	Asp	Asp				
	290					295					300								
Ile	Leu	Asp	Val	Thr	Lys	Ser	Ser	Lys	Glu	Leu	Gly	Lys	Thr	Ala	Gly				
305					310					315					320				

Lys Asp Leu Val Ala Asp Lys Thr Thr Tyr Pro Lys Leu Ile Gly Val
325 330 335

Glu Lys Ser Lys Glu Phe Ala Asp Arg Leu Asn Arg Glu Ala Gln Glu
340 345 350

Gln Leu Leu His Phe His Pro His Arg Ala Ala Pro Leu Ile Ala Leu
355 360 365

Ala Asn Tyr Ile Ala Tyr Arg Asp Asn
370 375

<210> 6
<211> 313
<212> PRT
<213> Mentha x piperita

<400> 6

Met Ala Ile Asn Leu Ser His Ile Asn Ser Lys Thr Cys Phe Pro Leu
1 5 10 15

Lys Thr Arg Ser Asp Leu Ser Arg Ser Ser Ser Ala Arg Cys Met Pro
20 25 30

Thr Ala Ala Ala Ala Ala Phe Pro Thr Ile Ala Thr Ala Ala Gln Ser
35 40 45

Gln Pro Tyr Trp Ala Ala Ile Glu Ala Asp Ile Glu Arg Tyr Leu Lys
50 55 60

Lys Ser Ile Thr Ile Arg Pro Pro Glu Thr Val Phe Gly Pro Met His
65 70 75 80

His Leu Thr Phe Ala Ala Pro Ala Thr Ala Ala Ser Thr Leu Cys Leu
85 90 95

Ala Ala Cys Glu Leu Val Gly Gly Asp Arg Ser Gln Ala Met Ala Ala
100 105 110

Ala Ala Ala Ile His Leu Val His Ala Ala Ala Tyr Val His Glu His
115 120 125

Leu Pro Leu Thr Asp Gly Ser Arg Pro Val Ser Lys Pro Ala Ile Gln
130 135 140

His Lys Tyr Gly Pro Asn Val Glu Leu Leu Thr Gly Asp Gly Ile Val
145 150 155 160

Pro Phe Gly Phe Glu Leu Leu Ala Gly Ser Val Asp Pro Ala Arg Thr
165 170 175

Asp Asp Pro Asp Arg Ile Leu Arg Val Ile Ile Glu Ile Ser Arg Ala
180 185 190

Gly Gly Pro Glu Gly Met Ile Ser Gly Leu His Arg Glu Glu Glu Ile
195 200 205

Val Asp Gly Asn Thr Ser Leu Asp Phe Ile Glu Tyr Val Cys Lys Lys
210 215 220

Lys Tyr Gly Glu Met His Ala Cys Gly Ala Ala Cys Gly Ala Ile Leu
225 230 235 240

Gly Gly Ala Ala Glu Glu Glu Ile Gln Lys Leu Arg Asn Phe Gly Leu
245 250 255

Tyr Gln Gly Thr Leu Arg Gly Met Met Glu Met Lys Asn Ser His Gln
260 265 270

Leu Ile Asp Glu Asn Ile Ile Gly Lys Leu Lys Glu Leu Ala Leu Glu
275 280 285

Glu Leu Gly Gly Phe His Gly Lys Asn Ala Glu Leu Met Ser Ser Leu
290 295 300

Val Ala Glu Pro Ser Leu Tyr Ala Ala
305 310

<210> 7
<211> 352
<212> PRT
<213> Saccharomyces sp.

<400> 7

Met Ala Ser Glu Lys Glu Ile Arg Arg Glu Arg Phe Leu Asn Val Phe
1 5 10 15

Pro Lys Leu Val Glu Glu Leu Asn Ala Ser Leu Leu Ala Tyr Gly Met
20 25 30

Pro Lys Glu Ala Cys Asp Trp Tyr Ala His Ser Leu Asn Tyr Asn Thr
35 40 45

Pro Gly Gly Lys Leu Asn Arg Gly Leu Ser Val Val Asp Thr Tyr Ala
50 55 60

Ile Leu Ser Asn Lys Thr Val Glu Gln Leu Gly Gln Glu Glu Tyr Glu
65 70 75 80

Lys Val Ala Ile Leu Gly Trp Cys Ile Glu Leu Leu Gln Ala Tyr Phe
85 90 95

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

Pro Cys Trp Tyr Lys Val Pro Glu Val Gly Glu Ile Ala Ile Asn Asp
115 120 125

Ala Phe Met Leu Glu Ala Ala Ile Tyr Lys Leu Leu Lys Ser His Phe
130 135 140

Arg Asn Glu Lys Tyr Tyr Ile Asp Ile Thr Glu Leu Phe His Glu Val
145 150 155 160

Thr Phe Gln Thr Glu Leu Gly Gln Leu Met Asp Leu Ile Thr Ala Pro
165 170 175

Glu Asp Lys Val Asp Leu Ser Lys Phe Ser Leu Lys Lys His Ser Phe
180 185 190

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

Leu Ala Met Tyr Val Ala Gly Ile Thr Asp Glu Lys Asp Leu Lys Gln
210 215 220

Ala Arg Asp Val Leu Ile Pro Leu Gly Glu Tyr Phe Gln Ile Gln Asp
225 230 235 240

Asp Tyr Leu Asp Cys Phe Gly Thr Pro Glu Gln Ile Gly Lys Ile Gly
245 250 255

Thr Asp Ile Gln Asp Asn Lys Cys Ser Trp Val Ile Asn Lys Ala Leu
260 265 270

Glu Leu Ala Ser Ala Glu Gln Arg Lys Thr Leu Asp Glu Asn Tyr Gly
275 280 285

Lys Lys Asp Ser Val Ala Glu Ala Lys Cys Lys Lys Ile Phe Asn Asp
290 295 300

Leu Lys Ile Glu Gln Leu Tyr His Glu Tyr Glu Glu Ser Ile Ala Lys
305 310 315 320

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

Ala Asp Val Leu Thr Ala Phe Leu Asn Lys Val Tyr Lys Arg Ser Lys
340 345 350

<210> 8
<211> 352
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutated Erg20 farnesylpyrophosphate synthase (K197G)

<400> 8

Met Ala Ser Glu Lys Glu Ile Arg Arg Glu Arg Phe Leu Asn Val Phe
1 5 10 15

Pro Lys Leu Val Glu Glu Leu Asn Ala Ser Leu Leu Ala Tyr Gly Met
20 25 30

Pro Lys Glu Ala Cys Asp Trp Tyr Ala His Ser Leu Asn Tyr Asn Thr
35 40 45

Pro Gly Gly Lys Leu Asn Arg Gly Leu Ser Val Val Asp Thr Tyr Ala
50 55 60

Ile Leu Ser Asn Lys Thr Val Glu Gln Leu Gly Gln Glu Glu Tyr Glu
65 70 75 80

Lys Val Ala Ile Leu Gly Trp Cys Ile Glu Leu Leu Gln Ala Tyr Phe
85 90 95

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

Pro Cys Trp Tyr Lys Val Pro Glu Val Gly Glu Ile Ala Ile Asn Asp
115 120 125

Ala Phe Met Leu Glu Ala Ala Ile Tyr Lys Leu Leu Lys Ser His Phe
130 135 140

Arg Asn Glu Lys Tyr Tyr Ile Asp Ile Thr Glu Leu Phe His Glu Val
145 150 155 160

Thr Phe Gln Thr Glu Leu Gly Gln Leu Met Asp Leu Ile Thr Ala Pro
165 170 175

Glu Asp Lys Val Asp Leu Ser Lys Phe Ser Leu Lys Lys His Ser Phe
180 185 190

Ile Val Thr Phe Gly Thr Ala Tyr Tyr Ser Phe Tyr Leu Pro Val Ala
195 200 205

Leu Ala Met Tyr Val Ala Gly Ile Thr Asp Glu Lys Asp Leu Lys Gln
210 215 220

Ala Arg Asp Val Leu Ile Pro Leu Gly Glu Tyr Phe Gln Ile Gln Asp
225 230 235 240

Asp Tyr Leu Asp Cys Phe Gly Thr Pro Glu Gln Ile Gly Lys Ile Gly

245

250

255

Thr Asp Ile Gln Asp Asn Lys Cys Ser Trp Val Ile Asn Lys Ala Leu
 260 265 270

Glu Leu Ala Ser Ala Glu Gln Arg Lys Thr Leu Asp Glu Asn Tyr Gly
 275 280 285

Lys Lys Asp Ser Val Ala Glu Ala Lys Cys Lys Lys Ile Phe Asn Asp
 290 295 300

Leu Lys Ile Glu Gln Leu Tyr His Glu Tyr Glu Glu Ser Ile Ala Lys
 305 310 315 320

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

Ala Asp Val Leu Thr Ala Phe Leu Asn Lys Val Tyr Lys Arg Ser Lys
 340 345 350

<210> 9

<211> 496

<212> PRT

<213> Rhizophagus irregularis

<400> 9

Met Arg Ala Gln Ala His Leu Gly Gly Gly Leu Lys Arg Ile Glu Thr
 1 5 10 15

Gln His Gln Lys Gly Lys Leu Thr Ala Arg Glu Arg Ala Glu Leu Leu
 20 25 30

Leu Asp Pro Gly Ser Phe Asn Glu Tyr Asp Thr Phe Val Glu His Gln
 35 40 45

Cys Thr Asp Phe Gly Met Asp Lys Asn Lys Ile Ile Gly Asp Gly Val
 50 55 60

Val Thr Gly His Gly Thr Ile Asn Gly Arg Arg Val Phe Thr Phe Ser
 65 70 75 80

Gln Asp Phe Thr Ala Phe Gly Gly Ser Leu Ser Lys Met His Ala Gln
85 90 95

Lys Ile Cys Lys Ile Met Asp Lys Ala Met Leu Val Gly Ala Pro Val
100 105 110

Ile Gly Leu Asn Asp Ser Gly Gly Ala Arg Ile Gln Glu Gly Val Asp
115 120 125

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

Gly Val Val Pro Gln Leu Ser Leu Ile Met Gly Pro Cys Ala Gly Gly
145 150 155 160

Ala Val Tyr Ser Pro Ala Leu Thr Asp Phe Thr Phe Met Val Arg Asp
165 170 175

Thr Ser Tyr Leu Phe Val Thr Gly Pro Glu Val Val Lys Ala Val Cys
180 185 190

Asn Glu Asp Val Thr Gln Glu Glu Leu Gly Gly Ala Asn Thr His Thr
195 200 205

Val Ile Ser Gly Val Ala His Ala Ala Phe Glu Asn Asp Ile Glu Ala
210 215 220

Ile Gln Arg Ile Arg Asp Phe Met Asp Phe Leu Pro Leu Ser Asn Arg
225 230 235 240

Glu Gln Ala Pro Thr Arg Tyr Ser Asp Asp Pro Ile Asp Arg Glu Asp
245 250 255

Pro Ser Leu Asn His Ile Ile Pro Val Asp Ser Thr Lys Ala Tyr Asp
260 265 270

Met Arg Glu Ile Ile Thr Arg Leu Ile Asp Asp Gly His Phe Phe Glu
275 280 285

Ile Met Pro Asp Tyr Ala Lys Asn Ile Val Val Gly Phe Ala Arg Met
290 295 300

Gly Gly Lys Thr Val Ser Ile Val Gly Asn Gln Pro Leu Val Ser Ser
305 310 315 320

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

Phe Cys Asp Ala Phe Asn Ile Pro Ile Ile Thr Leu Val Asp Val Pro
340 345 350

Gly Phe Leu Pro Gly Thr Ala Gln Glu His Asn Gly Ile Ile Arg His
355 360 365

Gly Ala Lys Leu Leu Tyr Ala Tyr Ala Glu Ala Thr Val Pro Lys Ile
370 375 380

Thr Ile Ile Thr Arg Lys Ala Tyr Gly Gly Ala Tyr Asp Val Met Ser
385 390 395 400

Ser Lys His Leu Arg Gly Asp Met Asn Tyr Ser Trp Pro Thr Gly Glu
405 410 415

Ile Ala Val Met Gly Ala Lys Gly Ala Val Glu Ile Ile Phe Arg His
420 425 430

Val Glu Asp Arg Thr Gln Ser Glu His Glu Tyr Ile Asp Lys Phe Ala
435 440 445

Asn Pro Ile Pro Ala Ala Gln Arg Gly Tyr Ile Asp Asp Ile Ile Leu
450 455 460

Pro Ala Ala Thr Arg Lys Arg Ile Ile Glu Asp Leu Phe Val Leu Ser
465 470 475 480

His Lys Gln Leu Pro Leu Ile Tyr Lys Lys His Asp Asn Cys Pro Leu
485 490 495

<210> 10
<211> 101
<212> PRT
<213> Cannabis sativa

<400> 10

Met Ala Val Lys His Leu Ile Val Leu Lys Phe Lys Asp Glu Ile Thr
1 5 10 15

Glu Ala Gln Lys Glu Glu Phe Phe Lys Thr Tyr Val Asn Leu Val Asn
20 25 30

Ile Ile Pro Ala Met Lys Asp Val Tyr Trp Gly Lys Asp Val Thr Gln
35 40 45

Lys Asn Lys Glu Glu Gly Tyr Thr His Ile Val Glu Val Thr Phe Glu
50 55 60

Ser Val Glu Thr Ile Gln Asp Tyr Ile Ile His Pro Ala His Val Gly
65 70 75 80

Phe Gly Asp Val Tyr Arg Ser Phe Trp Glu Lys Leu Leu Ile Phe Asp
85 90 95

Tyr Thr Pro Arg Lys
100

<210> 11

<211> 385

<212> PRT

<213> Cannabis sativa

<400> 11

Met Asn His Leu Arg Ala Glu Gly Pro Ala Ser Val Leu Ala Ile Gly
1 5 10 15

Thr Ala Asn Pro Glu Asn Ile Leu Leu Gln Asp Glu Phe Pro Asp Tyr
20 25 30

Tyr Phe Arg Val Thr Lys Ser Glu His Met Thr Gln Leu Lys Glu Lys
35 40 45

Phe Arg Lys Ile Cys Asp Lys Ser Met Ile Arg Lys Arg Asn Cys Phe
50 55 60

Leu Asn Glu Glu His Leu Lys Gln Asn Pro Arg Leu Val Glu His Glu
65 70 75 80

Met Gln Thr Leu Asp Ala Arg Gln Asp Met Leu Val Val Glu Val Pro
85 90 95

Lys Leu Gly Lys Asp Ala Cys Ala Lys Ala Ile Lys Glu Trp Gly Gln
100 105 110

Pro Lys Ser Lys Ile Thr His Leu Ile Phe Thr Ser Ala Ser Thr Thr
115 120 125

Asp Met Pro Gly Ala Asp Tyr His Cys Ala Lys Leu Leu Gly Leu Ser
130 135 140

Pro Ser Val Lys Arg Val Met Met Tyr Gln Leu Gly Cys Tyr Gly Gly
145 150 155 160

Gly Thr Val Leu Arg Ile Ala Lys Asp Ile Ala Glu Asn Asn Lys Gly
165 170 175

Ala Arg Val Leu Ala Val Cys Cys Asp Ile Met Ala Cys Leu Phe Arg
180 185 190

Gly Pro Ser Glu Ser Asp Leu Glu Leu Leu Val Gly Gln Ala Ile Phe
195 200 205

Gly Asp Gly Ala Ala Ala Val Ile Val Gly Ala Glu Pro Asp Glu Ser
210 215 220

Val Gly Glu Arg Pro Ile Phe Glu Leu Val Ser Thr Gly Gln Thr Ile
225 230 235 240

Leu Pro Asn Ser Glu Gly Thr Ile Gly Gly His Ile Arg Glu Ala Gly
245 250 255

Leu Ile Phe Asp Leu His Lys Asp Val Pro Met Leu Ile Ser Asn Asn
260 265 270

Ile Glu Lys Cys Leu Ile Glu Ala Phe Thr Pro Ile Gly Ile Ser Asp
275 280 285

Trp Asn Ser Ile Phe Trp Ile Thr His Pro Gly Gly Lys Ala Ile Leu
290 295 300

Asp Lys Val Glu Glu Lys Leu His Leu Lys Ser Asp Lys Phe Val Asp
305 310 315 320

Ser Arg His Val Leu Ser Glu His Gly Asn Met Ser Ser Ser Thr Val
325 330 335

Leu Phe Val Met Asp Glu Leu Arg Lys Arg Ser Leu Glu Glu Gly Lys
340 345 350

Ser Thr Thr Gly Asp Gly Phe Glu Trp Gly Val Leu Phe Gly Phe Gly
355 360 365

Pro Gly Leu Thr Val Glu Arg Val Val Val Arg Ser Val Pro Ile Lys
370 375 380

Tyr
385

<210> 12
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated geranyl pyrophosphate olivetolic acid
geranyltransferase (GOT)

<400> 12

Met Asn Ser Ile Arg Ala Ala Thr Thr Asn Gln Thr Glu Pro Pro Glu
1 5 10 15

Ser Asp Asn His Ser Val Ala Thr Lys Ile Leu Asn Phe Gly Lys Ala
20 25 30

Cys Trp Lys Leu Gln Arg Pro Tyr Thr Ile Ile Ala Phe Thr Ser Cys
35 40 45

Ala Cys Gly Leu Phe Gly Lys Glu Leu Leu His Asn Thr Asn Leu Ile

50

55

60

Ser Trp Ser Leu Met Phe Lys Ala Phe Phe Phe Leu Val Ala Ile Leu
65 70 75 80

Cys Ile Ala Ser Phe Thr Thr Thr Ile Asn Gln Ile Tyr Asp Leu His
85 90 95

Ile Asp Arg Ile Asn Lys Pro Asp Leu Pro Leu Ala Ser Gly Glu Ile
100 105 110

Ser Val Asn Thr Ala Trp Ile Met Ser Ile Ile Val Ala Leu Phe Gly
115 120 125

Leu Ile Ile Thr Ile Lys Met Lys Gly Gly Pro Leu Tyr Ile Phe Gly
130 135 140

Tyr Cys Phe Gly Ile Phe Gly Gly Ile Val Tyr Ser Val Pro Pro Phe
145 150 155 160

Arg Trp Lys Gln Asn Pro Ser Thr Ala Phe Leu Leu Asn Phe Leu Ala
165 170 175

His Ile Ile Thr Asn Phe Thr Phe Tyr Tyr Ala Ser Arg Ala Ala Leu
180 185 190

Gly Leu Pro Phe Glu Leu Arg Pro Ser Phe Thr Phe Leu Leu Ala Phe
195 200 205

Met Lys Ser Met Gly Ser Ala Leu Ala Leu Ile Lys Asp Ala Ser Asp
210 215 220

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

Gly Ser Arg Asn Leu Thr Leu Phe Cys Ser Gly Ile Val Leu Leu Ser
245 250 255

Tyr Val Ala Ala Ile Leu Ala Gly Ile Ile Trp Pro Gln Ala Phe Asn
260 265 270

Ser Asn Val Met Leu Leu Ser His Ala Ile Leu Ala Phe Trp Leu Ile
275 280 285

Leu Gln Thr Arg Asp Phe Ala Leu Thr Asn Tyr Asp Pro Glu Ala Gly
290 295 300

Arg Arg Phe Tyr Glu Phe Met Trp Lys Leu Tyr Tyr Ala Glu Tyr Leu
305 310 315 320

Val Tyr Val Phe Ile Gly Ser
325

<210> 13
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered geranyl pyrophosphate olivetolic acid
geranyltransferase (GOT)

<400> 13

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

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

Asp Phe Val Ser Val Cys Trp Glu Tyr Val Arg Pro Tyr Thr Ala Lys
35 40 45

Gly Val Ile Ile Cys Ser Ser Cys Leu Phe Gly Arg Glu Leu Leu Glu
50 55 60

Asn Pro Asn Leu Phe Ser Trp Pro Leu Ile Phe Lys Ala Phe Phe Phe
65 70 75 80

Leu Val Ala Ile Leu Cys Ile Ala Ser Phe Thr Thr Thr Ile Asn Gln
85 90 95

Ile Tyr Asp Leu His Ile Asp Arg Ile Asn Lys Pro Asp Leu Pro Leu
100 105 110

Ala Ser Gly Glu Ile Ser Val Asn Thr Ala Trp Ile Met Ser Ile Ile
115 120 125

Val Ala Leu Phe Gly Leu Ile Ile Thr Ile Lys Met Lys Gly Gly Pro
130 135 140

Leu Tyr Ile Phe Gly Tyr Cys Phe Gly Ile Phe Gly Gly Ile Val Tyr
145 150 155 160

Ser Val Pro Pro Phe Arg Trp Lys Gln Asn Pro Ser Thr Ala Phe Leu
165 170 175

Leu Asn Phe Leu Ala His Ile Ile Thr Asn Phe Thr Phe Tyr Tyr Ala
180 185 190

Ser Arg Ala Ala Leu Gly Leu Pro Phe Glu Leu Arg Pro Ser Phe Thr
195 200 205

Phe Leu Leu Ala Phe Met Lys Ser Met Gly Ser Ala Leu Ala Leu Ile
210 215 220

Lys Asp Ala Ser Asp Val Glu Gly Asp Thr Lys Phe Gly Ile Ser Thr
225 230 235 240

Leu Ala Ser Lys Tyr Gly Ser Arg Asn Leu Thr Leu Phe Cys Ser Gly
245 250 255

Ile Val Leu Leu Ser Tyr Val Ala Ala Ile Leu Ala Gly Ile Ile Trp
260 265 270

Pro Gln Ala Phe Asn Ser Asn Val Met Leu Leu Ser His Ala Ile Leu
275 280 285

Ala Phe Trp Leu Ile Leu Gln Thr Arg Asp Phe Ala Leu Thr Asn Tyr
290 295 300

Asp Pro Glu Ala Gly Arg Arg Phe Tyr Glu Phe Met Trp Lys Leu Tyr
305 310 315 320

Tyr Ala Glu Tyr Leu Val Tyr Val Phe Ile Gly Ser
325 330

<210> 14
<211> 547
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutant tetrahydro cannabinolic acid synthase (THCAS)

<400> 14

Met Asn Cys Ser Ala Phe Ser Phe Trp Phe Val Cys Lys Ile Ile Phe
1 5 10 15

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

Asn Phe Leu Lys Cys Phe Ser Lys His Ile Pro Asn Asn Val Ala Asn
35 40 45

Pro Lys Leu Val Tyr Thr Gln His Asp Gln Leu Tyr Met Ser Ile Leu
50 55 60

Asn Ser Thr Ile Gln Asn Leu Arg Phe Ile Ser Asp Thr Thr Pro Lys
65 70 75 80

Pro Leu Val Ile Val Thr Pro Ser Asn Asn Ser His Ile Gln Ala Thr
85 90 95

Ile Leu Cys Ser Lys Lys Val Gly Leu Gln Ile Arg Thr Arg Ser Gly
100 105 110

Gly His Asp Ala Glu Gly Met Ser Tyr Ile Ser Gln Val Pro Phe Val
115 120 125

Val Val Asp Leu Arg Asn Met His Ser Ile Lys Ile Asp Val His Ser
130 135 140

Gln Thr Ala Trp Val Glu Ala Gly Ala Thr Leu Gly Glu Val Tyr Tyr
145 150 155 160

Trp Ile Asn Glu Lys Asn Glu Asn Leu Ser Phe Pro Gly Gly Tyr Cys
165 170 175

Pro Thr Val Gly Val Gly Gly His Phe Ser Gly Gly Gly Tyr Gly Ala
180 185 190

Leu Met Arg Asn Tyr Gly Leu Ala Ala Asp Asn Ile Ile Asp Ala His
195 200 205

Leu Val Asn Val Asp Gly Lys Val Leu Asp Arg Lys Ser Met Gly Glu
210 215 220

Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Glu Asn Phe Gly Ile
225 230 235 240

Ile Ala Ala Trp Lys Ile Lys Leu Val Ala Val Pro Ser Lys Ser Thr
245 250 255

Ile Phe Ser Val Lys Lys Asn Met Glu Ile His Gly Leu Val Lys Leu
260 265 270

Phe Asn Lys Trp Gln Asn Ile Ala Tyr Lys Tyr Asp Lys Asp Leu Val
275 280 285

Leu Met Thr His Phe Ile Thr Lys Asn Ile Thr Asp Asn His Gly Lys
290 295 300

Asn Lys Thr Thr Val His Gly Tyr Phe Ser Ser Ile Phe His Gly Gly
305 310 315 320

Val Asp Ser Leu Val Asp Leu Met Asn Lys Ser Phe Pro Glu Leu Gly
325 330 335

Ile Lys Lys Thr Asp Cys Lys Glu Phe Ser Trp Ile Asp Thr Thr Ile
340 345 350

Phe Tyr Ser Gly Val Val Asn Phe Asn Thr Ala Asn Phe Lys Lys Glu
355 360 365

Ile Leu Leu Asp Arg Ser Ala Gly Lys Lys Thr Ala Phe Ser Ile Lys
370 375 380

Leu Asp Tyr Val Lys Lys Pro Ile Pro Glu Thr Ala Met Val Lys Ile
385 390 395 400

Leu Glu Lys Leu Tyr Glu Glu Asp Val Gly Ala Gly Met Tyr Val Leu
405 410 415

Tyr Pro Tyr Gly Gly Ile Met Glu Glu Ile Ser Glu Ser Ala Ile Pro
420 425 430

Phe Pro His Arg Ala Gly Ile Met Tyr Glu Leu Trp Tyr Thr Ala Ser
435 440 445

Trp Glu Lys Gln Glu Asp Asn Glu Lys His Ile Asn Trp Val Arg Ser
450 455 460

Val Tyr Asn Phe Thr Thr Pro Tyr Val Ser Gln Asn Pro Arg Leu Ala
465 470 475 480

Tyr Leu Asn Tyr Arg Asp Leu Asp Leu Gly Lys Thr Asn His Ala Ser
485 490 495

Pro Asn Asn Tyr Thr Gln Ala Arg Ile Trp Gly Glu Lys Tyr Phe Gly
500 505 510

Lys Asn Phe Asn Arg Leu Val Lys Val Lys Thr Lys Val Asp Pro Asn
515 520 525

Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro Pro Leu Pro Pro His His
530 535 540

His Gly Ser
545

<210> 15
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated tetrahydro cannabinolic acid synthase (THCAS)

<400> 15

Met Asn Pro Arg Glu Asn Phe Leu Lys Cys Phe Ser Lys His Ile Pro
1 5 10 15

Asn Asn Val Ala Asn Pro Lys Leu Val Tyr Thr Gln His Asp Gln Leu
20 25 30

Tyr Met Ser Ile Leu Asn Ser Thr Ile Gln Asn Leu Arg Phe Ile Ser
35 40 45

Asp Thr Thr Pro Lys Pro Leu Val Ile Val Thr Pro Ser Asn Asn Ser
50 55 60

His Ile Gln Ala Thr Ile Leu Cys Ser Lys Lys Val Gly Leu Gln Ile
65 70 75 80

Arg Thr Arg Ser Gly Gly His Asp Ala Glu Gly Met Ser Tyr Ile Ser
85 90 95

Gln Val Pro Phe Val Val Val Asp Leu Arg Asn Met His Ser Ile Lys
100 105 110

Ile Asp Val His Ser Gln Thr Ala Trp Val Glu Ala Gly Ala Thr Leu
115 120 125

Gly Glu Val Tyr Tyr Trp Ile Asn Glu Lys Asn Glu Asn Leu Ser Phe
130 135 140

Pro Gly Gly Tyr Cys Pro Thr Val Gly Val Gly Gly His Phe Ser Gly
145 150 155 160

Gly Gly Tyr Gly Ala Leu Met Arg Asn Tyr Gly Leu Ala Ala Asp Asn
165 170 175

Ile Ile Asp Ala His Leu Val Asn Val Asp Gly Lys Val Leu Asp Arg
180 185 190

Lys Ser Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly
195 200 205

Glu Asn Phe Gly Ile Ile Ala Ala Trp Lys Ile Lys Leu Val Ala Val
210 215 220

Pro Ser Lys Ser Thr Ile Phe Ser Val Lys Lys Asn Met Glu Ile His
225 230 235 240

Gly Leu Val Lys Leu Phe Asn Lys Trp Gln Asn Ile Ala Tyr Lys Tyr
245 250 255

Asp Lys Asp Leu Val Leu Met Thr His Phe Ile Thr Lys Asn Ile Thr
260 265 270

Asp Asn His Gly Lys Asn Lys Thr Thr Val His Gly Tyr Phe Ser Ser
275 280 285

Ile Phe His Gly Gly Val Asp Ser Leu Val Asp Leu Met Asn Lys Ser
290 295 300

Phe Pro Glu Leu Gly Ile Lys Lys Thr Asp Cys Lys Glu Phe Ser Trp
305 310 315 320

Ile Asp Thr Thr Ile Phe Tyr Ser Gly Val Val Asn Phe Asn Thr Ala
325 330 335

Asn Phe Lys Lys Glu Ile Leu Leu Asp Arg Ser Ala Gly Lys Lys Thr
340 345 350

Ala Phe Ser Ile Lys Leu Asp Tyr Val Lys Lys Pro Ile Pro Glu Thr
355 360 365

Ala Met Val Lys Ile Leu Glu Lys Leu Tyr Glu Glu Asp Val Gly Ala
370 375 380

Gly Met Tyr Val Leu Tyr Pro Tyr Gly Gly Ile Met Glu Glu Ile Ser
385 390 395 400

Glu Ser Ala Ile Pro Phe Pro His Arg Ala Gly Ile Met Tyr Glu Leu
405 410 415

Trp Tyr Thr Ala Ser Trp Glu Lys Gln Glu Asp Asn Glu Lys His Ile
420 425 430

Asn Trp Val Arg Ser Val Tyr Asn Phe Thr Thr Pro Tyr Val Ser Gln
435 440 445

Asn Pro Arg Leu Ala Tyr Leu Asn Tyr Arg Asp Leu Asp Leu Gly Lys
450 455 460

Thr Asn His Ala Ser Pro Asn Asn Tyr Thr Gln Ala Arg Ile Trp Gly
465 470 475 480

Glu Lys Tyr Phe Gly Lys Asn Phe Asn Arg Leu Val Lys Val Lys Thr
485 490 495

Lys Val Asp Pro Asn Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro Pro
500 505 510

Leu Pro Pro His His His Gly Ser
515 520

<210> 16

<211> 519

<212> PRT

<213> Artificial Sequence

<220>

<223> Truncated cannabidiolic acid synthase (CBDAS)

<400> 16

Met Asn Pro Arg Glu Asn Phe Leu Lys Cys Phe Ser Gln Tyr Ile Pro
1 5 10 15

Asn Asn Ala Thr Asn Leu Lys Leu Val Tyr Thr Gln Asn Asn Pro Leu
20 25 30

Tyr Met Ser Val Leu Asn Ser Thr Ile His Asn Leu Arg Phe Thr Ser
35 40 45

Asp Thr Thr Pro Lys Pro Leu Val Ile Val Thr Pro Ser His Val Ser
50 55 60

His Ile Gln Gly Thr Ile Leu Cys Ser Lys Lys Val Gly Leu Gln Ile
65 70 75 80

Arg Thr Arg Ser Gly Gly His Asp Ser Glu Gly Met Ser Tyr Ile Ser
85 90 95

Gln Val Pro Phe Val Ile Val Asp Leu Arg Asn Met Arg Ser Ile Lys
100 105 110

Ile Asp Val His Ser Gln Thr Ala Trp Val Glu Ala Gly Ala Thr Leu
115 120 125

Gly Glu Val Tyr Tyr Trp Val Asn Glu Lys Asn Glu Asn Leu Ser Leu
130 135 140

Ala Ala Gly Tyr Cys Pro Thr Val Cys Ala Gly Gly His Phe Gly Gly
145 150 155 160

Gly Gly Tyr Gly Pro Leu Met Arg Asn Tyr Gly Leu Ala Ala Asp Asn
165 170 175

Ile Ile Asp Ala His Leu Val Asn Val His Gly Lys Val Leu Asp Arg
180 185 190

Lys Ser Met Gly Glu Asp Leu Phe Trp Ala Leu Arg Gly Gly Gly Ala
195 200 205

Glu Ser Phe Gly Ile Ile Val Ala Trp Lys Ile Arg Leu Val Ala Val
210 215 220

Pro Lys Ser Thr Met Phe Ser Val Lys Lys Ile Met Glu Ile His Glu
225 230 235 240

Leu Val Lys Leu Val Asn Lys Trp Gln Asn Ile Ala Tyr Lys Tyr Asp
245 250 255

Lys Asp Leu Leu Leu Met Thr His Phe Ile Thr Arg Asn Ile Thr Asp
260 265 270

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

Phe Leu Gly Gly Val Asp Ser Leu Val Asp Leu Met Asn Lys Ser Phe
290 295 300

Pro Glu Leu Gly Ile Lys Lys Thr Asp Cys Arg Gln Leu Ser Trp Ile
305 310 315 320

Asp Thr Ile Ile Phe Tyr Ser Gly Val Val Asn Tyr Asp Thr Asp Asn
325 330 335

Phe Asn Lys Glu Ile Leu Leu Asp Arg Ser Ala Gly Gln Asn Gly Ala
340 345 350

Phe Lys Ile Lys Leu Asp Tyr Val Lys Lys Pro Ile Pro Glu Ser Val
355 360 365

Phe Val Gln Ile Leu Glu Lys Leu Tyr Glu Glu Asp Ile Gly Ala Gly
370 375 380

Met Tyr Ala Leu Tyr Pro Tyr Gly Gly Ile Met Asp Glu Ile Ser Glu
385 390 395 400

Ser Ala Ile Pro Phe Pro His Arg Ala Gly Ile Leu Tyr Glu Leu Trp
405 410 415

Tyr Ile Cys Ser Trp Glu Lys Gln Glu Asp Asn Glu Lys His Leu Asn
420 425 430

Trp Ile Arg Asn Ile Tyr Asn Phe Met Thr Pro Tyr Val Ser Lys Asn
435 440 445

Pro Arg Leu Ala Tyr Leu Asn Tyr Arg Asp Leu Asp Ile Gly Ile Asn
450 455 460

Asp Pro Lys Asn Pro Asn Asn Tyr Thr Gln Ala Arg Ile Trp Gly Glu
465 470 475 480

Lys Tyr Phe Gly Lys Asn Phe Asp Arg Leu Val Lys Val Lys Thr Leu
485 490 495

Val Asp Pro Asn Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro Pro Leu
500 505 510

Pro Arg His Arg His Gly Ser
515

<210> 17
<211> 502
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated 3-hydroxy-3-methyl-glutaryl-CoA reductase (HMGR)

<400> 17

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

Leu Ser Ser Ala Gln Ser Ser Ser Ser Gly Pro Ser Ser Ser Ser Glu
20 25 30

Glu Asp Asp Ser Arg Asp Ile Glu Ser Leu Asp Lys Lys Ile Arg Pro
35 40 45

Leu Glu Glu Leu Glu Ala Leu Leu Ser Ser Gly Asn Thr Lys Gln Leu
50 55 60

Lys Asn Lys Glu Val Ala Ala Leu Val Ile His Gly Lys Leu Pro Leu
65 70 75 80

Tyr Ala Leu Glu Lys Lys Leu Gly Asp Thr Thr Arg Ala Val Ala Val
85 90 95

Arg Arg Lys Ala Leu Ser Ile Leu Ala Glu Ala Pro Val Leu Ala Ser
100 105 110

Asp Arg Leu Pro Tyr Lys Asn Tyr Asp Tyr Asp Arg Val Phe Gly Ala
115 120 125

Cys Cys Glu Asn Val Ile Gly Tyr Met Pro Leu Pro Val Gly Val Ile
130 135 140

Gly Pro Leu Val Ile Asp Gly Thr Ser Tyr His Ile Pro Met Ala Thr
145 150 155 160

Thr Glu Gly Cys Leu Val Ala Ser Ala Met Arg Gly Cys Lys Ala Ile
165 170 175

Asn Ala Gly Gly Gly Ala Thr Thr Val Leu Thr Lys Asp Gly Met Thr
180 185 190

Arg Gly Pro Val Val Arg Phe Pro Thr Leu Lys Arg Ser Gly Ala Cys
195 200 205

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

Phe Asn Ser Thr Ser Arg Phe Ala Arg Leu Gln His Ile Gln Thr Cys
225 230 235 240

Leu Ala Gly Asp Leu Leu Phe Met Arg Phe Arg Thr Thr Thr Gly Asp
245 250 255

Ala Met Gly Met Asn Met Ile Ser Lys Gly Val Glu Tyr Ser Leu Lys
260 265 270

Gln Met Val Glu Glu Tyr Gly Trp Glu Asp Met Glu Val Val Ser Val
275 280 285

Ser Gly Asn Tyr Cys Thr Asp Lys Lys Pro Ala Ala Ile Asn Trp Ile
290 295 300

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

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

Asn Ile Ala Lys Asn Leu Val Gly Ser Ala Met Ala Gly Ser Val Gly
340 345 350

Gly Phe Asn Ala His Ala Ala Asn Leu Val Thr Ala Val Phe Leu Ala
355 360 365

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

Leu Met Lys Glu Val Asp Gly Asp Leu Arg Ile Ser Val Ser Met Pro
385 390 395 400

Ser Ile Glu Val Gly Thr Ile Gly Gly Gly Thr Val Leu Glu Pro Gln
405 410 415

Gly Ala Met Leu Asp Leu Leu Gly Val Arg Gly Pro His Ala Thr Ala
420 425 430

Pro Gly Thr Asn Ala Arg Gln Leu Ala Arg Ile Val Ala Cys Ala Val
435 440 445

Leu Ala Gly Glu Leu Ser Leu Cys Ala Ala Leu Ala Ala Gly His Leu
450 455 460

Val Gln Ser His Met Thr His Asn Arg Lys Pro Ala Glu Pro Thr Lys
465 470 475 480

Pro Asn Asn Leu Asp Ala Thr Asp Ile Asn Arg Leu Lys Asp Gly Ser
485 490 495

Val Thr Cys Ile Lys Ser
500

<210> 18
<211> 284
<212> PRT
<213> Ralstonia sp.

<400> 18

Met Ser Ile Arg Thr Val Gly Ile Val Gly Ala Gly Thr Met Gly Asn
1 5 10 15

Gly Ile Ala Gln Ala Cys Ala Val Val Gly Leu Asn Val Val Met Val
20 25 30

Asp Ile Ser Asp Ala Ala Val Gln Lys Gly Val Ala Thr Val Ala Ser
35 40 45

Ser Leu Asp Arg Leu Ile Lys Lys Glu Lys Leu Thr Glu Ala Asp Lys
50 55 60

Ala Ser Ala Leu Ala Arg Ile Lys Gly Ser Thr Ser Tyr Asp Asp Leu
65 70 75 80

Lys Ala Thr Asp Ile Val Ile Glu Ala Ala Thr Glu Asn Tyr Asp Leu
85 90 95

Lys Val Lys Ile Leu Lys Gln Ile Asp Gly Ile Val Gly Glu Asn Val
100 105 110

Ile Ile Ala Ser Asn Thr Ser Ser Ile Ser Ile Thr Lys Leu Ala Ala
115 120 125

Val Thr Ser Arg Ala Asp Arg Phe Ile Gly Met His Phe Phe Asn Pro
130 135 140

Val Pro Val Met Ala Leu Val Glu Leu Ile Arg Gly Leu Gln Thr Ser
145 150 155 160

Asp Thr Thr His Ala Ala Val Glu Ala Leu Ser Lys Gln Leu Gly Lys
165 170 175

Tyr Pro Ile Thr Val Lys Asn Ser Pro Gly Phe Val Val Asn Arg Ile
180 185 190

Leu Cys Pro Met Ile Asn Glu Ala Phe Cys Val Leu Gly Glu Gly Leu
195 200 205

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

Pro Ile Gly Pro Leu Ala Leu Ala Asp Met Ile Gly Leu Asp Thr Met
225 230 235 240

Leu Ala Val Met Glu Val Leu Tyr Thr Glu Phe Ala Asp Pro Lys Tyr
245 250 255

Arg Pro Ala Met Leu Met Arg Glu Met Val Ala Ala Gly Tyr Leu Gly

260

265

270

Arg Lys Thr Gly Arg Gly Val Tyr Val Tyr Ser Lys
 275 280

<210> 19

<211> 261

<212> PRT

<213> Clostridium sp.

<400> 19

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

Val Thr Ile Asn Arg Pro Lys Ala Leu Asn Ala Leu Asn Ser Asp Thr
 20 25 30

Leu Lys Glu Met Asp Tyr Val Ile Gly Glu Ile Glu Asn Asp Ser Glu
 35 40 45

Val Leu Ala Val Ile Leu Thr Gly Ala Gly Glu Lys Ser Phe Val Ala
 50 55 60

Gly Ala Asp Ile Ser Glu Met Lys Glu Met Asn Thr Ile Glu Gly Arg
 65 70 75 80

Lys Phe Gly Ile Leu Gly Asn Lys Val Phe Arg Arg Leu Glu Leu Leu
 85 90 95

Glu Lys Pro Val Ile Ala Ala Val Asn Gly Phe Ala Leu Gly Gly Gly
 100 105 110

Cys Glu Ile Ala Met Ser Cys Asp Ile Arg Ile Ala Ser Ser Asn Ala
 115 120 125

Arg Phe Gly Gln Pro Glu Val Gly Leu Gly Ile Thr Pro Gly Phe Gly
 130 135 140

Gly Thr Gln Arg Leu Ser Arg Leu Val Gly Met Gly Met Ala Lys Gln
 145 150 155 160

Leu Ile Phe Thr Ala Gln Asn Ile Lys Ala Asp Glu Ala Leu Arg Ile
165 170 175

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

Lys Glu Ile Ala Asn Lys Ile Val Ser Asn Ala Pro Val Ala Val Lys
195 200 205

Leu Ser Lys Gln Ala Ile Asn Arg Gly Met Gln Cys Asp Ile Asp Thr
210 215 220

Ala Leu Ala Phe Glu Ser Glu Ala Phe Gly Glu Cys Phe Ser Thr Glu
225 230 235 240

Asp Gln Lys Asp Ala Met Thr Ala Phe Ile Glu Lys Arg Lys Ile Glu
245 250 255

Gly Phe Lys Asn Arg
260

<210> 20
<211> 397
<212> PRT
<213> Treponema sp.

<400> 20

Met Ile Val Lys Pro Met Val Arg Asn Asn Ile Cys Leu Asn Ala His
1 5 10 15

Pro Gln Gly Cys Lys Lys Gly Val Glu Asp Gln Ile Glu Tyr Thr Lys
20 25 30

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

Val Leu Val Leu Gly Cys Ser Asn Gly Tyr Gly Leu Ala Ser Arg Ile
50 55 60

Thr Ala Ala Phe Gly Tyr Gly Ala Ala Thr Ile Gly Val Ser Phe Glu
65 70 75 80

Lys Ala Gly Ser Glu Thr Lys Tyr Gly Thr Pro Gly Trp Tyr Asn Asn
85 90 95

Leu Ala Phe Asp Glu Ala Ala Lys Arg Glu Gly Leu Tyr Ser Val Thr
100 105 110

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

Glu Ala Lys Lys Lys Gly Ile Lys Phe Asp Leu Ile Val Tyr Ser Leu
130 135 140

Ala Ser Pro Val Arg Thr Asp Pro Asp Thr Gly Ile Met His Lys Ser
145 150 155 160

Val Leu Lys Pro Phe Gly Lys Thr Phe Thr Gly Lys Thr Val Asp Pro
165 170 175

Phe Thr Gly Glu Leu Lys Glu Ile Ser Ala Glu Pro Ala Asn Asp Glu
180 185 190

Glu Ala Ala Ala Thr Val Lys Val Met Gly Gly Glu Asp Trp Glu Arg
195 200 205

Trp Ile Lys Gln Leu Ser Lys Glu Gly Leu Leu Glu Glu Gly Cys Ile
210 215 220

Thr Leu Ala Tyr Ser Tyr Ile Gly Pro Glu Ala Thr Gln Ala Leu Tyr
225 230 235 240

Arg Lys Gly Thr Ile Gly Lys Ala Lys Glu His Leu Glu Ala Thr Ala
245 250 255

His Arg Leu Asn Lys Glu Asn Pro Ser Ile Arg Ala Phe Val Ser Val
260 265 270

Asn Lys Gly Leu Val Thr Arg Ala Ser Ala Val Ile Pro Val Ile Pro
275 280 285

Leu Tyr Leu Ala Ser Leu Phe Lys Val Met Lys Glu Lys Gly Asn His

290

295

300

Glu Gly Cys Ile Glu Gln Ile Thr Arg Leu Tyr Ala Glu Arg Leu Tyr
 305 310 315 320

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

Asp Asp Trp Glu Leu Glu Glu Asp Val Gln Lys Ala Val Ser Ala Leu
 340 345 350

Met Glu Lys Val Thr Gly Glu Asn Ala Glu Ser Leu Thr Asp Leu Ala
 355 360 365

Gly Tyr Arg His Asp Phe Leu Ala Ser Asn Gly Phe Asp Val Glu Gly
 370 375 380

Ile Asn Tyr Glu Ala Glu Val Glu Arg Phe Asp Arg Ile
 385 390 395

<210> 21
 <211> 394
 <212> PRT
 <213> Ralstonia sp.

<400> 21

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

Thr Phe Gly Gly Ser Leu Lys Asp Val Ala Pro Ala Glu Leu Gly Ala
 20 25 30

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

Val Gly His Val Val Phe Gly Asn Val Ile Gln Thr Glu Pro Arg Asp
 50 55 60

Met Tyr Leu Gly Arg Val Ala Ala Val Asn Gly Gly Val Thr Ile Asn
 65 70 75 80

Ala Pro Ala Leu Thr Val Asn Arg Leu Cys Gly Ser Gly Leu Gln Ala
85 90 95

Ile Val Ser Ala Ala Gln Thr Ile Leu Leu Gly Asp Thr Asp Val Ala
100 105 110

Ile Gly Gly Gly Ala Glu Ser Met Ser Arg Ala Pro Tyr Leu Ala Pro
115 120 125

Ala Ala Arg Trp Gly Ala Arg Met Gly Asp Ala Gly Leu Val Asp Met
130 135 140

Met Leu Gly Ala Leu His Asp Pro Phe His Arg Ile His Met Gly Val
145 150 155 160

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

Asp Glu Ala Ala Leu Glu Ser His Arg Arg Ala Ser Ala Ala Ile Lys
180 185 190

Ala Gly Tyr Phe Lys Asp Gln Ile Val Pro Val Val Ser Lys Gly Arg
195 200 205

Lys Gly Asp Val Thr Phe Asp Thr Asp Glu His Val Arg His Asp Ala
210 215 220

Thr Ile Asp Asp Met Thr Lys Leu Arg Pro Val Phe Val Lys Glu Asn
225 230 235 240

Gly Thr Val Thr Ala Gly Asn Ala Ser Gly Leu Asn Asp Ala Ala Ala
245 250 255

Ala Val Val Met Met Glu Arg Ala Glu Ala Glu Arg Arg Gly Leu Lys
260 265 270

Pro Leu Ala Arg Leu Val Ser Tyr Gly His Ala Gly Val Asp Pro Lys
275 280 285

Ala Met Gly Ile Gly Pro Val Pro Ala Thr Lys Ile Ala Leu Glu Arg
290 295 300

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

Phe Ala Ala Gln Ala Cys Ala Val Thr Lys Ala Leu Gly Leu Asp Pro
325 330 335

Ala Lys Val Asn Pro Asn Gly Ser Gly Ile Ser Leu Gly His Pro Ile
340 345 350

Gly Ala Thr Gly Ala Leu Ile Thr Val Lys Ala Leu His Glu Leu Asn
355 360 365

Arg Val Gln Gly Arg Tyr Ala Leu Val Thr Met Cys Ile Gly Gly Gly
370 375 380

Gln Gly Ile Ala Ala Ile Phe Glu Arg Ile
385 390

<210> 22
<211> 813
<212> PRT
<213> Enterococcus sp.

<400> 22

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

Tyr Arg Gly Ser Leu Ser Pro Phe Thr Ala Val Glu Leu Gly Thr Leu
20 25 30

Val Thr Lys Gly Leu Leu Asp Lys Thr Lys Leu Lys Lys Asp Lys Ile
35 40 45

Asp Gln Val Ile Phe Gly Asn Val Leu Gln Ala Gly Asn Gly Gln Asn
50 55 60

Val Ala Arg Gln Ile Ala Leu Asn Ser Gly Leu Pro Val Asp Val Pro
65 70 75 80

Ala Met Thr Ile Asn Glu Val Cys Gly Ser Gly Met Lys Ala Val Ile

85

90

95

Leu Ala Arg Gln Leu Ile Gln Leu Gly Glu Ala Glu Leu Val Ile Ala
 100 105 110

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

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

Gly Leu Thr Asp Ala Phe Ser Asn Ala His Met Gly Leu Thr Ala Glu
 145 150 155 160

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

Ala Leu Ser Ser Gln Leu Lys Ala Ala His Ala Val Glu Ala Gly Val
 180 185 190

Phe Ser Glu Glu Ile Ile Pro Val Lys Ile Ser Asp Glu Asp Val Leu
 195 200 205

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

Thr Leu Arg Thr Val Phe Ser Glu Glu Gly Thr Val Thr Ala Gly Asn
 225 230 235 240

Ala Ser Pro Leu Asn Asp Gly Ala Ser Val Val Ile Leu Ala Ser Lys
 245 250 255

Glu Tyr Ala Glu Asn Asn Asn Leu Pro Tyr Leu Ala Thr Ile Lys Glu
 260 265 270

Val Ala Glu Val Gly Ile Asp Pro Ser Ile Met Gly Ile Ala Pro Ile
 275 280 285

Lys Ala Ile Gln Lys Leu Thr Asp Arg Ser Gly Met Asn Leu Ser Thr
 290 295 300

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

Val Ser Gln Glu Leu Gln Leu Asp Glu Glu Lys Val Asn Ile Tyr Gly
325 330 335

Gly Ala Ile Ala Leu Gly His Pro Ile Gly Ala Ser Gly Ala Arg Ile
340 345 350

Leu Thr Thr Leu Ala Tyr Gly Leu Leu Arg Glu Gln Lys Arg Tyr Gly
355 360 365

Ile Ala Ser Leu Cys Ile Gly Gly Gly Leu Gly Leu Ala Val Leu Leu
370 375 380

Glu Ala Asn Met Glu Gln Thr His Lys Asp Val Gln Lys Lys Lys Phe
385 390 395 400

Tyr Gln Leu Thr Pro Ser Glu Arg Arg Ser Gln Leu Ile Glu Lys Asn
405 410 415

Val Leu Thr Gln Glu Thr Ala Leu Ile Phe Gln Glu Gln Thr Leu Ser
420 425 430

Glu Glu Leu Ser Asp His Met Ile Glu Asn Gln Val Ser Glu Val Glu
435 440 445

Ile Pro Met Gly Ile Ala Gln Asn Phe Gln Ile Asn Gly Lys Lys Lys
450 455 460

Trp Ile Pro Met Ala Thr Glu Glu Pro Ser Val Ile Ala Ala Ala Ser
465 470 475 480

Asn Gly Ala Lys Ile Cys Gly Asn Ile Cys Ala Glu Thr Pro Gln Arg
485 490 495

Leu Met Arg Gly Gln Ile Val Leu Ser Gly Lys Ser Glu Tyr Gln Ala
500 505 510

Val Ile Asn Ala Val Asn His Arg Lys Glu Glu Leu Ile Leu Cys Ala

515

520

525

Asn Glu Ser Tyr Pro Ser Ile Val Lys Arg Gly Gly Gly Val Gln Asp
 530 535 540

Ile Ser Thr Arg Glu Phe Met Gly Ser Phe His Ala Tyr Leu Ser Ile
 545 550 555 560

Asp Phe Leu Val Asp Val Lys Asp Ala Met Gly Ala Asn Met Ile Asn
 565 570 575

Ser Ile Leu Glu Ser Val Ala Asn Lys Leu Arg Glu Trp Phe Pro Glu
 580 585 590

Glu Glu Ile Leu Phe Ser Ile Leu Ser Asn Phe Ala Thr Glu Ser Leu
 595 600 605

Ala Ser Ala Cys Cys Glu Ile Pro Phe Glu Arg Leu Gly Arg Asn Lys
 610 615 620

Glu Ile Gly Glu Gln Ile Ala Lys Lys Ile Gln Gln Ala Gly Glu Tyr
 625 630 635 640

Ala Lys Leu Asp Pro Tyr Arg Ala Ala Thr His Asn Lys Gly Ile Met
 645 650 655

Asn Gly Ile Glu Ala Val Val Ala Ala Thr Gly Asn Asp Thr Arg Ala
 660 665 670

Val Ser Ala Ser Ile His Ala Tyr Ala Ala Arg Asn Gly Leu Tyr Gln
 675 680 685

Gly Leu Thr Asp Trp Gln Ile Lys Gly Asp Lys Leu Val Gly Lys Leu
 690 695 700

Thr Val Pro Leu Ala Val Ala Thr Val Gly Gly Ala Ser Asn Ile Leu
 705 710 715 720

Pro Lys Ala Lys Ala Ser Leu Ala Met Leu Asp Ile Asp Ser Ala Lys
 725 730 735

Glu Leu Ala Gln Val Ile Ala Ala Val Gly Leu Ala Gln Asn Leu Ala
740 745 750

Ala Leu Arg Ala Leu Val Thr Glu Gly Ile Gln Lys Gly His Met Gly
755 760 765

Leu Gln Ala Arg Ser Leu Ala Ile Ser Ile Gly Ala Ile Gly Glu Glu
770 775 780

Ile Glu Gln Val Ala Lys Lys Leu Arg Glu Ala Glu Lys Met Asn Gln
785 790 795 800

Gln Thr Ala Ile Gln Ile Leu Glu Lys Ile Arg Glu Lys
805 810

<210> 23

<211> 389

<212> PRT

<213> Lactobacillus plantarum

<400> 23

Met Lys Ile Gly Ile Asp Lys Leu His Phe Ala Thr Ser His Leu Tyr
1 5 10 15

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

Tyr Leu Ile Gly Ile Gly Gln Ser Lys Met Ala Val Ile Pro Pro Ser
35 40 45

Gln Asp Val Val Thr Leu Ala Ala Asn Ala Ala Ala Pro Met Leu Thr
50 55 60

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

Gly Ile Asp Asn Ser Lys Ala Ser Ala Ile Tyr Val Ala Lys Leu Leu
85 90 95

Gly Leu Ser Gln Arg Val Arg Thr Ile Glu Met Lys Glu Ala Cys Tyr
100 105 110

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

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

Leu Asn Thr Pro Gly Glu Pro Thr Gln Gly Gly Gly Ala Val Ala Met
145 150 155 160

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

Leu Leu Ser Glu Asp Val Met Asp Phe Trp Arg Pro Leu Tyr His Thr
180 185 190

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

Phe Gln Asp Val Phe Lys Asn Tyr Leu Gln Thr Thr Gln Thr Ser Pro
210 215 220

Asp Thr Leu Thr Ala Leu Val Phe His Leu Pro Tyr Thr Lys Met Gly
225 230 235 240

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

Ala Gln Trp Leu Ala His Phe Glu His Ala Arg Gln Leu Asn Arg Gln
260 265 270

Val Gly Asn Leu Tyr Thr Gly Ser Leu Tyr Leu Ser Leu Leu Ser Gln
275 280 285

Leu Leu Thr Asp Pro Gln Leu Gln Pro Gly Asn Arg Leu Gly Leu Phe
290 295 300

Ser Tyr Gly Ser Gly Ala Glu Gly Glu Phe Tyr Thr Gly Val Ile Gln
305 310 315 320

Pro Asp Tyr Gln Thr Gly Leu Asp His Gly Leu Pro Gln Arg Leu Ala
325 330 335

Arg Arg Arg Arg Val Ser Val Ala Glu Tyr Glu Ala Leu Phe Ser His
340 345 350

Gln Leu Gln Trp Arg Ala Asp Asp Gln Ser Val Ser Tyr Ala Asp Asp
355 360 365

Pro His Arg Phe Val Leu Thr Gly Gln Lys Asn Glu Gln Arg Gln Tyr
370 375 380

Leu Asp Gln Gln Val
385

<210> 24
<211> 491
<212> PRT
<213> Saccharomyces cerevisiae

<400> 24

Met Lys Leu Ser Thr Lys Leu Cys Trp Cys Gly Ile Lys Gly Arg Leu
1 5 10 15

Arg Pro Gln Lys Gln Gln Gln Leu His Asn Thr Asn Leu Gln Met Thr
20 25 30

Glu Leu Lys Lys Gln Lys Thr Ala Glu Gln Lys Thr Arg Pro Gln Asn
35 40 45

Val Gly Ile Lys Gly Ile Gln Ile Tyr Ile Pro Thr Gln Cys Val Asn
50 55 60

Gln Ser Glu Leu Glu Lys Phe Asp Gly Val Ser Gln Gly Lys Tyr Thr
65 70 75 80

Ile Gly Leu Gly Gln Thr Asn Met Ser Phe Val Asn Asp Arg Glu Asp
85 90 95

Ile Tyr Ser Met Ser Leu Thr Val Leu Ser Lys Leu Ile Lys Ser Tyr
100 105 110

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

Leu Ile Asp Lys Ser Lys Ser Val Lys Ser Val Leu Met Gln Leu Phe
130 135 140

Gly Glu Asn Thr Asp Val Glu Gly Ile Asp Thr Leu Asn Ala Cys Tyr
145 150 155 160

Gly Gly Thr Asn Ala Leu Phe Asn Ser Leu Asn Trp Ile Glu Ser Asn
165 170 175

Ala Trp Asp Gly Arg Asp Ala Ile Val Val Cys Gly Asp Ile Ala Ile
180 185 190

Tyr Asp Lys Gly Ala Ala Arg Pro Thr Gly Gly Ala Gly Thr Val Ala
195 200 205

Met Trp Ile Gly Pro Asp Ala Pro Ile Val Phe Asp Ser Val Arg Ala
210 215 220

Ser Tyr Met Glu His Ala Tyr Asp Phe Tyr Lys Pro Asp Phe Thr Ser
225 230 235 240

Glu Tyr Pro Tyr Val Asp Gly His Phe Ser Leu Thr Cys Tyr Val Lys
245 250 255

Ala Leu Asp Gln Val Tyr Lys Ser Tyr Ser Lys Lys Ala Ile Ser Lys
260 265 270

Gly Leu Val Ser Asp Pro Ala Gly Ser Asp Ala Leu Asn Val Leu Lys
275 280 285

Tyr Phe Asp Tyr Asn Val Phe His Val Pro Thr Cys Lys Leu Val Thr
290 295 300

Lys Ser Tyr Gly Arg Leu Leu Tyr Asn Asp Phe Arg Ala Asn Pro Gln
305 310 315 320

Leu Phe Pro Glu Val Asp Ala Glu Leu Ala Thr Arg Asp Tyr Asp Glu

325

330

335

Ser Leu Thr Asp Lys Asn Ile Glu Lys Thr Phe Val Asn Val Ala Lys
 340 345 350

Pro Phe His Lys Glu Arg Val Ala Gln Ser Leu Ile Val Pro Thr Asn
 355 360 365

Thr Gly Asn Met Tyr Thr Ala Ser Val Tyr Ala Ala Phe Ala Ser Leu
 370 375 380

Leu Asn Tyr Val Gly Ser Asp Asp Leu Gln Gly Lys Arg Val Gly Leu
 385 390 395 400

Phe Ser Tyr Gly Ser Gly Leu Ala Ala Ser Leu Tyr Ser Cys Lys Ile
 405 410 415

Val Gly Asp Val Gln His Ile Ile Lys Glu Leu Asp Ile Thr Asn Lys
 420 425 430

Leu Ala Lys Arg Ile Thr Glu Thr Pro Lys Asp Tyr Glu Ala Ala Ile
 435 440 445

Glu Leu Arg Glu Asn Ala His Leu Lys Lys Asn Phe Lys Pro Gln Gly
 450 455 460

Ser Ile Glu His Leu Gln Ser Gly Val Tyr Tyr Leu Thr Asn Ile Asp
 465 470 475 480

Asp Lys Phe Arg Arg Ser Tyr Asp Val Lys Lys
 485 490

<210> 25

<211> 398

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 25

Met Ser Gln Asn Val Tyr Ile Val Ser Thr Ala Arg Thr Pro Ile Gly
 1 5 10 15

Ser Phe Gln Gly Ser Leu Ser Ser Lys Thr Ala Val Glu Leu Gly Ala
20 25 30

Val Ala Leu Lys Gly Ala Leu Ala Lys Val Pro Glu Leu Asp Ala Ser
35 40 45

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

Gly Gln Ala Pro Ala Arg Gln Val Ala Leu Ala Ala Gly Leu Ser Asn
65 70 75 80

His Ile Val Ala Ser Thr Val Asn Lys Val Cys Ala Ser Ala Met Lys
85 90 95

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

Val Val Ala Gly Gly Cys Glu Ser Met Thr Asn Ala Pro Tyr Tyr Met
115 120 125

Pro Ala Ala Arg Ala Gly Ala Lys Phe Gly Gln Thr Val Leu Val Asp
130 135 140

Gly Val Glu Arg Asp Gly Leu Asn Asp Ala Tyr Asp Gly Leu Ala Met
145 150 155 160

Gly Val His Ala Glu Lys Cys Ala Arg Asp Trp Asp Ile Thr Arg Glu
165 170 175

Gln Gln Asp Asn Phe Ala Ile Glu Ser Tyr Gln Lys Ser Gln Lys Ser
180 185 190

Gln Lys Glu Gly Lys Phe Asp Asn Glu Ile Val Pro Val Thr Ile Lys
195 200 205

Gly Phe Arg Gly Lys Pro Asp Thr Gln Val Thr Lys Asp Glu Glu Pro
210 215 220

Ala Arg Leu His Val Glu Lys Leu Arg Ser Ala Arg Thr Val Phe Gln
225 230 235 240

Lys Glu Asn Gly Thr Val Thr Ala Ala Asn Ala Ser Pro Ile Asn Asp
245 250 255

Gly Ala Ala Ala Val Ile Leu Val Ser Glu Lys Val Leu Lys Glu Lys
260 265 270

Asn Leu Lys Pro Leu Ala Ile Ile Lys Gly Trp Gly Glu Ala Ala His
275 280 285

Gln Pro Ala Asp Phe Thr Trp Ala Pro Ser Leu Ala Val Pro Lys Ala
290 295 300

Leu Lys His Ala Gly Ile Glu Asp Ile Asn Ser Val Asp Tyr Phe Glu
305 310 315 320

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

Lys Leu Asp Pro Ser Lys Val Asn Val Tyr Gly Gly Ala Val Ala Leu
340 345 350

Gly His Pro Leu Gly Cys Ser Gly Ala Arg Val Val Val Thr Leu Leu
355 360 365

Ser Ile Leu Gln Gln Glu Gly Gly Lys Ile Gly Val Ala Ala Ile Cys
370 375 380

Asn Gly Gly Gly Gly Ala Ser Ser Ile Val Ile Glu Lys Ile
385 390 395

<210> 26
<211> 247
<212> PRT
<213> Bacteroides sp.

<400> 26

Met Ser Asp Asp Lys Lys Ile Gly Ser Tyr Lys Phe Ile Ala Glu Pro
1 5 10 15

Phe His Val Asp Phe Asn Gly Arg Leu Thr Met Gly Val Leu Gly Asn

20

25

30

His Leu Leu Asn Cys Ala Gly Phe His Ala Ser Glu Arg Gly Phe Gly
 35 40 45

Ile Ala Thr Leu Asn Glu Asp Asn Tyr Thr Trp Val Leu Ser Arg Leu
 50 55 60

Ala Ile Asp Leu Glu Glu Met Pro Tyr Gln Tyr Glu Glu Phe Thr Val
 65 70 75 80

Gln Thr Trp Val Glu Asn Val Tyr Arg Leu Phe Thr Asp Arg Asn Phe
 85 90 95

Ala Ile Ile Asp Lys Asp Gly Lys Lys Ile Gly Tyr Ala Arg Ser Val
 100 105 110

Trp Ala Met Ile Asn Leu Asn Thr Arg Lys Pro Ala Asp Leu Leu Thr
 115 120 125

Leu His Gly Gly Ser Ile Val Asp Tyr Val Cys Asp Glu Pro Cys Pro
 130 135 140

Ile Glu Lys Pro Ser Arg Ile Lys Val Ala Thr Asp Gln Pro Cys Ala
 145 150 155 160

Lys Leu Thr Ala Lys Tyr Ser Asp Ile Asp Ile Asn Gly His Val Asn
 165 170 175

Ser Ile Arg Tyr Ile Glu His Ile Leu Asp Leu Phe Pro Ile Asp Leu
 180 185 190

Tyr Lys Ser Lys Arg Ile Gln Arg Phe Glu Met Ala Tyr Val Ala Glu
 195 200 205

Ser Tyr Tyr Gly Asp Glu Leu Ser Phe Phe Glu Glu Glu Val Ser Glu
 210 215 220

Asn Glu Tyr His Val Glu Ile Lys Lys Asn Gly Ser Glu Val Val Cys
 225 230 235 240

Arg Ala Lys Val Lys Phe Val
245

<210> 27

<211> 247

<212> PRT

<213> Bacteroides thetaiotaomicron

<400> 27

Met Ser Glu Glu Asn Lys Ile Gly Thr Tyr Gln Phe Val Ala Glu Pro
1 5 10 15

Phe His Val Asp Phe Asn Gly Arg Leu Thr Met Gly Val Leu Gly Asn
20 25 30

His Leu Leu Asn Cys Ala Gly Phe His Ala Ser Asp Arg Gly Phe Gly
35 40 45

Ile Ala Thr Leu Asn Glu Asp Asn Tyr Thr Trp Val Leu Ser Arg Leu
50 55 60

Ala Ile Glu Leu Asp Glu Met Pro Tyr Gln Tyr Glu Lys Phe Ser Val
65 70 75 80

Gln Thr Trp Val Glu Asn Val Tyr Arg Leu Phe Thr Asp Arg Asn Phe
85 90 95

Ala Val Ile Asp Lys Asp Gly Lys Lys Ile Gly Tyr Ala Arg Ser Val
100 105 110

Trp Ala Met Ile Asn Leu Asn Thr Arg Lys Pro Ala Asp Leu Leu Ala
115 120 125

Leu His Gly Gly Ser Ile Val Asp Tyr Ile Cys Asp Glu Pro Cys Pro
130 135 140

Ile Glu Lys Pro Ser Arg Ile Lys Val Thr Ser Asn Gln Pro Val Ala
145 150 155 160

Thr Leu Thr Ala Lys Tyr Ser Asp Ile Asp Ile Asn Gly His Val Asn
165 170 175

Ser Ile Arg Tyr Ile Glu His Ile Leu Asp Leu Phe Pro Ile Glu Leu
180 185 190

Tyr Gln Thr Lys Arg Ile Arg Arg Phe Glu Met Ala Tyr Val Ala Glu
195 200 205

Ser Tyr Phe Gly Asp Glu Leu Ser Phe Phe Cys Asp Glu Val Ser Glu
210 215 220

Asn Glu Phe His Val Glu Val Lys Lys Asn Gly Ser Glu Val Val Cys
225 230 235 240

Arg Ser Lys Val Ile Phe Glu
245

<210> 28

<211> 238

<212> PRT

<213> Bryantella formatexigen

<400> 28

Met Ile Tyr Met Ala Tyr Gln Tyr Arg Ser Arg Ile Arg Tyr Ser Glu
1 5 10 15

Ile Gly Glu Asp Lys Lys Leu Thr Leu Pro Gly Leu Val Asn Tyr Phe
20 25 30

Gln Asp Cys Ser Thr Phe Gln Ser Glu Ala Leu Gly Ile Gly Leu Asp
35 40 45

Thr Leu Gly Ala Arg Gln Arg Ala Trp Leu Leu Ala Ser Trp Lys Ile
50 55 60

Val Ile Asp Arg Leu Pro Arg Leu Gly Glu Glu Val Val Thr Glu Thr
65 70 75 80

Trp Pro Tyr Gly Phe Lys Gly Phe Gln Gly Asn Arg Asn Phe Arg Met
85 90 95

Leu Asp Gln Glu Gly His Thr Leu Ala Ala Ala Ala Ser Val Trp Ile

100

105

110

Tyr Leu Asn Val Glu Ser Gly His Pro Cys Arg Ile Asp Gly Asp Val
 115 120 125

Leu Glu Ala Tyr Glu Leu Glu Glu Glu Leu Pro Leu Gly Pro Phe Ser
 130 135 140

Arg Lys Ile Pro Val Pro Glu Glu Ser Thr Glu Arg Asp Ser Phe Leu
 145 150 155 160

Val Met Arg Ser His Leu Asp Thr Asn His His Val Asn Asn Gly Gln
 165 170 175

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

Gln Ile Arg Val Glu Tyr Arg Lys Ala Ala Val Leu His Asp Thr Ile
 195 200 205

Val Pro Phe Val Cys Thr Glu Pro Gln Arg Cys Thr Val Ser Leu Cys
 210 215 220

Gly Ser Asp Glu Lys Pro Phe Ala Val Val Glu Phe Ser Glu
 225 230 235

<210> 29

<211> 246

<212> PRT

<213> Lactobacillus brevis

<400> 29

Met Ala Ala Asn Glu Phe Ser Glu Thr His Arg Val Val Tyr Tyr Glu
 1 5 10 15

Ala Asp Asp Thr Gly Gln Leu Thr Leu Ala Met Leu Ile Asn Leu Phe
 20 25 30

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

Phe Val Gln Ser His Gly Val Gly Trp Val Val Thr Gln Tyr His Leu
50 55 60

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

Arg Ala Thr Ala Tyr Asn Arg Tyr Phe Ala Tyr Arg Glu Tyr Trp Leu
85 90 95

Leu Asp Asp Ala Gly Gln Val Leu Ala Tyr Gly Glu Gly Ile Trp Val
100 105 110

Thr Met Ser Tyr Ala Thr Arg Lys Ile Thr Thr Ile Pro Ala Glu Val
115 120 125

Met Ala Pro Tyr His Ser Glu Glu Gln Thr Arg Leu Pro Arg Leu Pro
130 135 140

Arg Pro Asp His Phe Asp Glu Ala Val Asn Gln Thr Leu Lys Pro Tyr
145 150 155 160

Thr Val Arg Tyr Phe Asp Ile Asp Gly Asn Gly His Val Asn Asn Ala
165 170 175

His Tyr Phe Asp Trp Met Leu Asp Val Leu Pro Ala Thr Phe Leu Arg
180 185 190

Ala His His Pro Thr Asp Val Lys Ile Arg Phe Glu Asn Glu Val Gln
195 200 205

Tyr Gly His Gln Val Thr Ser Glu Leu Ser Gln Ala Ala Ala Leu Thr
210 215 220

Thr Gln His Met Ile Lys Val Gly Asp Leu Thr Ala Val Lys Ala Thr
225 230 235 240

Ile Gln Trp Asp Asn Arg
245

<210> 30

<211> 261

<212> PRT

<213> Lactobacillus plantarum

<400> 30

Met Ala Thr Leu Gly Ala Asn Ala Ser Leu Tyr Ser Glu Gln His Arg
1 5 10 15

Ile Thr Tyr Tyr Glu Cys Asp Arg Thr Gly Arg Ala Thr Leu Thr Thr
20 25 30

Leu Ile Asp Ile Ala Val Leu Ala Ser Glu Asp Gln Ser Asp Ala Leu
35 40 45

Gly Leu Thr Thr Glu Met Val Gln Ser His Gly Val Gly Trp Val Val
50 55 60

Thr Gln Tyr Ala Ile Asp Ile Thr Arg Met Pro Arg Gln Asp Glu Val
65 70 75 80

Val Thr Ile Ala Val Arg Gly Ser Ala Tyr Asn Pro Tyr Phe Ala Tyr
85 90 95

Arg Glu Phe Trp Ile Arg Asp Ala Asp Gly Gln Gln Leu Ala Tyr Ile
100 105 110

Thr Ser Ile Trp Val Met Met Ser Gln Thr Thr Arg Arg Ile Val Lys
115 120 125

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

Ile Pro Arg Leu Pro Arg Pro Ile Ser Phe Glu Ala Thr Asp Thr Thr
145 150 155 160

Ile Thr Lys Pro Tyr His Val Arg Phe Phe Asp Ile Asp Pro Asn Arg
165 170 175

His Val Asn Asn Ala His Tyr Phe Asp Trp Leu Val Asp Thr Leu Pro
180 185 190

Ala Thr Phe Leu Leu Gln His Asp Leu Val His Val Asp Val Arg Tyr

195

200

205

Glu Asn Glu Val Lys Tyr Gly Gln Thr Val Thr Ala His Ala Asn Ile
 210 215 220

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

Val Asp Asp Glu Lys Cys Cys Glu Val Thr Ile Gln Trp Arg Thr Leu
 245 250 255

Pro Glu Pro Ile Gln
 260

<210> 31

<211> 250

<212> PRT

<213> Streptococcus dysgalactiae

<400> 31

Met Gly Leu Ser Tyr Arg Glu Asp Ile Lys Leu Pro Phe Glu Leu Cys
 1 5 10 15

Asp Val Lys Ser Asp Ile Lys Phe Pro Leu Leu Leu Asp Tyr Cys Leu
 20 25 30

Thr Val Ser Gly Arg Gln Ser Ala Gln Leu Gly Arg Ser Asn Asp Tyr
 35 40 45

Leu Leu Glu Gln Tyr Gly Leu Ile Trp Ile Val Thr Asp Tyr Glu Ala
 50 55 60

Thr Ile His Arg Leu Pro His Phe Gln Glu Thr Ile Thr Ile Glu Thr
 65 70 75 80

Lys Ala Leu Ser Tyr Asn Lys Phe Phe Cys Tyr Arg Gln Phe Tyr Ile
 85 90 95

Tyr Asp Gln Glu Gly Gly Leu Leu Val Asp Ile Leu Ala Tyr Phe Ala
 100 105 110

Leu Leu Asn Pro Asp Thr Arg Lys Val Ala Thr Ile Pro Glu Asp Leu
115 120 125

Val Ala Pro Phe Glu Thr Asp Phe Val Lys Lys Leu His Arg Val Pro
130 135 140

Lys Met Pro Leu Leu Glu Gln Ser Ile Asp Arg Asp Tyr Tyr Val Arg
145 150 155 160

Tyr Phe Asp Ile Asp Met Asn Gly His Val Asn Asn Ser Lys Tyr Leu
165 170 175

Asp Trp Met Tyr Asp Val Leu Gly Cys Glu Phe Leu Lys Thr His Gln
180 185 190

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

Gln Ile Thr Ser Ser Tyr His Leu Asp Gln Leu Thr Ser Tyr His Gln
210 215 220

Ile Thr Ser Asp Gly Gln Leu Asn Ala Gln Ala Met Ile Glu Trp Arg
225 230 235 240

Ala Ile Lys Gln Thr Glu Ser Glu Ile Asp
245 250

<210> 32
<211> 620
<212> PRT
<213> Escherichia coli

<400> 32

Met Ser Phe Asp Ile Ala Lys Tyr Pro Thr Leu Ala Leu Val Asp Ser
1 5 10 15

Thr Gln Glu Leu Arg Leu Leu Pro Lys Glu Ser Leu Pro Lys Leu Cys
20 25 30

Asp Glu Leu Arg Arg Tyr Leu Leu Asp Ser Val Ser Arg Ser Ser Gly
35 40 45

His Phe Ala Ser Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His
50 55 60

Tyr Val Tyr Asn Thr Pro Phe Asp Gln Leu Ile Trp Asp Val Gly His
65 70 75 80

Gln Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Ile Gly
85 90 95

Thr Ile Arg Gln Lys Gly Gly Leu His Pro Phe Pro Trp Arg Gly Glu
100 105 110

Ser Glu Tyr Asp Val Leu Ser Val Gly His Ser Ser Thr Ser Ile Ser
115 120 125

Ala Gly Ile Gly Ile Ala Val Ala Ala Glu Lys Glu Gly Lys Asn Arg
130 135 140

Arg Thr Val Cys Val Ile Gly Asp Gly Ala Ile Thr Ala Gly Met Ala
145 150 155 160

Phe Glu Ala Met Asn His Ala Gly Asp Ile Arg Pro Asp Met Leu Val
165 170 175

Ile Leu Asn Asp Asn Glu Met Ser Ile Ser Glu Asn Val Gly Ala Leu
180 185 190

Asn Asn His Leu Ala Gln Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu
195 200 205

Arg Glu Gly Gly Lys Lys Val Phe Ser Gly Val Pro Pro Ile Lys Glu
210 215 220

Leu Leu Lys Arg Thr Glu Glu His Ile Lys Gly Met Val Val Pro Gly
225 230 235 240

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

His Asp Val Leu Gly Leu Ile Thr Thr Leu Lys Asn Met Arg Asp Leu

260

265

270

Lys Gly Pro Gln Phe Leu His Ile Met Thr Lys Lys Gly Arg Gly Tyr
 275 280 285

Glu Pro Ala Glu Lys Asp Pro Ile Thr Phe His Ala Val Pro Lys Phe
 290 295 300

Asp Pro Ser Ser Gly Cys Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser
 305 310 315 320

Tyr Ser Lys Ile Phe Gly Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp
 325 330 335

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

Val Glu Phe Ser Arg Lys Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile
 355 360 365

Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly
 370 375 380

Tyr Lys Pro Ile Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr
 385 390 395 400

Asp Gln Val Leu His Asp Val Ala Ile Gln Lys Leu Pro Val Leu Phe
 405 410 415

Ala Ile Asp Arg Ala Gly Ile Val Gly Ala Asp Gly Gln Thr His Gln
 420 425 430

Gly Ala Phe Asp Leu Ser Tyr Leu Arg Cys Ile Pro Glu Met Val Ile
 435 440 445

Met Thr Pro Ser Asp Glu Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly
 450 455 460

Tyr His Tyr Asn Asp Gly Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn
 465 470 475 480

Ala Val Gly Val Glu Leu Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys
485 490 495

Gly Ile Val Lys Arg Arg Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly
500 505 510

Thr Leu Met Pro Glu Ala Ala Lys Val Ala Glu Ser Leu Asn Ala Thr
515 520 525

Leu Val Asp Met Arg Phe Val Lys Pro Leu Asp Glu Ala Leu Ile Leu
530 535 540

Glu Met Ala Ala Ser His Glu Ala Leu Val Thr Val Glu Glu Asn Ala
545 550 555 560

Ile Met Gly Gly Ala Gly Ser Gly Val Asn Glu Val Leu Met Ala His
565 570 575

Arg Lys Pro Val Pro Val Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile
580 585 590

Pro Gln Gly Thr Gln Glu Glu Met Arg Ala Glu Leu Gly Leu Asp Ala
595 600 605

Ala Gly Met Glu Ala Lys Ile Lys Ala Trp Leu Ala
610 615 620

<210> 33
<211> 398
<212> PRT
<213> Escherichia coli

<400> 33

Met Lys Gln Leu Thr Ile Leu Gly Ser Thr Gly Ser Ile Gly Cys Ser
1 5 10 15

Thr Leu Asp Val Val Arg His Asn Pro Glu His Phe Arg Val Val Ala
20 25 30

Leu Val Ala Gly Lys Asn Val Thr Arg Met Val Glu Gln Cys Leu Glu
35 40 45

Phe Ser Pro Arg Tyr Ala Val Met Asp Asp Glu Ala Ser Ala Lys Leu
50 55 60

Leu Lys Thr Met Leu Gln Gln Gln Gly Ser Arg Thr Glu Val Leu Ser
65 70 75 80

Gly Gln Gln Ala Ala Cys Asp Met Ala Ala Leu Glu Asp Val Asp Gln
85 90 95

Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu Pro Thr Leu Ala
100 105 110

Ala Ile Arg Ala Gly Lys Thr Ile Leu Leu Ala Asn Lys Glu Ser Leu
115 120 125

Val Thr Cys Gly Arg Leu Phe Met Asp Ala Val Lys Gln Ser Lys Ala
130 135 140

Gln Leu Leu Pro Val Asp Ser Glu His Asn Ala Ile Phe Gln Ser Leu
145 150 155 160

Pro Gln Pro Ile Gln His Asn Leu Gly Tyr Ala Asp Leu Glu Gln Asn
165 170 175

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

Thr Pro Leu Arg Asp Leu Ala Thr Met Thr Pro Asp Gln Ala Cys Arg
195 200 205

His Pro Asn Trp Ser Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr
210 215 220

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

Ala Ser Ala Ser Gln Met Glu Val Leu Ile His Pro Gln Ser Val Ile
245 250 255

His Ser Met Val Arg Tyr Gln Asp Gly Ser Val Leu Ala Gln Leu Gly
260 265 270

Glu Pro Asp Met Arg Thr Pro Ile Ala His Thr Met Ala Trp Pro Asn
275 280 285

Arg Val Asn Ser Gly Val Lys Pro Leu Asp Phe Cys Lys Leu Ser Ala
290 295 300

Leu Thr Phe Ala Ala Pro Asp Tyr Asp Arg Tyr Pro Cys Leu Lys Leu
305 310 315 320

Ala Met Glu Ala Phe Glu Gln Gly Gln Ala Ala Thr Thr Ala Leu Asn
325 330 335

Ala Ala Asn Glu Ile Thr Val Ala Ala Phe Leu Ala Gln Gln Ile Arg
340 345 350

Phe Thr Asp Ile Ala Ala Leu Asn Leu Ser Val Leu Glu Lys Met Asp
355 360 365

Met Arg Glu Pro Gln Cys Val Asp Asp Val Leu Ser Val Asp Ala Asn
370 375 380

Ala Arg Glu Val Ala Arg Lys Glu Val Met Arg Leu Ala Ser
385 390 395

<210> 34
<211> 236
<212> PRT
<213> Escherichia coli

<400> 34

Met Ala Thr Thr His Leu Asp Val Cys Ala Val Val Pro Ala Ala Gly
1 5 10 15

Phe Gly Arg Arg Met Gln Thr Glu Cys Pro Lys Gln Tyr Leu Ser Ile
20 25 30

Gly Asn Gln Thr Ile Leu Glu His Ser Val His Ala Leu Leu Ala His
35 40 45

Pro Arg Val Lys Arg Val Val Ile Ala Ile Ser Pro Gly Asp Ser Arg
50 55 60

Phe Ala Gln Leu Pro Leu Ala Asn His Pro Arg Ile Thr Val Val Asp
65 70 75 80

Gly Gly Glu Glu Arg Ala Asp Ser Val Leu Ala Gly Leu Lys Ala Ala
85 90 95

Gly Asp Ala Gln Trp Val Leu Val His Asp Ala Ala Arg Pro Cys Leu
100 105 110

His Gln Asp Asp Leu Ala Arg Leu Leu Ala Leu Ser Glu Thr Ser Arg
115 120 125

Thr Gly Gly Ile Leu Ala Ala Pro Val Arg Asp Thr Met Lys Arg Ala
130 135 140

Glu Pro Gly Lys Asn Ala Ile Ala His Thr Val Asp Arg Asn Gly Leu
145 150 155 160

Trp His Ala Leu Thr Pro Gln Phe Phe Pro Arg Glu Leu Leu His Asp
165 170 175

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

Ser Ala Leu Glu Tyr Cys Gly Phe His Pro Gln Leu Val Glu Gly Arg
195 200 205

Ala Asp Asn Ile Lys Val Thr Arg Pro Glu Asp Leu Ala Leu Ala Glu
210 215 220

Phe Tyr Leu Thr Arg Thr Ile His Gln Glu Asn Thr
225 230 235

<210> 35
<211> 283
<212> PRT
<213> Escherichia coli

<400> 35

Met Arg Thr Gln Trp Pro Ser Pro Ala Lys Leu Asn Leu Phe Leu Tyr
1 5 10 15

Ile Thr Gly Gln Arg Ala Asp Gly Tyr His Thr Leu Gln Thr Leu Phe
20 25 30

Gln Phe Leu Asp Tyr Gly Asp Thr Ile Ser Ile Glu Leu Arg Asp Asp
35 40 45

Gly Asp Ile Arg Leu Leu Thr Pro Val Glu Gly Val Glu His Glu Asp
50 55 60

Asn Leu Ile Val Arg Ala Ala Arg Leu Leu Met Lys Thr Ala Ala Asp
65 70 75 80

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

Arg Leu Pro Met Gly Gly Gly Leu Gly Gly Gly Ser Ser Asn Ala Ala
100 105 110

Thr Val Leu Val Ala Leu Asn His Leu Trp Gln Cys Gly Leu Ser Met
115 120 125

Asp Glu Leu Ala Glu Met Gly Leu Thr Leu Gly Ala Asp Val Pro Val
130 135 140

Phe Val Arg Gly His Ala Ala Phe Ala Glu Gly Val Gly Glu Ile Leu
145 150 155 160

Thr Pro Val Asp Pro Pro Glu Lys Trp Tyr Leu Val Ala His Pro Gly
165 170 175

Val Ser Ile Pro Thr Pro Val Ile Phe Lys Asp Pro Glu Leu Pro Arg
180 185 190

Asn Thr Pro Lys Arg Ser Ile Glu Thr Leu Leu Lys Cys Glu Phe Ser
195 200 205

Asn Asp Cys Glu Val Ile Ala Arg Lys Arg Phe Arg Glu Val Asp Ala
210 215 220

Val Leu Ser Trp Leu Leu Glu Tyr Ala Pro Ser Arg Leu Thr Gly Thr
225 230 235 240

Gly Ala Cys Val Phe Ala Glu Phe Asp Thr Glu Ser Glu Ala Arg Gln
245 250 255

Val Leu Glu Gln Ala Pro Glu Trp Leu Asn Gly Phe Val Ala Lys Gly
260 265 270

Ala Asn Leu Ser Pro Leu His Arg Ala Met Leu
275 280

<210> 36
<211> 159
<212> PRT
<213> Escherichia coli

<400> 36

Met Arg Ile Gly His Gly Phe Asp Val His Ala Phe Gly Gly Glu Gly
1 5 10 15

Pro Ile Ile Ile Gly Gly Val Arg Ile Pro Tyr Glu Lys Gly Leu Leu
20 25 30

Ala His Ser Asp Gly Asp Val Val Leu His Ala Leu Thr Asp Ala Leu
35 40 45

Leu Gly Ala Ala Ala Leu Gly Asp Ile Gly Lys Leu Phe Pro Asp Thr
50 55 60

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

Trp Arg Arg Ile Gln Ala Lys Gly Tyr Ala Leu Gly Asn Val Asp Val
85 90 95

Thr Ile Ile Ala Gln Ala Pro Arg Met Leu Pro His Ile Pro Gln Met
100 105 110

Arg Val Phe Ile Ala Glu Asp Leu Gly Cys His Met Asp Asp Val Asn
115 120 125

Val Lys Ala Thr Thr Thr Glu Lys Leu Gly Phe Thr Gly Arg Gly Glu
130 135 140

Gly Ile Ala Cys Glu Ala Val Ala Leu Leu Ile Lys Ala Thr Lys
145 150 155

<210> 37

<211> 372

<212> PRT

<213> Escherichia coli

<400> 37

Met His Asn Gln Ala Pro Ile Gln Arg Arg Lys Ser Thr Arg Ile Tyr
1 5 10 15

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

Met Thr Asn Thr Arg Thr Thr Asp Val Glu Ala Thr Val Asn Gln Ile
35 40 45

Lys Ala Leu Glu Arg Val Gly Ala Asp Ile Val Arg Val Ser Val Pro
50 55 60

Thr Met Asp Ala Ala Glu Ala Phe Lys Leu Ile Lys Gln Gln Val Asn
65 70 75 80

Val Pro Leu Val Ala Asp Ile His Phe Asp Tyr Arg Ile Ala Leu Lys
85 90 95

Val Ala Glu Tyr Gly Val Asp Cys Leu Arg Ile Asn Pro Gly Asn Ile
100 105 110

Gly Asn Glu Glu Arg Ile Arg Met Val Val Asp Cys Ala Arg Asp Lys
115 120 125

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

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

Ala Met Arg His Val Asp His Leu Asp Arg Leu Asn Phe Asp Gln Phe
165 170 175

Lys Val Ser Val Lys Ala Ser Asp Val Phe Leu Ala Val Glu Ser Tyr
180 185 190

Arg Leu Leu Ala Lys Gln Ile Asp Gln Pro Leu His Leu Gly Ile Thr
195 200 205

Glu Ala Gly Gly Ala Arg Ser Gly Ala Val Lys Ser Ala Ile Gly Leu
210 215 220

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

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

Ser Leu Arg Ile Arg Ser Arg Gly Ile Asn Phe Ile Ala Cys Pro Thr
260 265 270

Cys Ser Arg Gln Glu Phe Asp Val Ile Gly Thr Val Asn Ala Leu Glu
275 280 285

Gln Arg Leu Glu Asp Ile Ile Thr Pro Met Asp Val Ser Ile Ile Gly
290 295 300

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

Thr Gly Gly Asn Lys Lys Ser Gly Leu Tyr Glu Asp Gly Val Arg Lys
325 330 335

Asp Arg Leu Asp Asn Asn Asp Met Ile Asp Gln Leu Glu Ala Arg Ile
340 345 350

Arg Ala Lys Ala Ser Gln Leu Asp Glu Ala Arg Arg Ile Asp Val Gln
355 360 365

Gln Val Glu Lys
370

<210> 38
<211> 316
<212> PRT
<213> Escherichia coli

<400> 38

Met Gln Ile Leu Leu Ala Asn Pro Arg Gly Phe Cys Ala Gly Val Asp
1 5 10 15

Arg Ala Ile Ser Ile Val Glu Asn Ala Leu Ala Ile Tyr Gly Ala Pro
20 25 30

Ile Tyr Val Arg His Glu Val Val His Asn Arg Tyr Val Val Asp Ser
35 40 45

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

Asp Gly Ala Ile Leu Ile Phe Ser Ala His Gly Val Ser Gln Ala Val
65 70 75 80

Arg Asn Glu Ala Lys Ser Arg Asp Leu Thr Val Phe Asp Ala Thr Cys
85 90 95

Pro Leu Val Thr Lys Val His Met Glu Val Ala Arg Ala Ser Arg Arg
100 105 110

Gly Glu Glu Ser Ile Leu Ile Gly His Ala Gly His Pro Glu Val Glu
115 120 125

Gly Thr Met Gly Gln Tyr Ser Asn Pro Glu Gly Gly Met Tyr Leu Val
130 135 140

Glu Ser Pro Asp Asp Val Trp Lys Leu Thr Val Lys Asn Glu Glu Lys
145 150 155 160

Leu Ser Phe Met Thr Gln Thr Thr Leu Ser Val Asp Asp Thr Ser Asp
165 170 175

Val Ile Asp Ala Leu Arg Lys Arg Phe Pro Lys Ile Val Gly Pro Arg
180 185 190

Lys Asp Asp Ile Cys Tyr Ala Thr Thr Asn Arg Gln Glu Ala Val Arg
195 200 205

Ala Leu Ala Glu Gln Ala Glu Val Val Leu Val Val Gly Ser Lys Asn
210 215 220

Ser Ser Asn Ser Asn Arg Leu Ala Glu Leu Ala Gln Arg Met Gly Lys
225 230 235 240

Arg Ala Phe Leu Ile Asp Asp Ala Thr Asp Ile Gln Glu Glu Trp Val
245 250 255

Lys Glu Ala Lys Cys Val Gly Val Thr Ala Gly Ala Ser Ala Pro Asp
260 265 270

Ile Leu Val Gln Asn Val Val Ala Arg Leu Gln Gln Leu Gly Gly Gly
275 280 285

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

Pro Lys Glu Leu Arg Val Asp Ile Arg Glu Val Asp
305 310 315

<210> 39

<211> 182

<212> PRT

<213> Escherichia coli

<400> 39

Met Gln Thr Glu His Val Ile Leu Leu Asn Ala Gln Gly Val Pro Thr
1 5 10 15

Gly Thr Leu Glu Lys Tyr Ala Ala His Thr Ala Asp Thr Arg Leu His
20 25 30

Leu Ala Phe Ser Ser Trp Leu Phe Asn Ala Lys Gly Gln Leu Leu Val
35 40 45

Thr Arg Arg Ala Leu Ser Lys Lys Ala Trp Pro Gly Val Trp Thr Asn
50 55 60

Ser Val Cys Gly His Pro Gln Leu Gly Glu Ser Asn Glu Asp Ala Val
65 70 75 80

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

Ser Ile Tyr Pro Asp Phe Arg Tyr Arg Ala Thr Asp Pro Ser Gly Ile
100 105 110

Val Glu Asn Glu Val Cys Pro Val Phe Ala Ala Arg Thr Thr Ser Ala
115 120 125

Leu Gln Ile Asn Asp Asp Glu Val Met Asp Tyr Gln Trp Cys Asp Leu
130 135 140

Ala Asp Val Leu His Gly Ile Asp Ala Thr Pro Trp Ala Phe Ser Pro
145 150 155 160

Trp Met Val Met Gln Ala Thr Asn Arg Glu Ala Arg Lys Arg Leu Ser
165 170 175

Ala Phe Thr Gln Leu Lys
180

<210> 40
<211> 299
<212> PRT
<213> Escherichia coli

<400> 40

Met Asp Phe Pro Gln Gln Leu Glu Ala Cys Val Lys Gln Ala Asn Gln
1 5 10 15

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

20

25

30

Val Glu Thr Met Gln Tyr Gly Ala Leu Leu Gly Gly Lys Arg Leu Arg
 35 40 45

Pro Phe Leu Val Tyr Ala Thr Gly His Met Phe Gly Val Ser Thr Asn
 50 55 60

Thr Leu Asp Ala Pro Ala Ala Val Glu Cys Ile His Ala Tyr Ser
 65 70 75 80

Leu Ile His Asp Asp Leu Pro Ala Met Asp Asp Asp Asp Leu Arg Arg
 85 90 95

Gly Leu Pro Thr Cys His Val Lys Phe Gly Glu Ala Asn Ala Ile Leu
 100 105 110

Ala Gly Asp Ala Leu Gln Thr Leu Ala Phe Ser Ile Leu Ser Asp Ala
 115 120 125

Asp Met Pro Glu Val Ser Asp Arg Asp Arg Ile Ser Met Ile Ser Glu
 130 135 140

Leu Ala Ser Ala Ser Gly Ile Ala Gly Met Cys Gly Gly Gln Ala Leu
 145 150 155 160

Asp Leu Asp Ala Glu Gly Lys His Val Pro Leu Asp Ala Leu Glu Arg
 165 170 175

Ile His Arg His Lys Thr Gly Ala Leu Ile Arg Ala Ala Val Arg Leu
 180 185 190

Gly Ala Leu Ser Ala Gly Asp Lys Gly Arg Arg Ala Leu Pro Val Leu
 195 200 205

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

Ile Leu Asp Val Val Gly Asp Thr Ala Thr Leu Gly Lys Arg Gln Gly
 225 230 235 240

Ala Asp Gln Gln Leu Gly Lys Ser Thr Tyr Pro Ala Leu Leu Gly Leu
245 250 255

Glu Gln Ala Arg Lys Lys Ala Arg Asp Leu Ile Asp Asp Ala Arg Gln
260 265 270

Ser Leu Lys Gln Leu Ala Glu Gln Ser Leu Asp Thr Ser Ala Leu Glu
275 280 285

Ala Leu Ala Asp Tyr Ile Ile Gln Arg Asn Lys
290 295

<210> 41
<211> 1083
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 41
atgaagctac taaccttccc aggtcaaggg acctccatct ccatttcgat attaaaagcg 60
ataataagaa acaaatcaag agaattccaa acaataactga gtcagaacgg caaggaatca 120
aatgatctat tgcagtacat cttccagaac cttccagcc ccggaagcat tgcagtctgc 180
tccaaccttt tctatcaatt gtaccagata ctctcgaatc cttctgatcc tcaagatcaa 240
gcaccaaaaa atatgactaa gatcgattcc cccgacaaga aagacaatga acaatgttac 300
cttttgggtc actcgctagg cgagttaaca tgtctgagtg ttaattcact gttttcgtta 360
aaggatcttt ttgatattgc taattttaga aataagttaa tggtaacatc tactgaaaag 420
tacttagtag ccacacaatat caacagatcc aacaaatttg aaatgtgggc actctcttct 480
ccgagggcca cagatttacc gcaagaagtg caaaaactac taaattcccc taatttatta 540
tcatcttcac aaaataccat ttctgtagca aatgcaaatt cagtaaagca atgtgtagtc 600
accggtctgg ttgatgattt agagtcctta agaacagaat tgaacttaag gttcccgcgt 660
ttaagaatta cagaattaac taaccatac aacatcccct tccataatag cactgtgttg 720
aggcccgttc aggaaccact ctatgactac atttgggata tattaaagaa aaacggaact 780
cacacgttga tggagttgaa ccatccaata atagctaact tagatggtaa tatatcttac 840
tatattcatc atgccctaga tagattcggt aagtgttcaa gcaggactgt gcaattcacc 900
atgtgttatg ataccataaa ctctggaacc ccagtggaaa ttgataagag tatttgcttt 960

ggcccgggca atgtgattta taaccttatt cggagaaatt gtccccaagt ggacactata 1020
gaatacacct ctttagcaac tatagacgct tatcacaagg cggcagagga gaacaaagat 1080
tga 1083

<210> 42
<211> 360
<212> PRT
<213> *Saccharomyces cerevisiae*
<400> 42

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

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

Leu Ser Gln Asn Gly Lys Glu Ser Asn Asp Leu Leu Gln Tyr Ile Phe
35 40 45

Gln Asn Pro Ser Ser Pro Gly Ser Ile Ala Val Cys Ser Asn Leu Phe
50 55 60

Tyr Gln Leu Tyr Gln Ile Leu Ser Asn Pro Ser Asp Pro Gln Asp Gln
65 70 75 80

Ala Pro Lys Asn Met Thr Lys Ile Asp Ser Pro Asp Lys Lys Asp Asn
85 90 95

Glu Gln Cys Tyr Leu Leu Gly His Ser Leu Gly Glu Leu Thr Cys Leu
100 105 110

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

Phe Arg Asn Lys Leu Met Val Thr Ser Thr Glu Lys Tyr Leu Val Ala
130 135 140

His Asn Ile Asn Arg Ser Asn Lys Phe Glu Met Trp Ala Leu Ser Ser
145 150 155 160

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

Pro Asn Leu Leu Ser Ser Ser Gln Asn Thr Ile Ser Val Ala Asn Ala
180 185 190

Asn Ser Val Lys Gln Cys Val Val Thr Gly Leu Val Asp Asp Leu Glu
195 200 205

Ser Leu Arg Thr Glu Leu Asn Leu Arg Phe Pro Arg Leu Arg Ile Thr
210 215 220

Glu Leu Thr Asn Pro Tyr Asn Ile Pro Phe His Asn Ser Thr Val Leu
225 230 235 240

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

Lys Asn Gly Thr His Thr Leu Met Glu Leu Asn His Pro Ile Ile Ala
260 265 270

Asn Leu Asp Gly Asn Ile Ser Tyr Tyr Ile His His Ala Leu Asp Arg
275 280 285

Phe Val Lys Cys Ser Ser Arg Thr Val Gln Phe Thr Met Cys Tyr Asp
290 295 300

Thr Ile Asn Ser Gly Thr Pro Val Glu Ile Asp Lys Ser Ile Cys Phe
305 310 315 320

Gly Pro Gly Asn Val Ile Tyr Asn Leu Ile Arg Arg Asn Cys Pro Gln
325 330 335

Val Asp Thr Ile Glu Tyr Thr Ser Leu Ala Thr Ile Asp Ala Tyr His
340 345 350

Lys Ala Ala Glu Glu Asn Lys Asp
355 360

<211> 1191
<212> DNA
<213> Artificial Sequence

<220>

<223> Artificial beta-ketothiolase (BktB) nucleotide sequence

<400> 43

```
atgactagag aagttgtcgt cgtttccggt gtccgtaccg ctatcggtac tttcgggtggt      60
tccttaaagg atgttgctcc tgctgaattg ggtgcttttag ttgttagaga agctttggcc      120
agagcccaag tctccggtga cgacgttggt cacgtcgttt tcggtaacgt catccaaact      180
gaaccacgtg acatgtactt gggtagagtc gccgctgtta acggtggtgt caccatcaac      240
gctcctgcct taactgttaa cagattatgt ggttccggtt tacaagctat tgtctctgcc      300
gccccaaacta tcttgttggg tgatactgac gttgctattg gtggtggtgc tgaatctatg      360
tctagagctc catacttggc tccagctgcc cgttgggggtg ctagaatggg tgacgccggt      420
ttggtcgata tgatgttggg tgccttgcac gatcctttcc acagaatcca catgggtggt      480
accgctgaaa acgttgctaa ggaatacgat atctctagag ctcaacaaga tgaagccgct      540
ttagaatctc acagacgtgc ctccgccgct attaaggctg gttacttcaa ggaccaaatt      600
gttccagttg tctctaaggg tcgtaaaggt gatgttacct ttgatactga cgaacacgtt      660
agacacgacg ccactattga cgatatgact aaattaagac cagtctttgt taaggagaat      720
ggtagcgtta ctgctggtaa cgcttctggt ttgaacgatg ccgccgctgc cgttgttatg      780
atggaaagag ctgaagccga aagacgtggt ttaaagccat tggccagatt agtctcctac      840
ggtcacgctg gtgtcgaccc aaaggctatg ggtatcggtc cagttcctgc tactaagatt      900
gctttagaaa gagctggttt gcaagtttct gacttggacg tcacgaagc caacgaagcc      960
ttcgctgctc aagcttgtgc tgtcaccaag gctttgggtt tggatccagc taaagttaac     1020
cctaattggt ctggtatttc cttgggtcac ccaatcggtg ctaccggtgc tttaatcact     1080
gttaaagcct tacacgaatt gaacagagtt caaggtagat acgctttggt cactatgtgc     1140
atcgggtggt gtcaaggat cgctgctatc ttcgaaagaa tcggatccta a              1191
```

<210> 44
<211> 396
<212> PRT
<213> Artificial Sequence

<220>

<223> Engineered beta-ketothiolase (BktB)

<400> 44

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

Thr Phe Gly Gly Ser Leu Lys Asp Val Ala Pro Ala Glu Leu Gly Ala
20 25 30

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

Val Gly His Val Val Phe Gly Asn Val Ile Gln Thr Glu Pro Arg Asp
50 55 60

Met Tyr Leu Gly Arg Val Ala Ala Val Asn Gly Gly Val Thr Ile Asn
65 70 75 80

Ala Pro Ala Leu Thr Val Asn Arg Leu Cys Gly Ser Gly Leu Gln Ala
85 90 95

Ile Val Ser Ala Ala Gln Thr Ile Leu Leu Gly Asp Thr Asp Val Ala
100 105 110

Ile Gly Gly Gly Ala Glu Ser Met Ser Arg Ala Pro Tyr Leu Ala Pro
115 120 125

Ala Ala Arg Trp Gly Ala Arg Met Gly Asp Ala Gly Leu Val Asp Met
130 135 140

Met Leu Gly Ala Leu His Asp Pro Phe His Arg Ile His Met Gly Val
145 150 155 160

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

Asp Glu Ala Ala Leu Glu Ser His Arg Arg Ala Ser Ala Ala Ile Lys
180 185 190

Ala Gly Tyr Phe Lys Asp Gln Ile Val Pro Val Val Ser Lys Gly Arg

195

200

205

Lys Gly Asp Val Thr Phe Asp Thr Asp Glu His Val Arg His Asp Ala
 210 215 220

Thr Ile Asp Asp Met Thr Lys Leu Arg Pro Val Phe Val Lys Glu Asn
 225 230 235 240

Gly Thr Val Thr Ala Gly Asn Ala Ser Gly Leu Asn Asp Ala Ala Ala
 245 250 255

Ala Val Val Met Met Glu Arg Ala Glu Ala Glu Arg Arg Gly Leu Lys
 260 265 270

Pro Leu Ala Arg Leu Val Ser Tyr Gly His Ala Gly Val Asp Pro Lys
 275 280 285

Ala Met Gly Ile Gly Pro Val Pro Ala Thr Lys Ile Ala Leu Glu Arg
 290 295 300

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

Phe Ala Ala Gln Ala Cys Ala Val Thr Lys Ala Leu Gly Leu Asp Pro
 325 330 335

Ala Lys Val Asn Pro Asn Gly Ser Gly Ile Ser Leu Gly His Pro Ile
 340 345 350

Gly Ala Thr Gly Ala Leu Ile Thr Val Lys Ala Leu His Glu Leu Asn
 355 360 365

Arg Val Gln Gly Arg Tyr Ala Leu Val Thr Met Cys Ile Gly Gly Gly
 370 375 380

Gln Gly Ile Ala Ala Ile Phe Glu Arg Ile Gly Ser
 385 390 395

<210> 45

<211> 858

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial PaaH1: 3-hydroxyacyl-CoA dehydrogenase nucleotide sequence

<400> 45

atgtccatca gaactgtcgg tattgttggt gctggtacta tgggtaacgg tattgctcaa	60
gcctgtgctg tcgtcggttt gaacgtcgtc atggtcgaca tttctgacgc tgctgttcaa	120
aagggtgttg ctactgtcgc ttcctctttg gacagattaa ttaagaagga aaagttgacc	180
gaagccgaca aggcctctgc cttggccaga attaagggtt ccacttctta tgacgacttg	240
aaagctaccg acattgttat cgaagctgct actgaaaact acgatttgaa agttaagatc	300
ttgaagcaaa ttgatggtat cgtcggtag aacgtcatta ttgcttctaa cacttcctcc	360
atttctatca ctaaattagc cgccgtcacc tctagagccg acagatttat cggtatgcac	420
ttctttaatc cagttccagt catggctttg gtcgaattaa ttagagggtt gcaaacctcc	480
gacaccaccc acgccgccgt tgaagctttg tctaagcaat tgggtaagta cccaatcacc	540
gttaaaaatt cccaggttt cgttgtcaac cgtattttgt gcccaatgat caatgaagct	600
ttctgtgtct tgggtgaggg tttggcctcc ccagaagaaa tcgatgaagg tatgaagtta	660
ggttgtaacc accctattgg tccttttagc ttggccgaca tgatcggttt agacactatg	720
ttggccgtta tggaagtctt gtacactgaa ttcgctgacc caaagtacag accagctatg	780
ttaatgagag aaatggttgc tgccggttat ttgggtagaa agactggtcg tggtgtttat	840
gtctactcta aagggatc	858

<210> 46

<211> 286

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered PaaH1: 3-hydroxyacyl-CoA dehydrogenase

<400> 46

Met	Ser	Ile	Arg	Thr	Val	Gly	Ile	Val	Gly	Ala	Gly	Thr	Met	Gly	Asn
1				5				10					15		

Gly	Ile	Ala	Gln	Ala	Cys	Ala	Val	Val	Gly	Leu	Asn	Val	Val	Met	Val
			20					25				30			

Asp Ile Ser Asp Ala Ala Val Gln Lys Gly Val Ala Thr Val Ala Ser
35 40 45

Ser Leu Asp Arg Leu Ile Lys Lys Glu Lys Leu Thr Glu Ala Asp Lys
50 55 60

Ala Ser Ala Leu Ala Arg Ile Lys Gly Ser Thr Ser Tyr Asp Asp Leu
65 70 75 80

Lys Ala Thr Asp Ile Val Ile Glu Ala Ala Thr Glu Asn Tyr Asp Leu
85 90 95

Lys Val Lys Ile Leu Lys Gln Ile Asp Gly Ile Val Gly Glu Asn Val
100 105 110

Ile Ile Ala Ser Asn Thr Ser Ser Ile Ser Ile Thr Lys Leu Ala Ala
115 120 125

Val Thr Ser Arg Ala Asp Arg Phe Ile Gly Met His Phe Phe Asn Pro
130 135 140

Val Pro Val Met Ala Leu Val Glu Leu Ile Arg Gly Leu Gln Thr Ser
145 150 155 160

Asp Thr Thr His Ala Ala Val Glu Ala Leu Ser Lys Gln Leu Gly Lys
165 170 175

Tyr Pro Ile Thr Val Lys Asn Ser Pro Gly Phe Val Val Asn Arg Ile
180 185 190

Leu Cys Pro Met Ile Asn Glu Ala Phe Cys Val Leu Gly Glu Gly Leu
195 200 205

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

Pro Ile Gly Pro Leu Ala Leu Ala Asp Met Ile Gly Leu Asp Thr Met
225 230 235 240

Leu Ala Val Met Glu Val Leu Tyr Thr Glu Phe Ala Asp Pro Lys Tyr
245 250 255

Arg Pro Ala Met Leu Met Arg Glu Met Val Ala Ala Gly Tyr Leu Gly
260 265 270

Arg Lys Thr Gly Arg Gly Val Tyr Val Tyr Ser Lys Gly Ile
275 280 285

<210> 47
<211> 792
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial crotonase (Crt) nucleotide sequence

<400> 47
atggaattga acaacgttat tttggaaaag gaaggtaagg tcgctgtcgt tactatcaac 60
agaccaaagg ctttaaacgc tttgaactct gacaccttga aagaaatgga ttatgtttatc 120
ggtgaaatcg aaaatgactc tgaagttttg gccgttatct tgactgggtgc tggtgaaaaa 180
tctttcgttg ctgggtctga cttttctgaa atgaaggaga tgaataccat tgaaggtaga 240
aagttcggtg tcttgggtaa caaggttttt agaagattgg aattgttgga aaaaccagtc 300
atcgctgctg ttaacggttt cgcttttaggt ggtggttgtg aaatcgctat gtcctgtgac 360
attcgtatcg cctcctcaa tgctagattc ggtcaaccag aagttggttt aggtattact 420
ccaggtttcg gtggtacca aagattgtct agattggctg gtatgggtat ggctaagcaa 480
ttaattttca ctgctcaaaa cattaaggct gatgaagcct tacgtattgg tttggtcaac 540
aaggtcgttg aaccatctga attgatgaat accgctaagg aaattgctaa caaaattggt 600
tctaattgcc cagttgctgt caagttgtcc aagcaagcta ttaacagagg tatgcaatgt 660
gatattgaca ctgctttggc tttcgaatcc gaagcttttg gtgaatgttt ttctaccgaa 720
gatcaaaagg atgctatgac cgctttcatc gagaagagaa agatcgaagg tttcaaaaac 780
agaggatcct aa 792

<210> 48
<211> 263
<212> PRT
<213> Artificial Sequence

<220>

<223> Engineered crotonase (Crt)

<400> 48

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

Val Thr Ile Asn Arg Pro Lys Ala Leu Asn Ala Leu Asn Ser Asp Thr
20 25 30

Leu Lys Glu Met Asp Tyr Val Ile Gly Glu Ile Glu Asn Asp Ser Glu
35 40 45

Val Leu Ala Val Ile Leu Thr Gly Ala Gly Glu Lys Ser Phe Val Ala
50 55 60

Gly Ala Asp Ile Ser Glu Met Lys Glu Met Asn Thr Ile Glu Gly Arg
65 70 75 80

Lys Phe Gly Ile Leu Gly Asn Lys Val Phe Arg Arg Leu Glu Leu Leu
85 90 95

Glu Lys Pro Val Ile Ala Ala Val Asn Gly Phe Ala Leu Gly Gly Gly
100 105 110

Cys Glu Ile Ala Met Ser Cys Asp Ile Arg Ile Ala Ser Ser Asn Ala
115 120 125

Arg Phe Gly Gln Pro Glu Val Gly Leu Gly Ile Thr Pro Gly Phe Gly
130 135 140

Gly Thr Gln Arg Leu Ser Arg Leu Val Gly Met Gly Met Ala Lys Gln
145 150 155 160

Leu Ile Phe Thr Ala Gln Asn Ile Lys Ala Asp Glu Ala Leu Arg Ile
165 170 175

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

Lys Glu Ile Ala Asn Lys Ile Val Ser Asn Ala Pro Val Ala Val Lys
195 200 205

Leu Ser Lys Gln Ala Ile Asn Arg Gly Met Gln Cys Asp Ile Asp Thr
210 215 220

Ala Leu Ala Phe Glu Ser Glu Ala Phe Gly Glu Cys Phe Ser Thr Glu
225 230 235 240

Asp Gln Lys Asp Ala Met Thr Ala Phe Ile Glu Lys Arg Lys Ile Glu
245 250 255

Gly Phe Lys Asn Arg Gly Ser
260

<210> 49

<211> 1200

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial Ter: trans-2-enoyl-CoA reductase nucleotide sequence

<400> 49

atgattgtca aaccaatggt tcgtaacaac atttgtttta atgccacccc acaaggttgt 60

aagaagggtg ttgaagatca aatcgaatac actaaaaaga gaattaccgc tgaagttaaa 120

gctggtgcta aggcccaaaa gaacgttttg gttttgggtt gttccaacgg ttacggtttg 180

gcctccagaa ttactgctgc ttttggttac ggtgccgcta ccatcggtgt ctctttcgaa 240

aaggccggtt ccgaaactaa gtacgttact ccaggttggt acaataactt ggctttcgat 300

gaagctgcta agagagaagg tttgtattcc gttactattg acggtgatgc cttttctgac 360

gaaatcaaag ctcaagtcac cgaagaagcc aaaaagaaag gtatcaagtt cgatttgatt 420

gtctactctt tagcctctcc tgtagaact gatccagata ctggtattat gcacaaatcc 480

gttttgaagc cattcggtaa gaccttcact ggtaaaactg tcgatacctt cactggtgaa 540

ttaaaggaaa tctctgctga acctgccaac gacgaagaag ctgctgccac tgtaaggtt 600

atgggtggtg aagactggga aagatggatc aagcaattat ctaaggaagg tttgttgtaa 660

gaaggttgta tcaccttggc ttactcttac atcggccag aagctacca agctttgtac 720

agaaagggtg ccattggtaa ggctaaagaa cacttgagg ctactgctca tagattgaac 780

aaggaaaatc catccatcag agcctttgtt tccgtcaata aaggtttggt cactagagcc	840
tctgccgtca ttccagttat ccctttatac ttggcttctt tgtttaaagt catgaaggaa	900
aagggtaacc atgaagggtg tatcgaacaa atcactcgtt tgtacgctga acgtttatac	960
agaaaggacg gtaccatccc tgtcgaatgaa gaaaacagaa tcagaatcga cgattgggaa	1020
ttggaagaag atgttcaaaa agccgtttcc gccttgatgg aaaaggtcac cggtgaaaat	1080
gccgaatcct tgactgactt agctgggttac agacatgact ttttagcttc taatggtttc	1140
gatgttgaag gtattaacta tgaggctgaa gtcgaaagat ttgacagaat cggatcctaa	1200

<210> 50
 <211> 399
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Engineered Ter: trans-2-enoyl-CoA reductase

<400> 50

Met	Ile	Val	Lys	Pro	Met	Val	Arg	Asn	Asn	Ile	Cys	Leu	Asn	Ala	His
1				5					10					15	

Pro	Gln	Gly	Cys	Lys	Lys	Gly	Val	Glu	Asp	Gln	Ile	Glu	Tyr	Thr	Lys
			20					25					30		

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

Val	Leu	Val	Leu	Gly	Cys	Ser	Asn	Gly	Tyr	Gly	Leu	Ala	Ser	Arg	Ile
	50					55					60				

Thr	Ala	Ala	Phe	Gly	Tyr	Gly	Ala	Ala	Thr	Ile	Gly	Val	Ser	Phe	Glu
65					70					75					80

Lys	Ala	Gly	Ser	Glu	Thr	Lys	Tyr	Gly	Thr	Pro	Gly	Trp	Tyr	Asn	Asn
				85					90					95	

Leu	Ala	Phe	Asp	Glu	Ala	Ala	Lys	Arg	Glu	Gly	Leu	Tyr	Ser	Val	Thr
			100					105						110	

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

Glu Ala Lys Lys Lys Gly Ile Lys Phe Asp Leu Ile Val Tyr Ser Leu
130 135 140

Ala Ser Pro Val Arg Thr Asp Pro Asp Thr Gly Ile Met His Lys Ser
145 150 155 160

Val Leu Lys Pro Phe Gly Lys Thr Phe Thr Gly Lys Thr Val Asp Pro
165 170 175

Phe Thr Gly Glu Leu Lys Glu Ile Ser Ala Glu Pro Ala Asn Asp Glu
180 185 190

Glu Ala Ala Ala Thr Val Lys Val Met Gly Gly Glu Asp Trp Glu Arg
195 200 205

Trp Ile Lys Gln Leu Ser Lys Glu Gly Leu Leu Glu Glu Gly Cys Ile
210 215 220

Thr Leu Ala Tyr Ser Tyr Ile Gly Pro Glu Ala Thr Gln Ala Leu Tyr
225 230 235 240

Arg Lys Gly Thr Ile Gly Lys Ala Lys Glu His Leu Glu Ala Thr Ala
245 250 255

His Arg Leu Asn Lys Glu Asn Pro Ser Ile Arg Ala Phe Val Ser Val
260 265 270

Asn Lys Gly Leu Val Thr Arg Ala Ser Ala Val Ile Pro Val Ile Pro
275 280 285

Leu Tyr Leu Ala Ser Leu Phe Lys Val Met Lys Glu Lys Gly Asn His
290 295 300

Glu Gly Cys Ile Glu Gln Ile Thr Arg Leu Tyr Ala Glu Arg Leu Tyr
305 310 315 320

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

Asp Asp Trp Glu Leu Glu Glu Asp Val Gln Lys Ala Val Ser Ala Leu
340 345 350

Met Glu Lys Val Thr Gly Glu Asn Ala Glu Ser Leu Thr Asp Leu Ala
355 360 365

Gly Tyr Arg His Asp Phe Leu Ala Ser Asn Gly Phe Asp Val Glu Gly
370 375 380

Ile Asn Tyr Glu Ala Glu Val Glu Arg Phe Asp Arg Ile Gly Ser
385 390 395

<210> 51
<211> 812
<212> DNA
<213> Artificial Sequence

<220>
<223> Truncated 3-hydroxy-3-methyl-glutaryl-CoA reductase (tHMG1)

<400> 51
atggcgcgtg accaattggt gaaaactgaa gtcaccaaga agtcttttac tgctcctgta 60
caaaaggctt ctacaccagt tttaaccaat aaaacagtca tttctggatc gaaagtcaaa 120
agtttatcat ctgcgcaatc gagctcatca ggaccttcac catctagtga ggaagatgat 180
tcccgcgata ttgaaagctt ggataagaaa atacgtcctt tagaagaatt agaagcatta 240
ttaagtagtg gaaatacaaa acaattgaag aacaaagagg tcgctgcctt ggttattcac 300
ggtaagttac ctttgtacgc tttggagaaa aaattaggtg atactacgag agcggttgcg 360
gtacgtagga aggctctttc aattttggca gaagctcctg tattagcatc tgatcgttta 420
ccatataaaa attatgacta cgaccgcgta tttggcgctt gttgtgaaaa tgttataggt 480
tacatgcctt tgcccgttgg tgttatagga cccttggtta tcgatggtag atcttatcat 540
ataccaatgg caactacaga gggttgtttg gtagcttctg ccatgcgtgg ctgtaaggca 600
atcaatgctg gcggtggtgc aacaactgtt ttaactaagg atggtagtac aagaggccca 660
gtagtccgtt tccaactttt gaaaagatct ggtgcctgta agatatgggt agactcagaa 720
gagggacaaa acgcaattaa aaaagctttt aactctacat caagatttgc acgtctgcaa 780
catattcaaa cttgtctagc aggagatttg tt 812

<210> 52
 <211> 270
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Truncated 3-hydroxy-3-methyl-glutaryl-CoA reductase (tHMG1)

 <400> 52

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

Thr Ala Pro Val Gln Lys Ala Ser Thr Pro Val Leu Thr Asn Lys Thr
 20 25 30

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

Ser Ser Gly Pro Ser Ser Ser Ser Glu Glu Asp Asp Ser Arg Asp Ile
 50 55 60

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

Leu Ser Ser Gly Asn Thr Lys Gln Leu Lys Asn Lys Glu Val Ala Ala
 85 90 95

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

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

Leu Ala Glu Ala Pro Val Leu Ala Ser Asp Arg Leu Pro Tyr Lys Asn
 130 135 140

Tyr Asp Tyr Asp Arg Val Phe Gly Ala Cys Cys Glu Asn Val Ile Gly
 145 150 155 160

Tyr Met Pro Leu Pro Val Gly Val Ile Gly Pro Leu Val Ile Asp Gly
 165 170 175

Thr Ser Tyr His Ile Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala
180 185 190

Ser Ala Met Arg Gly Cys Lys Ala Ile Asn Ala Gly Gly Gly Ala Thr
195 200 205

Thr Val Leu Thr Lys Asp Gly Met Thr Arg Gly Pro Val Val Arg Phe
210 215 220

Pro Thr Leu Lys Arg Ser Gly Ala Cys Lys Ile Trp Leu Asp Ser Glu
225 230 235 240

Glu Gly Gln Asn Ala Ile Lys Lys Ala Phe Asn Ser Thr Ser Arg Phe
245 250 255

Ala Arg Leu Gln His Ile Gln Thr Cys Leu Ala Gly Asp Leu
260 265 270

<210> 53
<211> 2412
<212> DNA
<213> Enterococcus sp.

<400> 53
atgaagactg tcgttatcat agatgccttg agaacaccaa tcggtaaata caaaggttca 60
ttatcccaag tttccgccgt tgacttaggt actcatgtta ctacacaatt gttgaagaga 120
cactccacaa tcagtgaaga aatcgatcaa gtcattttcg gtaacgtatt gcaagctggt 180
aatggtcaaa acccagccag acaaataagct atcaattctg gtttatcaca tgaaattcct 240
gctatgacag taaacgaagt ttgtggttca ggcattgaaag cagtcatttt ggccaagcaa 300
ttgatacaat taggtgaagc agaagtttta atcgccggtg gtatagaaaa catgagtcaa 360
gctccaaaat tgcaaagatt caattacgaa actgaatctt acgatgcacc tttctcttcg 420
atgatgtatg atggtttgac tgacgctttt tctggtcaag caatgggttt aacagctgaa 480
aatgtcgcag aaaagtacca tgtaaccaga gaagaacaag atcaattttc cgttcacagt 540
caattaaaag ctgcacaagc acaagccgaa ggtatttttc cgcacgaaat agctccattg 600
gaagtttctg gtacattagt cgaaaaggat gaaggtatta gacctaacct cagtgttgaa 660

aaattgggta ctttgaagac agtattcaag gaagacggta cagttaccgc tggtaatgcc	720
tctaccatta acgatgggtgc tagtgcattg attatagctt ctcaagaata tgccgaagct	780
catggtttgc catacttagc tatcattaga gatagtgtag aagttgggtat tgaccagca	840
tacatgggta tctctcctat aaaagcaatc caaaagttgt tagccagaaa ccaattgacc	900
actgaagaaa ttgatttgta cgaaattaac gaagcatttg ccgctacatc aatcgttgtc	960
caaagagaat tggcattgcc agaagaaaag gttaacatct atgggtgggtg tatctccttg	1020
ggtcacgcta taggtgcaac cggtgccaga ttgttgactt ccttaagtta ccaattgaac	1080
caaaaggaaa agaaatacgg tgttgcttct ttatgcattg gtgggtggtt gggttttagca	1140
atgttgttag aaagaccaca acaaaagaaa aattctagat tctaccaa atgtcccctgaa	1200
gaaagattgg cctcattgtt aaatgaaggc caaatttccg cagatactaa gaaagaattt	1260
gaaaacaccg ctttatcttc acaaatcgca aaccatatga tcgaaaacca aatctctgaa	1320
acagaagttc caatgggtgt cggtttgcac ttaactgtcg atgaaacaga ctatttggtg	1380
ccaatggcta ccgaagaacc tagtgttatc gcagccttat ctaatgggtc taagatagca	1440
caaggtttta agactgttaa ccaacaaaga ttgatgagag gtcaaatcgt attctacgat	1500
gttgctgacc cagaatcatt aatcgataag ttgcaagtaa gagaagccga agtttttcaa	1560
caagctgaat tgtcttacc ttcaatagtt aagagagggt gtgggttgag agatttgcaa	1620
tacagaactt ttgacgaatc cttcgtcagt gtagatttct tagttgatgt caaggacgcc	1680
atgggtgcta atattgttaa cgcaatgttg gaagggtgcg ccgaattgtt tagagaatgg	1740
ttcgctgaac aaaagatttt gttttctatc ttgtcaaact acgctacaga atctgtagtt	1800
accatgaaaa ctgcaattcc agtttccaga ttgagtaagg gttctaacgg tagagaaatc	1860
gctgaaaaga ttgttttggc atcaagatat gcctccttag acccttacag agctgttact	1920
cataataagg gtataatgaa cggtatcgaa gctgtcgtat tagcaaccgg taatgatact	1980
agagcagtat ctgcctcatg tcacgcattc gccgttaagg aaggtagata ccaaggtttg	2040
acatcatgga ccttggtatg tgaacaatta attggtgaaa tatccgttcc attggcttta	2100
gcaactgttg gtgggtgtac aaaagtcttg cctaagagtc aagctgcagc cgatttggtt	2160
gccgtcactg acgctaagga attgtctaga gttgtcgctg cagtaggttt agctcaaaat	2220
ttggccgctt taagagcatt ggtttcagaa ggtattcaaa aaggtcatat ggctttgcaa	2280

gcaagatcct tagccatgac agttggtgct accggtaaag aagtcgaagc cgtagctcaa 2340
 caattaaaaa gacaaaagac aatgaaccaa gacagagcaa tggctatatt aaacgatttg 2400
 agaaagcaat aa 2412

<210> 54
 <211> 803
 <212> PRT
 <213> Enterococcus sp.

<400> 54

Met Lys Thr Val Val Ile Ile Asp Ala Leu Arg Thr Pro Ile Gly Lys
 1 5 10 15

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

Val Thr Thr Gln Leu Leu Lys Arg His Ser Thr Ile Ser Glu Glu Ile
 35 40 45

Asp Gln Val Ile Phe Gly Asn Val Leu Gln Ala Gly Asn Gly Gln Asn
 50 55 60

Pro Ala Arg Gln Ile Ala Ile Asn Ser Gly Leu Ser His Glu Ile Pro
 65 70 75 80

Ala Met Thr Val Asn Glu Val Cys Gly Ser Gly Met Lys Ala Val Ile
 85 90 95

Leu Ala Lys Gln Leu Ile Gln Leu Gly Glu Ala Glu Val Leu Ile Ala
 100 105 110

Gly Gly Ile Glu Asn Met Ser Gln Ala Pro Lys Leu Gln Arg Phe Asn
 115 120 125

Tyr Glu Thr Glu Ser Tyr Asp Ala Pro Phe Ser Ser Met Met Tyr Asp
 130 135 140

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

Asn Val Ala Glu Lys Tyr His Val Thr Arg Glu Glu Gln Asp Gln Phe
165 170 175

Ser Val His Ser Gln Leu Lys Ala Ala Gln Ala Gln Ala Glu Gly Ile
180 185 190

Phe Ala Asp Glu Ile Ala Pro Leu Glu Val Ser Gly Thr Leu Val Glu
195 200 205

Lys Asp Glu Gly Ile Arg Pro Asn Ser Ser Val Glu Lys Leu Gly Thr
210 215 220

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

Ser Thr Ile Asn Asp Gly Ala Ser Ala Leu Ile Ile Ala Ser Gln Glu
245 250 255

Tyr Ala Glu Ala His Gly Leu Pro Tyr Leu Ala Ile Ile Arg Asp Ser
260 265 270

Val Glu Val Gly Ile Asp Pro Ala Tyr Met Gly Ile Ser Pro Ile Lys
275 280 285

Ala Ile Gln Lys Leu Leu Ala Arg Asn Gln Leu Thr Thr Glu Glu Ile
290 295 300

Asp Leu Tyr Glu Ile Asn Glu Ala Phe Ala Ala Thr Ser Ile Val Val
305 310 315 320

Gln Arg Glu Leu Ala Leu Pro Glu Glu Lys Val Asn Ile Tyr Gly Gly
325 330 335

Gly Ile Ser Leu Gly His Ala Ile Gly Ala Thr Gly Ala Arg Leu Leu
340 345 350

Thr Ser Leu Ser Tyr Gln Leu Asn Gln Lys Glu Lys Lys Tyr Gly Val
355 360 365

Ala Ser Leu Cys Ile Gly Gly Gly Leu Gly Leu Ala Met Leu Leu Glu
370 375 380

Arg Pro Gln Gln Lys Lys Asn Ser Arg Phe Tyr Gln Met Ser Pro Glu
385 390 395 400

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

Lys Lys Glu Phe Glu Asn Thr Ala Leu Ser Ser Gln Ile Ala Asn His
420 425 430

Met Ile Glu Asn Gln Ile Ser Glu Thr Glu Val Pro Met Gly Val Gly
435 440 445

Leu His Leu Thr Val Asp Glu Thr Asp Tyr Leu Val Pro Met Ala Thr
450 455 460

Glu Glu Pro Ser Val Ile Ala Ala Leu Ser Asn Gly Ala Lys Ile Ala
465 470 475 480

Gln Gly Phe Lys Thr Val Asn Gln Gln Arg Leu Met Arg Gly Gln Ile
485 490 495

Val Phe Tyr Asp Val Ala Asp Pro Glu Ser Leu Ile Asp Lys Leu Gln
500 505 510

Val Arg Glu Ala Glu Val Phe Gln Gln Ala Glu Leu Ser Tyr Pro Ser
515 520 525

Ile Val Lys Arg Gly Gly Gly Leu Arg Asp Leu Gln Tyr Arg Thr Phe
530 535 540

Asp Glu Ser Phe Val Ser Val Asp Phe Leu Val Asp Val Lys Asp Ala
545 550 555 560

Met Gly Ala Asn Ile Val Asn Ala Met Leu Glu Gly Val Ala Glu Leu
565 570 575

Phe Arg Glu Trp Phe Ala Glu Gln Lys Ile Leu Phe Ser Ile Leu Ser
580 585 590

Asn Tyr Ala Thr Glu Ser Val Val Thr Met Lys Thr Ala Ile Pro Val
595 600 605

Ser Arg Leu Ser Lys Gly Ser Asn Gly Arg Glu Ile Ala Glu Lys Ile
610 615 620

Val Leu Ala Ser Arg Tyr Ala Ser Leu Asp Pro Tyr Arg Ala Val Thr
625 630 635 640

His Asn Lys Gly Ile Met Asn Gly Ile Glu Ala Val Val Leu Ala Thr
645 650 655

Gly Asn Asp Thr Arg Ala Val Ser Ala Ser Cys His Ala Phe Ala Val
660 665 670

Lys Glu Gly Arg Tyr Gln Gly Leu Thr Ser Trp Thr Leu Asp Gly Glu
675 680 685

Gln Leu Ile Gly Glu Ile Ser Val Pro Leu Ala Leu Ala Thr Val Gly
690 695 700

Gly Ala Thr Lys Val Leu Pro Lys Ser Gln Ala Ala Ala Asp Leu Leu
705 710 715 720

Ala Val Thr Asp Ala Lys Glu Leu Ser Arg Val Val Ala Ala Val Gly
725 730 735

Leu Ala Gln Asn Leu Ala Ala Leu Arg Ala Leu Val Ser Glu Gly Ile
740 745 750

Gln Lys Gly His Met Ala Leu Gln Ala Arg Ser Leu Ala Met Thr Val
755 760 765

Gly Ala Thr Gly Lys Glu Val Glu Ala Val Ala Gln Gln Leu Lys Arg
770 775 780

Gln Lys Thr Met Asn Gln Asp Arg Ala Met Ala Ile Leu Asn Asp Leu
785 790 795 800

Arg Lys Gln

<210> 55
<211> 1152
<212> DNA
<213> Enterococcus sp.

<400> 55
atgacaattg ggattgataa aattagtttt tttgtgcccc cttattatat tgatatgacg 60
gcactggctg aagccagaaa tgtagaccct ggaaaatttc atattggtat tgggcaagac 120
caaatggcgg tgaacccaat cagccaagat attgtgacat ttgcagccaa tgccgcagaa 180
gcgatcttga ccaaagaaga taaagaggcc attgatattg tgattgtcgg gactgagtcc 240
agtatcgatg agtcaaaagc ggccgcagtt gtcttacatc gtttaatggg gattcaacct 300
ttcgctcgct ctttcgaaat caaggaagct tgttacggag caacagcagg cttacagtta 360
gctaagaatc acgtagcctt acatccagat aaaaaagtct tggtcgtagc ggcagatatt 420
gcaaaatatg gcttaaattc tggcggtgag cctacacaag gagctggggc ggttgcaatg 480
ttagttgcta gtgaaccgcg ctttttggct ttaaaagagg ataatgtgat gctgacgcaa 540
gatatctatg acttttggcg tccaacaggc caccggtatc ctatggtcga tggtcctttg 600
tcaaacgaaa cctacatcca atcttttgcc caagtctggg atgaacataa aaaacgaacc 660
ggtcttgatt ttgcagatta tgatgcttta gcgttccata ttccttacac aaaaatgggc 720
aaaaaagcct tattagcaaa aatctccgac caaactgaag cagaacagga acgaatttta 780
gcccgttatg aagaaagtat cgtctatagt cgtcgcgtag gaaacttgta tacgggttca 840
ctttatctgg gactcatttc ctttttagaa aatgcaacga ctttaaccgc aggcaatcaa 900
attggtttat tcagttatgg ttctggtgct gtcgctgaat ttttactgg tgaattagta 960
gctggttatc aaaatcattt acaaaaagaa actcatttag cactgctgga taatcggaca 1020
gaactttcta tcgctgaata tgaagccatg tttgcagaaa ctttagacac agacattgat 1080
caaacgtag aagatgaatt aaaatatagt atttctgcta ttaataatac cgttcgttct 1140
tatcgaaact aa 1152

<210> 56
<211> 383
<212> PRT
<213> Enterococcus sp.

<400> 56

Met Thr Ile Gly Ile Asp Lys Ile Ser Phe Phe Val Pro Pro Tyr Tyr
1 5 10 15

Ile Asp Met Thr Ala Leu Ala Glu Ala Arg Asn Val Asp Pro Gly Lys
20 25 30

Phe His Ile Gly Ile Gly Gln Asp Gln Met Ala Val Asn Pro Ile Ser
35 40 45

Gln Asp Ile Val Thr Phe Ala Ala Asn Ala Ala Glu Ala Ile Leu Thr
50 55 60

Lys Glu Asp Lys Glu Ala Ile Asp Met Val Ile Val Gly Thr Glu Ser
65 70 75 80

Ser Ile Asp Glu Ser Lys Ala Ala Ala Val Val Leu His Arg Leu Met
85 90 95

Gly Ile Gln Pro Phe Ala Arg Ser Phe Glu Ile Lys Glu Ala Cys Tyr
100 105 110

Gly Ala Thr Ala Gly Leu Gln Leu Ala Lys Asn His Val Ala Leu His
115 120 125

Pro Asp Lys Lys Val Leu Val Val Ala Ala Asp Ile Ala Lys Tyr Gly
130 135 140

Leu Asn Ser Gly Gly Glu Pro Thr Gln Gly Ala Gly Ala Val Ala Met
145 150 155 160

Leu Val Ala Ser Glu Pro Arg Ile Leu Ala Leu Lys Glu Asp Asn Val
165 170 175

Met Leu Thr Gln Asp Ile Tyr Asp Phe Trp Arg Pro Thr Gly His Pro
180 185 190

Tyr Pro Met Val Asp Gly Pro Leu Ser Asn Glu Thr Tyr Ile Gln Ser
195 200 205

Phe Ala Gln Val Trp Asp Glu His Lys Lys Arg Thr Gly Leu Asp Phe
 210 215 220

Ala Asp Tyr Asp Ala Leu Ala Phe His Ile Pro Tyr Thr Lys Met Gly
 225 230 235 240

Lys Lys Ala Leu Leu Ala Lys Ile Ser Asp Gln Thr Glu Ala Glu Gln
 245 250 255

Glu Arg Ile Leu Ala Arg Tyr Glu Glu Ser Ile Val Tyr Ser Arg Arg
 260 265 270

Val Gly Asn Leu Tyr Thr Gly Ser Leu Tyr Leu Gly Leu Ile Ser Leu
 275 280 285

Leu Glu Asn Ala Thr Thr Leu Thr Ala Gly Asn Gln Ile Gly Leu Phe
 290 295 300

Ser Tyr Gly Ser Gly Ala Val Ala Glu Phe Phe Thr Gly Glu Leu Val
 305 310 315 320

Ala Gly Tyr Gln Asn His Leu Gln Lys Glu Thr His Leu Ala Leu Leu
 325 330 335

Asp Asn Arg Thr Glu Leu Ser Ile Ala Glu Tyr Glu Ala Met Phe Ala
 340 345 350

Glu Thr Leu Asp Thr Asp Ile Asp Gln Thr Leu Glu Asp Glu Leu Lys
 355 360 365

Tyr Ser Ile Ser Ala Ile Asn Asn Thr Val Arg Ser Tyr Arg Asn
 370 375 380

<210> 57
 <211> 867
 <212> DNA
 <213> Saccharomyces sp.

<400> 57
 atgactgccg acaacaatag tatgccccat ggtgcagtat ctagttacgc caaattagtg 60
 caaaacaaaa cacctgaaga cattttggaa gagtttcctg aaattattcc attacaacaa 120

agacctaata cccgatctag tgagacgtca aatgacgaaa gcggagaaac atgtttttct 180
 ggtcatgatg aggagcaaat taagttaatg aatgaaaatt gtattgtttt ggattgggac 240
 gataatgcta ttggtgccgg taccaagaaa gtttgtcatt taatggaaaa tattgaaaag 300
 ggtttactac atcgtgcatt ctccgtcttt attttcaatg aacaaggatga attactttta 360
 caacaaagag ccactgaaaa aataactttc cctgatcttt ggactaacac atgctgctct 420
 catccactat gtattgatga cgaattaggt ttgaagggtga agctagacga taagattaag 480
 ggcgctatta ctgcggcggg gagaaaacta gatcatgaat taggtattcc agaagatgaa 540
 actaagacaa ggggtaagtt tcacttttta aacagaatcc attacatggc accaagcaat 600
 gaaccatggg gtgaacatga aattgattac atcctatttt ataagatcaa cgctaaagaa 660
 aacttgactg tcaacccaaa cgtcaatgaa gttagagact tcaaatgggt ttcaccaaatt 720
 gatttgaaaa ctatgtttgc tgaccaagt tacaagttta cgccttggtt taagattatt 780
 tgcgagaatt acttattcaa ctggtgggag caattagatg acctttctga agtggaaaat 840
 gacaggcaaa ttcatagaat gctataa 867

<210> 58
 <211> 288
 <212> PRT
 <213> Saccharomyces sp.

<400> 58

Met Thr Ala Asp Asn Asn Ser Met Pro His Gly Ala Val Ser Ser Tyr
 1 5 10 15

Ala Lys Leu Val Gln Asn Gln Thr Pro Glu Asp Ile Leu Glu Glu Phe
 20 25 30

Pro Glu Ile Ile Pro Leu Gln Gln Arg Pro Asn Thr Arg Ser Ser Glu
 35 40 45

Thr Ser Asn Asp Glu Ser Gly Glu Thr Cys Phe Ser Gly His Asp Glu
 50 55 60

Glu Gln Ile Lys Leu Met Asn Glu Asn Cys Ile Val Leu Asp Trp Asp
 65 70 75 80

Asp Asn Ala Ile Gly Ala Gly Thr Lys Lys Val Cys His Leu Met Glu
85 90 95

Asn Ile Glu Lys Gly Leu Leu His Arg Ala Phe Ser Val Phe Ile Phe
100 105 110

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

Thr Phe Pro Asp Leu Trp Thr Asn Thr Cys Cys Ser His Pro Leu Cys
130 135 140

Ile Asp Asp Glu Leu Gly Leu Lys Gly Lys Leu Asp Asp Lys Ile Lys
145 150 155 160

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

Pro Glu Asp Glu Thr Lys Thr Arg Gly Lys Phe His Phe Leu Asn Arg
180 185 190

Ile His Tyr Met Ala Pro Ser Asn Glu Pro Trp Gly Glu His Glu Ile
195 200 205

Asp Tyr Ile Leu Phe Tyr Lys Ile Asn Ala Lys Glu Asn Leu Thr Val
210 215 220

Asn Pro Asn Val Asn Glu Val Arg Asp Phe Lys Trp Val Ser Pro Asn
225 230 235 240

Asp Leu Lys Thr Met Phe Ala Asp Pro Ser Tyr Lys Phe Thr Pro Trp
245 250 255

Phe Lys Ile Ile Cys Glu Asn Tyr Leu Phe Asn Trp Trp Glu Gln Leu
260 265 270

Asp Asp Leu Ser Glu Val Glu Asn Asp Arg Gln Ile His Arg Met Leu
275 280 285

<210> 59

<211> 1059

<212> DNA
<213> Artificial Sequence

<220>

<223> Mutant farnesyl pyrophosphate synthase (Erg20mut, F96W, N127W)

<400> 59

```
atggcttcag aaaaagaaat taggagagag agattcttga acgttttccc taaattagta      60
gaggaattga acgcatcgct tttggcttac ggtatgccta aggaagcatg tgactggtat      120
gccactcat tgaactacaa cactccaggc ggtaagctaa atagaggttt gtccgttgat      180
gacacgtatg ctattctctc caacaagacc gttgaacaat tggggcaaga agaatacgaa      240
aaggttgcca ttctaggttg gtgcattgag ttgttgcagg cttactgggtt ggtcgccgat      300
gatatgatgg acaagtccat taccagaaga ggccaacat gttggtacaa ggttcctgaa      360
gttggggaaa ttgccatctg ggacgcattc atgttagagg ctgctatcta caagcttttg      420
aaatctcact tcagaaacga aaaatactac atagatatca ccgaattggt ccatgaggtc      480
accttccaaa ccgaattggg ccaattgatg gacttaatca ctgcacctga agacaaagtc      540
gacttgagta agttctccct aaagaagcac tccttcatag ttactttcaa gactgcttac      600
tattctttct acttgcctgt cgcattggcc atgtacgttg ccggtatcac ggatgaaaag      660
gatttgaaac aagccagaga tgtcttgatt ccattgggtg aatacttcca aattcaagat      720
gactacttag actgcttcgg taccccagaa cagatcggtg agatcggtac agatatccaa      780
gataacaaat gttcttgggt aatcaacaag gcattggaac ttgcttccgc agaacaaaga      840
aagactttag acgaaaatta cggtagaag gactcagtcg cagaagccaa atgcaaaaag      900
atattcaatg acttgaaaat tgaacagcta taccacgaat atgaagagtc tattgccaag      960
gatttgaagg ccaaatttc tcaggtcgat gagtctcgtg gcttcaaagc tgatgtctta     1020
actgcgttct tgaacaaagt ttacaagaga agcaaatag                               1059
```

<210> 60
<211> 352
<212> PRT
<213> Artificial Sequence

<220>

<223> Mutant farnesyl pyrophosphate synthase (Erg20mut, F96W, N127W)

<400> 60

Met Ala Ser Glu Lys Glu Ile Arg Arg Glu Arg Phe Leu Asn Val Phe
1 5 10 15

Pro Lys Leu Val Glu Glu Leu Asn Ala Ser Leu Leu Ala Tyr Gly Met
20 25 30

Pro Lys Glu Ala Cys Asp Trp Tyr Ala His Ser Leu Asn Tyr Asn Thr
35 40 45

Pro Gly Gly Lys Leu Asn Arg Gly Leu Ser Val Val Asp Thr Tyr Ala
50 55 60

Ile Leu Ser Asn Lys Thr Val Glu Gln Leu Gly Gln Glu Glu Tyr Glu
65 70 75 80

Lys Val Ala Ile Leu Gly Trp Cys Ile Glu Leu Leu Gln Ala Tyr Trp
85 90 95

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

Pro Cys Trp Tyr Lys Val Pro Glu Val Gly Glu Ile Ala Ile Trp Asp
115 120 125

Ala Phe Met Leu Glu Ala Ala Ile Tyr Lys Leu Leu Lys Ser His Phe
130 135 140

Arg Asn Glu Lys Tyr Tyr Ile Asp Ile Thr Glu Leu Phe His Glu Val
145 150 155 160

Thr Phe Gln Thr Glu Leu Gly Gln Leu Met Asp Leu Ile Thr Ala Pro
165 170 175

Glu Asp Lys Val Asp Leu Ser Lys Phe Ser Leu Lys Lys His Ser Phe
180 185 190

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

Leu Ala Met Tyr Val Ala Gly Ile Thr Asp Glu Lys Asp Leu Lys Gln
210 215 220

Ala Arg Asp Val Leu Ile Pro Leu Gly Glu Tyr Phe Gln Ile Gln Asp
 225 230 235 240

Asp Tyr Leu Asp Cys Phe Gly Thr Pro Glu Gln Ile Gly Lys Ile Gly
 245 250 255

Thr Asp Ile Gln Asp Asn Lys Cys Ser Trp Val Ile Asn Lys Ala Leu
 260 265 270

Glu Leu Ala Ser Ala Glu Gln Arg Lys Thr Leu Asp Glu Asn Tyr Gly
 275 280 285

Lys Lys Asp Ser Val Ala Glu Ala Lys Cys Lys Lys Ile Phe Asn Asp
 290 295 300

Leu Lys Ile Glu Gln Leu Tyr His Glu Tyr Glu Glu Ser Ile Ala Lys
 305 310 315 320

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

Ala Asp Val Leu Thr Ala Phe Leu Asn Lys Val Tyr Lys Arg Ser Lys
 340 345 350

<210> 61
 <211> 1356
 <212> DNA
 <213> Saccharomyces sp.

<400> 61
 atgtcagagt tgagagcctt cagtgcccca gggaaagcgt tactagctgg tggatattta 60
 gttttagata caaaatatga agcatttgta gtcggattat cggcaagaat gcatgctgta 120
 gcccatcctt acggttcatt gcaagggtct gataagtttg aagtgcgtgt gaaaagtaaa 180
 caatttaaag atggggagtg gctgtaccat ataagtccta aaagtggcctt cattcctggt 240
 tcgataggcg gatctaagaa ccctttcatt gaaaaagtta tcgctaacgt atttagctac 300
 tttaaacctt acatggacga ctactgcaat agaaacttgt tcgttattga tattttctct 360
 gatgatgcct accattctca ggaggatagc gttaccgaac atcgtggcaa cagaagattg 420

agttttcatt cgcacagaat tgaagaagtt cccaaaacag ggctgggctc ctcggcaggt 480
 ttagtcacag ttttaactac agctttggcc tccttttttg tatcggacct ggaaaataat 540
 gtagacaaat atagagaagt tattcataat ttagcacaag ttgctcattg tcaagctcag 600
 ggtaaaattg gaagcggggtt tgatgtagcg gcggcagcat atggatctat cagatataga 660
 agattcccac ccgcattaat ctctaatttg ccagatatattg gaagtgctac ttacggcagt 720
 aaactggcgc atttgggttga tgaagaagac tggaatatta cgattaaaag taaccattta 780
 ccttcgggat taactttatg gatgggcgat attaagaatg gttcagaaac agtaaaactg 840
 gtccagaagg taaaaaattg gtatgattcg catatgccag aaagcttgaa aatatataca 900
 gaactcgatc atgcaaattc tagattttatg gatggactat ctaaactaga tcgcttacac 960
 gagactcatg acgattacag cgatcagata tttgagtctc ttgagaggaa tgactgtacc 1020
 tgtcaaaagt atcctgaaat cacagaagtt agagatgcag ttgccacaat tagacgttcc 1080
 tttagaaaaa taactaaaga atctggtgcc gatatcgaac ctcccgtaca aactagctta 1140
 ttggatgatt gccagacctt aaaaggagtt cttacttgct taatacctgg tgctggtggt 1200
 tatgacgcca ttgcagtgat tactaagcaa gatgttgatc ttagggctca aaccgctaata 1260
 gacaaaagat tttctaaggt tcaatggctg gatgtaactc aggctgactg gggtgttagg 1320
 aaagaaaaag atccggaaac ttatcttgat aaataa 1356

<210> 62
 <211> 451
 <212> PRT
 <213> Saccharomyces sp.

<400> 62

Met Ser Glu Leu Arg Ala Phe Ser Ala Pro Gly Lys Ala Leu Leu Ala
 1 5 10 15

Gly Gly Tyr Leu Val Leu Asp Thr Lys Tyr Glu Ala Phe Val Val Gly
 20 25 30

Leu Ser Ala Arg Met His Ala Val Ala His Pro Tyr Gly Ser Leu Gln
 35 40 45

Gly Ser Asp Lys Phe Glu Val Arg Val Lys Ser Lys Gln Phe Lys Asp
 50 55 60

Gly Glu Trp Leu Tyr His Ile Ser Pro Lys Ser Gly Phe Ile Pro Val
65 70 75 80

Ser Ile Gly Gly Ser Lys Asn Pro Phe Ile Glu Lys Val Ile Ala Asn
85 90 95

Val Phe Ser Tyr Phe Lys Pro Asn Met Asp Asp Tyr Cys Asn Arg Asn
100 105 110

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

Asp Ser Val Thr Glu His Arg Gly Asn Arg Arg Leu Ser Phe His Ser
130 135 140

His Arg Ile Glu Glu Val Pro Lys Thr Gly Leu Gly Ser Ser Ala Gly
145 150 155 160

Leu Val Thr Val Leu Thr Thr Ala Leu Ala Ser Phe Phe Val Ser Asp
165 170 175

Leu Glu Asn Asn Val Asp Lys Tyr Arg Glu Val Ile His Asn Leu Ala
180 185 190

Gln Val Ala His Cys Gln Ala Gln Gly Lys Ile Gly Ser Gly Phe Asp
195 200 205

Val Ala Ala Ala Ala Tyr Gly Ser Ile Arg Tyr Arg Arg Phe Pro Pro
210 215 220

Ala Leu Ile Ser Asn Leu Pro Asp Ile Gly Ser Ala Thr Tyr Gly Ser
225 230 235 240

Lys Leu Ala His Leu Val Asp Glu Glu Asp Trp Asn Ile Thr Ile Lys
245 250 255

Ser Asn His Leu Pro Ser Gly Leu Thr Leu Trp Met Gly Asp Ile Lys
260 265 270

Asn Gly Ser Glu Thr Val Lys Leu Val Gln Lys Val Lys Asn Trp Tyr
275 280 285

Asp Ser His Met Pro Glu Ser Leu Lys Ile Tyr Thr Glu Leu Asp His
290 295 300

Ala Asn Ser Arg Phe Met Asp Gly Leu Ser Lys Leu Asp Arg Leu His
305 310 315 320

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

Asn Asp Cys Thr Cys Gln Lys Tyr Pro Glu Ile Thr Glu Val Arg Asp
340 345 350

Ala Val Ala Thr Ile Arg Arg Ser Phe Arg Lys Ile Thr Lys Glu Ser
355 360 365

Gly Ala Asp Ile Glu Pro Pro Val Gln Thr Ser Leu Leu Asp Asp Cys
370 375 380

Gln Thr Leu Lys Gly Val Leu Thr Cys Leu Ile Pro Gly Ala Gly Gly
385 390 395 400

Tyr Asp Ala Ile Ala Val Ile Thr Lys Gln Asp Val Asp Leu Arg Ala
405 410 415

Gln Thr Ala Asn Asp Lys Arg Phe Ser Lys Val Gln Trp Leu Asp Val
420 425 430

Thr Gln Ala Asp Trp Gly Val Arg Lys Glu Lys Asp Pro Glu Thr Tyr
435 440 445

Leu Asp Lys
450

<210> 63

<211> 1332

<212> DNA

<213> Saccharomyces sp.

<400> 63

atgtcattac cgttcttaac ttctgcaccg ggaaagggtta ttatTTTTtg tgaacactct	60
gctgtgtaca acaagcctgc cgtcgctgct agtgtgtctg cgTTgagaac ctacctgcta	120
ataagcgagt catctgcacc agatactatt gaattggact tcccggacat tagctTTaat	180
cataagtggT ccatcaatga tttcaatgcc atcaccgagg atcaagtaaa ctccccaaaa	240
ttggccaagg ctcaacaagc caccgatggc ttgtctcagg aactcgTtag tctTTtgat	300
ccgttgTtag ctcaactatc cgaatccttC cactaccatg cagcgTTTTg tttcctgtat	360
atgtttgttt gcctatgccc ccatgccaaG aatattaagt tttctTTaaa gtctactTTa	420
cccatcggtg ctgggttggg ctcaagcgcc tctatTTctg tatcactggc cttagctatg	480
gcctacttgg gggggTTaat aggatctaat gacttggaaa agctgtcaga aaacgataag	540
catatagtga atcaatgggc cttcataggt gaaaagtgtA ttcacggTac ccTTcagga	600
atagataacg ctgtggccac ttatggtaat gccctgctat ttgaaaaaga ctcacataat	660
ggaacaataa acacaaacaa tTTtaagttc ttagatgatt tcccagccat tccaatgatc	720
ctaacctata ctagaattcc aaggTctaca aaagatcttg ttgctcgctg tcgtgtgttg	780
gtcaccgaga aatttctga agttatgaag ccaattctag atgcatggg tgaatgtgcc	840
ctacaaggct tagagatcat gactaagtta agtaaTgtA aaggcaccga tgacgaggct	900
gtagaaacta ataatgaact gtatgaacaa ctattggaat tgataagaat aaatcatgga	960
ctgcttgtct caatcggtgt ttctcatcct ggattagaac ttattaaaaa tctgagcgat	1020
gatttgagaa ttggctccac aaaacttacc ggtgctggTg gcggcggttg ctctttgact	1080
ttgttacgaa gagacattac tcaagagcaa attgacagct tcaaaaagaa attgcaagat	1140
gattttagtt acgagacatt tgaaacagac ttgggtggga ctggctgctg tttgttaagc	1200
gcaaaaaatt tgaataaaga tcttaaaatc aaatccctag tattccaatt atttgaaaat	1260
aaaactacca caaagcaaca aattgacgat ctattattgc caggaaacac gaatttacca	1320
tggaattcat aa	1332

<210> 64

<211> 443

<212> PRT

<213> Saccharomyces sp.

<400> 64

Met Ser Leu Pro Phe Leu Thr Ser Ala Pro Gly Lys Val Ile Ile Phe
1 5 10 15

Gly Glu His Ser Ala Val Tyr Asn Lys Pro Ala Val Ala Ala Ser Val
20 25 30

Ser Ala Leu Arg Thr Tyr Leu Leu Ile Ser Glu Ser Ser Ala Pro Asp
35 40 45

Thr Ile Glu Leu Asp Phe Pro Asp Ile Ser Phe Asn His Lys Trp Ser
50 55 60

Ile Asn Asp Phe Asn Ala Ile Thr Glu Asp Gln Val Asn Ser Gln Lys
65 70 75 80

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

Ser Leu Leu Asp Pro Leu Leu Ala Gln Leu Ser Glu Ser Phe His Tyr
100 105 110

His Ala Ala Phe Cys Phe Leu Tyr Met Phe Val Cys Leu Cys Pro His
115 120 125

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

Gly Leu Gly Ser Ser Ala Ser Ile Ser Val Ser Leu Ala Leu Ala Met
145 150 155 160

Ala Tyr Leu Gly Gly Leu Ile Gly Ser Asn Asp Leu Glu Lys Leu Ser
165 170 175

Glu Asn Asp Lys His Ile Val Asn Gln Trp Ala Phe Ile Gly Glu Lys
180 185 190

Cys Ile His Gly Thr Pro Ser Gly Ile Asp Asn Ala Val Ala Thr Tyr
195 200 205

Gly Asn Ala Leu Leu Phe Glu Lys Asp Ser His Asn Gly Thr Ile Asn
210 215 220

Thr Asn Asn Phe Lys Phe Leu Asp Asp Phe Pro Ala Ile Pro Met Ile
225 230 235 240

Leu Thr Tyr Thr Arg Ile Pro Arg Ser Thr Lys Asp Leu Val Ala Arg
245 250 255

Val Arg Val Leu Val Thr Glu Lys Phe Pro Glu Val Met Lys Pro Ile
260 265 270

Leu Asp Ala Met Gly Glu Cys Ala Leu Gln Gly Leu Glu Ile Met Thr
275 280 285

Lys Leu Ser Lys Cys Lys Gly Thr Asp Asp Glu Ala Val Glu Thr Asn
290 295 300

Asn Glu Leu Tyr Glu Gln Leu Leu Glu Leu Ile Arg Ile Asn His Gly
305 310 315 320

Leu Leu Val Ser Ile Gly Val Ser His Pro Gly Leu Glu Leu Ile Lys
325 330 335

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

Gly Gly Gly Gly Cys Ser Leu Thr Leu Leu Arg Arg Asp Ile Thr Gln
355 360 365

Glu Gln Ile Asp Ser Phe Lys Lys Lys Leu Gln Asp Asp Phe Ser Tyr
370 375 380

Glu Thr Phe Glu Thr Asp Leu Gly Gly Thr Gly Cys Cys Leu Leu Ser
385 390 395 400

Ala Lys Asn Leu Asn Lys Asp Leu Lys Ile Lys Ser Leu Val Phe Gln
405 410 415

Leu Phe Glu Asn Lys Thr Thr Thr Lys Gln Gln Ile Asp Asp Leu Leu
420 425 430

Leu Pro Gly Asn Thr Asn Leu Pro Trp Thr Ser
 435 440

<210> 65
 <211> 1191
 <212> DNA
 <213> Saccharomyces sp.

<400> 65
 atgaccgttt acacagcatc cgttaccgca cccgtcaaca tcgcaaccct taagtattgg 60
 gggaaaaggg acacgaagtt gaatctgccc accaattcgt ccatatcagt gactttatcg 120
 caagatgacc tcagaacggt gacctctgcg gctactgcac ctgagtttga acgcgacact 180
 ttgtggttaa atggagaacc acacagcatc gacaatgaaa gaactcaaaa ttgtctgcgc 240
 gacctacgcc aattaagaaa ggaaatggaa tcgaaggacg cctcattgcc cacattatct 300
 caatggaaac tccacattgt ctccgaaaat aactttccta cagcagctgg tttagcttcc 360
 tccgctgctg gctttgctgc attggtctct gcaattgcta agttatacca attaccacag 420
 tcaacttcag aaatatctag aatagcaaga aaggggtctg gttcagcttg tagatcgttg 480
 tttggcggat acgtggcctg ggaaatggga aaagctgaag atggtcatga ttccatggca 540
 gtacaaatcg cagacagctc tgactggcct cagatgaaag cttgtgtcct agttgtcagc 600
 gatattaaaa aggatgtgag ttccactcag ggtatgcaat tgaccgtggc aacctccgaa 660
 ctatttaaag aaagaattga acatgtcgta ccaaagagat ttgaagtcac gcgtaaagcc 720
 attgttgaaa aagatttcgc cacctttgca aaggaaacaa tgatggattc caactctttc 780
 catgccacat gtttggactc tttccctcca atattctaca tgaatgacac ttccaagcgt 840
 atcatcagtt ggtgccacac cattaatcag ttttacggag aaacaatcgt tgcatacacg 900
 tttgatgcag gtccaaatgc tgtgttgtag tacttagctg aaaatgagtc gaaactcttt 960
 gcatttatct ataaattggt tggctctggt cctggatggg acaagaaatt tactactgag 1020
 cagcttgagg ctttcaacca tcaatttgaa tcattctaact ttactgcacg tgaattggat 1080
 cttgagttgc aaaaggatgt tgccagagtg attttaactc aagtcggttc aggcccacaa 1140
 gaaacaaacg aatctttgat tgacgcaaag actggtctac caaaggaata a 1191

<210> 66
 <211> 396
 <212> PRT

<213> Saccharomyces sp.

<400> 66

Met Thr Val Tyr Thr Ala Ser Val Thr Ala Pro Val Asn Ile Ala Thr
1 5 10 15

Leu Lys Tyr Trp Gly Lys Arg Asp Thr Lys Leu Asn Leu Pro Thr Asn
20 25 30

Ser Ser Ile Ser Val Thr Leu Ser Gln Asp Asp Leu Arg Thr Leu Thr
35 40 45

Ser Ala Ala Thr Ala Pro Glu Phe Glu Arg Asp Thr Leu Trp Leu Asn
50 55 60

Gly Glu Pro His Ser Ile Asp Asn Glu Arg Thr Gln Asn Cys Leu Arg
65 70 75 80

Asp Leu Arg Gln Leu Arg Lys Glu Met Glu Ser Lys Asp Ala Ser Leu
85 90 95

Pro Thr Leu Ser Gln Trp Lys Leu His Ile Val Ser Glu Asn Asn Phe
100 105 110

Pro Thr Ala Ala Gly Leu Ala Ser Ser Ala Ala Gly Phe Ala Ala Leu
115 120 125

Val Ser Ala Ile Ala Lys Leu Tyr Gln Leu Pro Gln Ser Thr Ser Glu
130 135 140

Ile Ser Arg Ile Ala Arg Lys Gly Ser Gly Ser Ala Cys Arg Ser Leu
145 150 155 160

Phe Gly Gly Tyr Val Ala Trp Glu Met Gly Lys Ala Glu Asp Gly His
165 170 175

Asp Ser Met Ala Val Gln Ile Ala Asp Ser Ser Asp Trp Pro Gln Met
180 185 190

Lys Ala Cys Val Leu Val Val Ser Asp Ile Lys Lys Asp Val Ser Ser
195 200 205

Thr Gln Gly Met Gln Leu Thr Val Ala Thr Ser Glu Leu Phe Lys Glu
210 215 220

Arg Ile Glu His Val Val Pro Lys Arg Phe Glu Val Met Arg Lys Ala
225 230 235 240

Ile Val Glu Lys Asp Phe Ala Thr Phe Ala Lys Glu Thr Met Met Asp
245 250 255

Ser Asn Ser Phe His Ala Thr Cys Leu Asp Ser Phe Pro Pro Ile Phe
260 265 270

Tyr Met Asn Asp Thr Ser Lys Arg Ile Ile Ser Trp Cys His Thr Ile
275 280 285

Asn Gln Phe Tyr Gly Glu Thr Ile Val Ala Tyr Thr Phe Asp Ala Gly
290 295 300

Pro Asn Ala Val Leu Tyr Tyr Leu Ala Glu Asn Glu Ser Lys Leu Phe
305 310 315 320

Ala Phe Ile Tyr Lys Leu Phe Gly Ser Val Pro Gly Trp Asp Lys Lys
325 330 335

Phe Thr Thr Glu Gln Leu Glu Ala Phe Asn His Gln Phe Glu Ser Ser
340 345 350

Asn Phe Thr Ala Arg Glu Leu Asp Leu Glu Leu Gln Lys Asp Val Ala
355 360 365

Arg Val Ile Leu Thr Gln Val Gly Ser Gly Pro Gln Glu Thr Asn Glu
370 375 380

Ser Leu Ile Asp Ala Lys Thr Gly Leu Pro Lys Glu
385 390 395

<210> 67

<211> 2751

<212> DNA

<213> Artificial Sequence

<220>

<223> Engineered phosphomevalonate kinase/mevalonate kinase
(Erg8-T2A-Erg12)

<400> 67

atgtcagagt tgagagcctt cagtgcccca gggaaagcgt tactagctgg tggatattta	60
gttttagata caaaatatga agcatttgta gtcggattat cggcaagaat gcatgctgta	120
gccccatcctt acggttcatt gcaagggctct gataagtttg aagtgcgtgt gaaaagtaaa	180
caatttaaag atggggagtg gctgtaccat ataagtccta aaagtggctt cattcctgtt	240
tcgataggcg gatctaagaa ccttttcatt gaaaaagtta tcgctaacgt atttagctac	300
tttaaaccta acatggacga ctactgcaat agaaacttgt tcgttattga tattttctct	360
gatgatgcct accattctca ggaggatagc gttaccgaac atcgtggcaa cagaagattg	420
agttttcatt cgcacagaat tgaagaagtt cccaaaacag ggctgggctc ctcggcaggt	480
ttagtcacag ttttaactac agctttggcc tccttttttg tatcggacct ggaaaataat	540
gtagacaaat atagagaagt tattcataat ttagcacaag ttgctcattg tcaagctcag	600
ggtaaaattg gaagcgggtt tgatgtagcg gcggcagcat atggatctat cagatataga	660
agattcccac ccgcattaat ctctaatttg ccagatatg gaagtgctac ttacggcagt	720
aaactggcgc atttggttga tgaagaagac tggaatatta cgattaaaag taaccattta	780
ccttcgggat taactttatg gatgggcgat attaagaatg gttcagaaac agtaaaactg	840
gtccagaagg taaaaaattg gtatgattcg catatgccag aaagcttgaa aatatataca	900
gaactcgatc atgcaaattc tagatttatg gatggactat ctaaactaga tcgcttacac	960
gagactcatg acgattacag cgatcagata tttgagtctc ttgagaggaa tgactgtacc	1020
tgtcaaaagt atcctgaaat cacagaagtt agagatgcag ttgccacaat tagacgttcc	1080
tttagaaaaa taactaaaga atctggtgcc gatatcgaac ctcccgtaca aactagctta	1140
ttggatgatt gccagacctt aaaaggagtt cttacttgct taatacctgg tgctggtggt	1200
tatgacgcca ttgcagtgat tactaagcaa gatgttgatc ttagggctca aaccgcta	1260
gacaaaagat tttctaaggt tcaatggctg gatgtaactc aggctgactg ggggtgttagg	1320
aaagaaaaag atccggaaac ttatcttgat aaaaagcttg agggcagagg aagtcttcta	1380
acatgcggtg acgtggagga gaatcccggc cctgctagca tgtcattacc gttcttaact	1440

tctgcaccgg gaaaggttat tatttttggg gaacactctg ctgtgtacaa caagcctgcc	1500
gtcgtgcta gtgtgtctgc gttgagaacc tacctgctaa taagcgagtc atctgcacca	1560
gatactattg aattggactt cccggacatt agctttaatc ataagtggtc catcaatgat	1620
ttcaatgcca tcaccgagga tcaagtaaac tcccaaaaat tggccaaggc tcaacaaggc	1680
accgatggct tgtctcagga actcgttagt cttttggatc cgttgtttagc tcaactatcc	1740
gaatccttcc actaccatgc agcgttttgt ttcctgtata tgtttgtttg cctatgcccc	1800
catgccaaga atattaagtt ttctttaaaag tctactttac ccatcggtgc tgggttgggc	1860
tcaagcgctt ctatttctgt atcactggcc ttagctatgg cctacttggg ggggttaata	1920
ggatctaata acttggaata gctgtcagaa aacgataagc atatagtgaa tcaatgggccc	1980
ttcataggtg aaaagtgtat tcacgggtacc ctttcaggaa tagataacgc tgtggccact	2040
tatggtaatg ccctgctatt tgaaaaagac tcacataatg gaacaataaa cacaacaat	2100
tttaagttct tagatgattt cccagccatt ccaatgatcc taacctatac tagaattcca	2160
aggtctacaa aagatcttgt tgctcgcgtt cgtgtgttgg tcaccgagaa atttcctgaa	2220
gttatgaagc caattctaga tgccatgggt gaatgtgccc tacaaggctt agagatcatg	2280
actaagttaa gtaaatgtaa aggcaccgat gacgaggctg tagaaactaa taatgaactg	2340
tatgaacaac tattggaatt gataagaata aatcatggac tgcttgtctc aatcggtgtt	2400
tctcatcctg gattagaact tattaataat ctgagcgatg atttgagaat tggctccaca	2460
aaacttaccg gtgctgggtg cggcgggtgc tctttgactt tgttacgaag agacattact	2520
caagagcaaa ttgacagctt caaaaagaaa ttgcaagatg attttagtta cgagacattt	2580
gaaacagact tgggtgggac tggctgctgt ttgttaagcg caaaaaattt gaataaagat	2640
cttaaaatca aatccctagt attccaatta ttgaaaata aaactaccac aaagcaacaa	2700
attgacgatc tattattgcc aggaacacg aatttaccat ggacttcata a	2751

<210> 68

<211> 916

<212> PRT

<213> Artificial Sequence

<220>

<223> Engineered phosphomevalonate kinase/mevalonate kinase
(Erg8-T2A-Erg12)

<400> 68

Met Ser Glu Leu Arg Ala Phe Ser Ala Pro Gly Lys Ala Leu Leu Ala
1 5 10 15

Gly Gly Tyr Leu Val Leu Asp Thr Lys Tyr Glu Ala Phe Val Val Gly
20 25 30

Leu Ser Ala Arg Met His Ala Val Ala His Pro Tyr Gly Ser Leu Gln
35 40 45

Gly Ser Asp Lys Phe Glu Val Arg Val Lys Ser Lys Gln Phe Lys Asp
50 55 60

Gly Glu Trp Leu Tyr His Ile Ser Pro Lys Ser Gly Phe Ile Pro Val
65 70 75 80

Ser Ile Gly Gly Ser Lys Asn Pro Phe Ile Glu Lys Val Ile Ala Asn
85 90 95

Val Phe Ser Tyr Phe Lys Pro Asn Met Asp Asp Tyr Cys Asn Arg Asn
100 105 110

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

Asp Ser Val Thr Glu His Arg Gly Asn Arg Arg Leu Ser Phe His Ser
130 135 140

His Arg Ile Glu Glu Val Pro Lys Thr Gly Leu Gly Ser Ser Ala Gly
145 150 155 160

Leu Val Thr Val Leu Thr Thr Ala Leu Ala Ser Phe Phe Val Ser Asp
165 170 175

Leu Glu Asn Asn Val Asp Lys Tyr Arg Glu Val Ile His Asn Leu Ala
180 185 190

Gln Val Ala His Cys Gln Ala Gln Gly Lys Ile Gly Ser Gly Phe Asp
195 200 205

Val Ala Ala Ala Ala Tyr Gly Ser Ile Arg Tyr Arg Arg Phe Pro Pro
210 215 220

Ala Leu Ile Ser Asn Leu Pro Asp Ile Gly Ser Ala Thr Tyr Gly Ser
225 230 235 240

Lys Leu Ala His Leu Val Asp Glu Glu Asp Trp Asn Ile Thr Ile Lys
245 250 255

Ser Asn His Leu Pro Ser Gly Leu Thr Leu Trp Met Gly Asp Ile Lys
260 265 270

Asn Gly Ser Glu Thr Val Lys Leu Val Gln Lys Val Lys Asn Trp Tyr
275 280 285

Asp Ser His Met Pro Glu Ser Leu Lys Ile Tyr Thr Glu Leu Asp His
290 295 300

Ala Asn Ser Arg Phe Met Asp Gly Leu Ser Lys Leu Asp Arg Leu His
305 310 315 320

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

Asn Asp Cys Thr Cys Gln Lys Tyr Pro Glu Ile Thr Glu Val Arg Asp
340 345 350

Ala Val Ala Thr Ile Arg Arg Ser Phe Arg Lys Ile Thr Lys Glu Ser
355 360 365

Gly Ala Asp Ile Glu Pro Pro Val Gln Thr Ser Leu Leu Asp Asp Cys
370 375 380

Gln Thr Leu Lys Gly Val Leu Thr Cys Leu Ile Pro Gly Ala Gly Gly
385 390 395 400

Tyr Asp Ala Ile Ala Val Ile Thr Lys Gln Asp Val Asp Leu Arg Ala
405 410 415

Gln Thr Ala Asn Asp Lys Arg Phe Ser Lys Val Gln Trp Leu Asp Val
420 425 430

Thr Gln Ala Asp Trp Gly Val Arg Lys Glu Lys Asp Pro Glu Thr Tyr
435 440 445

Leu Asp Lys Lys Leu Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
450 455 460

Val Glu Glu Asn Pro Gly Pro Ala Ser Met Ser Leu Pro Phe Leu Thr
465 470 475 480

Ser Ala Pro Gly Lys Val Ile Ile Phe Gly Glu His Ser Ala Val Tyr
485 490 495

Asn Lys Pro Ala Val Ala Ala Ser Val Ser Ala Leu Arg Thr Tyr Leu
500 505 510

Leu Ile Ser Glu Ser Ser Ala Pro Asp Thr Ile Glu Leu Asp Phe Pro
515 520 525

Asp Ile Ser Phe Asn His Lys Trp Ser Ile Asn Asp Phe Asn Ala Ile
530 535 540

Thr Glu Asp Gln Val Asn Ser Gln Lys Leu Ala Lys Ala Gln Gln Ala
545 550 555 560

Thr Asp Gly Leu Ser Gln Glu Leu Val Ser Leu Leu Asp Pro Leu Leu
565 570 575

Ala Gln Leu Ser Glu Ser Phe His Tyr His Ala Ala Phe Cys Phe Leu
580 585 590

Tyr Met Phe Val Cys Leu Cys Pro His Ala Lys Asn Ile Lys Phe Ser
595 600 605

Leu Lys Ser Thr Leu Pro Ile Gly Ala Gly Leu Gly Ser Ser Ala Ser
610 615 620

Ile Ser Val Ser Leu Ala Leu Ala Met Ala Tyr Leu Gly Gly Leu Ile
625 630 635 640

Gly Ser Asn Asp Leu Glu Lys Leu Ser Glu Asn Asp Lys His Ile Val
645 650 655

Asn Gln Trp Ala Phe Ile Gly Glu Lys Cys Ile His Gly Thr Pro Ser
660 665 670

Gly Ile Asp Asn Ala Val Ala Thr Tyr Gly Asn Ala Leu Leu Phe Glu
675 680 685

Lys Asp Ser His Asn Gly Thr Ile Asn Thr Asn Asn Phe Lys Phe Leu
690 695 700

Asp Asp Phe Pro Ala Ile Pro Met Ile Leu Thr Tyr Thr Arg Ile Pro
705 710 715 720

Arg Ser Thr Lys Asp Leu Val Ala Arg Val Arg Val Leu Val Thr Glu
725 730 735

Lys Phe Pro Glu Val Met Lys Pro Ile Leu Asp Ala Met Gly Glu Cys
740 745 750

Ala Leu Gln Gly Leu Glu Ile Met Thr Lys Leu Ser Lys Cys Lys Gly
755 760 765

Thr Asp Asp Glu Ala Val Glu Thr Asn Asn Glu Leu Tyr Glu Gln Leu
770 775 780

Leu Glu Leu Ile Arg Ile Asn His Gly Leu Leu Val Ser Ile Gly Val
785 790 795 800

Ser His Pro Gly Leu Glu Leu Ile Lys Asn Leu Ser Asp Asp Leu Arg
805 810 815

Ile Gly Ser Thr Lys Leu Thr Gly Ala Gly Gly Gly Gly Cys Ser Leu
820 825 830

Thr Leu Leu Arg Arg Asp Ile Thr Gln Glu Gln Ile Asp Ser Phe Lys
835 840 845

Lys Lys Leu Gln Asp Asp Phe Ser Tyr Glu Thr Phe Glu Thr Asp Leu
850 855 860

Gly Gly Thr Gly Cys Cys Leu Leu Ser Ala Lys Asn Leu Asn Lys Asp
865 870 875 880

Leu Lys Ile Lys Ser Leu Val Phe Gln Leu Phe Glu Asn Lys Thr Thr
885 890 895

Thr Lys Gln Gln Ile Asp Asp Leu Leu Leu Pro Gly Asn Thr Asn Leu
900 905 910

Pro Trp Thr Ser
915

<210> 69
<211> 756
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial neryl pyrophosphate (NPP) synthase (NPPS) nucleotide
sequence

<400> 69
atgtgctcac ttaatttgca aacggaaaag ctatgctatg aagacaatga caatgacttg 60
gacgaggaac tgatgccgaa gcacatagcg ctaatcatgg atggtaatag acgttgggca 120
aaagacaagg gcttagaagt gtacgaaggg cacaacata taatcccgaa actaaaagaa 180
atatgtgaca tatcctcaa gttggggatt cagatcatca cagcgttcgc gttctccaca 240
gagaactgga agagatcaa ggaggaagtc gatttcctat tgcagatggt tgaagaaatc 300
tatgacgaat ttagccgttc tggggtgaga gtgagtatca tcggatgcaa aagcgatttg 360
ccgatgaccc ttcaaaaatg tatcgcatg acagaggaaa cgacgaaagg caataaggga 420
ttacacctgg tcatagcact taactacggt gggtattacg atatcctaca agcaacgaag 480
tccattgtaa acaaggctat gaatggttta ttggacgttg aagacatcaa taaaaatctg 540
ttcgaccaag aattagaaag caaatgccct aaccctgact tgctgatcag aactggggga 600
gaacagaggg tctctaattt tcttctatgg caattggctt atactgagtt ctattttacc 660
aatactttat tccctgactt tgggtgaagag gacctgaaag aagccatcat gaattttcaa 720
cagagacacc gtagattcgg aggacatact tattga 756

<210> 70
<211> 251
<212> PRT
<213> Solanum sp.

<400> 70

Met Cys Ser Leu Asn Leu Gln Thr Glu Lys Leu Cys Tyr Glu Asp Asn
1 5 10 15

Asp Asn Asp Leu Asp Glu Glu Leu Met Pro Lys His Ile Ala Leu Ile
20 25 30

Met Asp Gly Asn Arg Arg Trp Ala Lys Asp Lys Gly Leu Glu Val Tyr
35 40 45

Glu Gly His Lys His Ile Ile Pro Lys Leu Lys Glu Ile Cys Asp Ile
50 55 60

Ser Ser Lys Leu Gly Ile Gln Ile Ile Thr Ala Phe Ala Phe Ser Thr
65 70 75 80

Glu Asn Trp Lys Arg Ser Lys Glu Glu Val Asp Phe Leu Leu Gln Met
85 90 95

Phe Glu Glu Ile Tyr Asp Glu Phe Ser Arg Ser Gly Val Arg Val Ser
100 105 110

Ile Ile Gly Cys Lys Ser Asp Leu Pro Met Thr Leu Gln Lys Cys Ile
115 120 125

Ala Leu Thr Glu Glu Thr Thr Lys Gly Asn Lys Gly Leu His Leu Val
130 135 140

Ile Ala Leu Asn Tyr Gly Gly Tyr Tyr Asp Ile Leu Gln Ala Thr Lys
145 150 155 160

Ser Ile Val Asn Lys Ala Met Asn Gly Leu Leu Asp Val Glu Asp Ile
165 170 175

Asn Lys Asn Leu Phe Asp Gln Glu Leu Glu Ser Lys Cys Pro Asn Pro
180 185 190

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

Leu Trp Gln Leu Ala Tyr Thr Glu Phe Tyr Phe Thr Asn Thr Leu Phe
210 215 220

Pro Asp Phe Gly Glu Glu Asp Leu Lys Glu Ala Ile Met Asn Phe Gln
225 230 235 240

Gln Arg His Arg Arg Phe Gly Gly His Thr Tyr
245 250

<210> 71
<211> 1113
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial geranylgeranyl pyrophosphate synthase large subunit
(GPPSlsu) nucleotide sequence

<400> 71
atgagcaccg tgaatctgac ctgggtgcag acgtgctcta tgttcaacca gggcgggcgt 60
tcccgttcat tgtcaacctt caacttaaatt ctgtaccatc cattgaagaa aacgcctttc 120
tctatccaga cacctaagca gaaaaggcca acttccccct tctcatctat cagtgccgta 180
ttaacggagc aggaagcagt aaaggagggt gacgaggaaa aaagcatatt taacttcaaa 240
tcttatatgg ttcagaaagc taatagcgtg aatcaggcac tagattctgc ggtgttattg 300
agagacccca ttatgataca tgaatctatg cgttactctt tgcttgcggg cggcaagcgt 360
gtcagaccga tgttatgctt aagtgcgtgc gagttagtag gaggtaaaga gtctgtagca 420
atgcccgcag catgtgctgt agaaatgata cacacaatgt cactgattca cgatgatctt 480
ccttgcatgg ataacgacga tcttcgtaga ggtaagccaa ccaaccacaa ggtattcggg 540
gaagacgtgg cagtttttagc aggagacgcg ctactagcgt tcgctgttga acacatggca 600
gtagcacag taggagttcc agcagcaaaa atagttaggg ctataggaga gtagcaaaag 660
tccatcggtg gcgagggcct tgttgccgga caggtagttg atatcgatag tgaagggttg 720
gctaacgtgg gactagaaca actggagttc atccacctac acaagacagg ggcactgctt 780

gaagcgagtg ttgtacttgg ggctattctg gggggaggaa cagatgagga ggtagaaaaa 840
ctacgtagtt ttgccagggtg tataggacta ctatttcaag ttgtagatga taticcttgac 900
gtcacgaaga gtagtcaaga gttaggaaaa acagcaggga aagatctagt tgccgataaa 960
gtaacctacc ccaggctaata gggatatcat aaatctcgtg agttcgccga acaattaaat 1020
actgaggcta agcaacattt aagcgggttt gatcctatta aggctgcgcc gctgattgct 1080
ctagcaaact atattgcata tagacagaac tga 1113

<210> 72
<211> 370
<212> PRT
<213> Cannabis sativa

<400> 72

Met Ser Thr Val Asn Leu Thr Trp Val Gln Thr Cys Ser Met Phe Asn
1 5 10 15

Gln Gly Gly Arg Ser Arg Ser Leu Ser Thr Phe Asn Leu Asn Leu Tyr
20 25 30

His Pro Leu Lys Lys Thr Pro Phe Ser Ile Gln Thr Pro Lys Gln Lys
35 40 45

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

Glu Ala Val Lys Glu Gly Asp Glu Glu Lys Ser Ile Phe Asn Phe Lys
65 70 75 80

Ser Tyr Met Val Gln Lys Ala Asn Ser Val Asn Gln Ala Leu Asp Ser
85 90 95

Ala Val Leu Leu Arg Asp Pro Ile Met Ile His Glu Ser Met Arg Tyr
100 105 110

Ser Leu Leu Ala Gly Gly Lys Arg Val Arg Pro Met Leu Cys Leu Ser
115 120 125

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

Cys Ala Val Glu Met Ile His Thr Met Ser Leu Ile His Asp Asp Leu
145 150 155 160

Pro Cys Met Asp Asn Asp Asp Leu Arg Arg Gly Lys Pro Thr Asn His
165 170 175

Lys Val Phe Gly Glu Asp Val Ala Val Leu Ala Gly Asp Ala Leu Leu
180 185 190

Ala Phe Ala Phe Glu His Met Ala Val Ser Thr Val Gly Val Pro Ala
195 200 205

Ala Lys Ile Val Arg Ala Ile Gly Glu Leu Ala Lys Ser Ile Gly Ser
210 215 220

Glu Gly Leu Val Ala Gly Gln Val Val Asp Ile Asp Ser Glu Gly Leu
225 230 235 240

Ala Asn Val Gly Leu Glu Gln Leu Glu Phe Ile His Leu His Lys Thr
245 250 255

Gly Ala Leu Leu Glu Ala Ser Val Val Leu Gly Ala Ile Leu Gly Gly
260 265 270

Gly Thr Asp Glu Glu Val Glu Lys Leu Arg Ser Phe Ala Arg Cys Ile
275 280 285

Gly Leu Leu Phe Gln Val Val Asp Asp Ile Leu Asp Val Thr Lys Ser
290 295 300

Ser Gln Glu Leu Gly Lys Thr Ala Gly Lys Asp Leu Val Ala Asp Lys
305 310 315 320

Val Thr Tyr Pro Arg Leu Met Gly Ile Asp Lys Ser Arg Glu Phe Ala
325 330 335

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

Ile Lys Ala Ala Pro Leu Ile Ala Leu Ala Asn Tyr Ile Ala Tyr Arg
355 360 365

Gln Asn
370

<210> 73
<211> 948
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial geranylgeranyl pyrophosphate synthase small subunit
(GPPSssu) nucleotide sequence

<400> 73
atggctgttt acaacctttc aatcaactgt tctcccagat tcgtccatca tgtatacgtg 60
ccccatttta catgtaaadc aaataagagc ctgagccatg tccccatgag aatcacgatg 120
tcaaagcagc atcatcactc atactttgcc tctacaacgg cagatgtcga tgccccatcta 180
aaacaatcaa tcacaattaa acccccgttg tctgtccacg aagccatgta taactttatc 240
ttcagtagcg caccgaattt ggcgccatca ttatgtgtcg cagcatgtga attggttggg 300
ggtcaccagg gacaggcgat ggagcgggcc agcgcatata gggtaatata tgctagcatc 360
gttaccacag atcaccttcc gttaacggga aggccaaacc ccacctcacc ggaggccgct 420
acgcacaatt cctataatcc aaacatacag ttgttattac ctgacgccat tacacccttc 480
gggtttgagc tattagcgtc cagtgatgat cttacacaca acaagagtga gagagttctt 540
agggtgatcg ttgaatttac gaggactttc ggttccagag gcactataga cgcccaatac 600
cacgaaaagt tggctagtag gtttgatgtg gatagccatg aggcaaagac cgtaggatgg 660
gggcattacc catcattgaa aaaggaggga gccatgcacg catgtgctgc tgcctgcgga 720
gcaatattgg gtgaggctca tgaagaagaa gtggaaaaat tgcgtacatt cgggctgtat 780
gtcggcatga tccaaggtta tgcgaacaga ttcacatga gcagtacaga ggagaaaaaa 840
gaggctgaca ggataattga ggagcttacc aatttagcgc gtcaggagct gaaatacttc 900
gatggaagga acctagaacc gttttcaaca ttcttgttcc gtttgtag 948

<210> 74
<211> 315
<212> PRT

<213> Cannabis sativa

<400> 74

Met Ala Val Tyr Asn Leu Ser Ile Asn Cys Ser Pro Arg Phe Val His
1 5 10 15

His Val Tyr Val Pro His Phe Thr Cys Lys Ser Asn Lys Ser Leu Ser
20 25 30

His Val Pro Met Arg Ile Thr Met Ser Lys Gln His His His Ser Tyr
35 40 45

Phe Ala Ser Thr Thr Ala Asp Val Asp Ala His Leu Lys Gln Ser Ile
50 55 60

Thr Ile Lys Pro Pro Leu Ser Val His Glu Ala Met Tyr Asn Phe Ile
65 70 75 80

Phe Ser Thr Pro Pro Asn Leu Ala Pro Ser Leu Cys Val Ala Ala Cys
85 90 95

Glu Leu Val Gly Gly His Gln Gly Gln Ala Met Ala Ala Ala Ser Ala
100 105 110

Leu Arg Val Ile His Ala Ser Ile Val Thr His Asp His Leu Pro Leu
115 120 125

Thr Gly Arg Pro Asn Pro Thr Ser Pro Glu Ala Ala Thr His Asn Ser
130 135 140

Tyr Asn Pro Asn Ile Gln Leu Leu Leu Pro Asp Ala Ile Thr Pro Phe
145 150 155 160

Gly Phe Glu Leu Leu Ala Ser Ser Asp Asp Leu Thr His Asn Lys Ser
165 170 175

Glu Arg Val Leu Arg Val Ile Val Glu Phe Thr Arg Thr Phe Gly Ser
180 185 190

Arg Gly Thr Ile Asp Ala Gln Tyr His Glu Lys Leu Ala Ser Arg Phe
195 200 205

Asp Val Asp Ser His Glu Ala Lys Thr Val Gly Trp Gly His Tyr Pro
210 215 220

Ser Leu Lys Lys Glu Gly Ala Met His Ala Cys Ala Ala Ala Cys Gly
225 230 235 240

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

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

Met Ser Ser Thr Glu Glu Lys Lys Glu Ala Asp Arg Ile Ile Glu Glu
275 280 285

Leu Thr Asn Leu Ala Arg Gln Glu Leu Lys Tyr Phe Asp Gly Arg Asn
290 295 300

Leu Glu Pro Phe Ser Thr Phe Leu Phe Arg Leu
305 310 315

<210> 75
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial tetraketide synthase (TKS) nucleotide sequence

<400> 75
atgaatcatt taagagctga aggtccagcc tccgttttgg ccatcggtac cgctaaccct 60
gaaaacattt tgttgcaaga cgaattccca gactactact tcagagtcac taagtccgaa 120
cacatgaccc aattgaagga gaagttcaga aagatttgtg acaagtccat gattagaaag 180
agaaactgtt tcttgaacga agaacacttg aagcaaaacc caagattggt tgaacatgaa 240
atgcaaactt tggacgctag acaagacatg ttggttggtg aagtccttaa gttgggtaag 300
gatgcctgtg ctaaggccat taaagaatgg ggtcaaccta agtccaagat taccacttg 360
attttcacct ctgcctccac cactgacatg cctggtgctg attaccactg cgctaagtta 420
ttgggtttgt ctccatccgt taagagagtt atgatgtacc aattgggttg ctacggtggt 480

```

ggtactgttt taagaattgc taaggatatt gctgaaaaca acaagggtgc cagagtctta      540
gctgtctgct gtgacattat ggcttgttta ttcagaggtc catctgaatc cgacttggaa      600
ttgttggttg gtcaagctat cttcggtgac ggtgctgctg ccgttattgt tggtgctgaa      660
ccagacgaat ccgttggtga aagaccaatt tttgaattgg tttccaccgg tcaaactatt      720
ttgccaaatt ccgaaggtag catcggtggt catatcagag aagccggttt gatcttcgac      780
ttacataagg atgtcccaat gttgatctct aacaacattg aaaagtgttt gatcgaagct      840
tttaccctaa ttggtatttc tgactggaac tctatcttct ggattacca tcctggtggt      900
aaggctatth ttgataaggt cgaggaaaaa ttgcacttga agtctgacaa gttcgttgac      960
tctagacacg tcttgtccga acatggtaat atgtcctctt ccaccgtttt attcgttatg     1020
gatgagttga gaaagagatc cttagaagaa ggtaagtcca ccaccggtga tggttttgag     1080
tggggtgttt tgttcggttt cgggtccaggt ttgaccgtcg aaagagttgt tgtttagatct     1140
gtcccaatta agtacggatc c                                                    1161

```

```

<210> 76
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial tetraketide synthase (TKS)

<400> 76

```

```

Met Asn His Leu Arg Ala Glu Gly Pro Ala Ser Val Leu Ala Ile Gly
1           5           10          15

```

```

Thr Ala Asn Pro Glu Asn Ile Leu Leu Gln Asp Glu Phe Pro Asp Tyr
          20          25          30

```

```

Tyr Phe Arg Val Thr Lys Ser Glu His Met Thr Gln Leu Lys Glu Lys
          35          40          45

```

```

Phe Arg Lys Ile Cys Asp Lys Ser Met Ile Arg Lys Arg Asn Cys Phe
          50          55          60

```

```

Leu Asn Glu Glu His Leu Lys Gln Asn Pro Arg Leu Val Glu His Glu
65           70           75          80

```

Met Gln Thr Leu Asp Ala Arg Gln Asp Met Leu Val Val Glu Val Pro
85 90 95

Lys Leu Gly Lys Asp Ala Cys Ala Lys Ala Ile Lys Glu Trp Gly Gln
100 105 110

Pro Lys Ser Lys Ile Thr His Leu Ile Phe Thr Ser Ala Ser Thr Thr
115 120 125

Asp Met Pro Gly Ala Asp Tyr His Cys Ala Lys Leu Leu Gly Leu Ser
130 135 140

Pro Ser Val Lys Arg Val Met Met Tyr Gln Leu Gly Cys Tyr Gly Gly
145 150 155 160

Gly Thr Val Leu Arg Ile Ala Lys Asp Ile Ala Glu Asn Asn Lys Gly
165 170 175

Ala Arg Val Leu Ala Val Cys Cys Asp Ile Met Ala Cys Leu Phe Arg
180 185 190

Gly Pro Ser Glu Ser Asp Leu Glu Leu Leu Val Gly Gln Ala Ile Phe
195 200 205

Gly Asp Gly Ala Ala Ala Val Ile Val Gly Ala Glu Pro Asp Glu Ser
210 215 220

Val Gly Glu Arg Pro Ile Phe Glu Leu Val Ser Thr Gly Gln Thr Ile
225 230 235 240

Leu Pro Asn Ser Glu Gly Thr Ile Gly Gly His Ile Arg Glu Ala Gly
245 250 255

Leu Ile Phe Asp Leu His Lys Asp Val Pro Met Leu Ile Ser Asn Asn
260 265 270

Ile Glu Lys Cys Leu Ile Glu Ala Phe Thr Pro Ile Gly Ile Ser Asp
275 280 285

Trp Asn Ser Ile Phe Trp Ile Thr His Pro Gly Gly Lys Ala Ile Leu
290 295 300

Asp Lys Val Glu Glu Lys Leu His Leu Lys Ser Asp Lys Phe Val Asp
305 310 315 320

Ser Arg His Val Leu Ser Glu His Gly Asn Met Ser Ser Ser Thr Val
325 330 335

Leu Phe Val Met Asp Glu Leu Arg Lys Arg Ser Leu Glu Glu Gly Lys
340 345 350

Ser Thr Thr Gly Asp Gly Phe Glu Trp Gly Val Leu Phe Gly Phe Gly
355 360 365

Pro Gly Leu Thr Val Glu Arg Val Val Val Arg Ser Val Pro Ile Lys
370 375 380

Tyr Gly Ser
385

<210> 77
<211> 309
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial olivetolic acid cyclase (OAC) nucleotide sequence

<400> 77
atggccgtca agcacttgat cgttttgaag ttcaaggatg aaatcactga agctcaaaag 60
gaagaattct tcaaaaccta cgtcaactta gtcaatatta ttccagccat gaaggacgtc 120
tattggggta aggacgttac tcaaaagaat aaggaggaag gttatactca tatcgttgag 180
gtcactttcg aatctgttga gactattcaa gactacatca tccaccagc ccacgttggt 240
ttcggatgatg tttatcgttc cttctgggaa aaattgttga tcttcgacta caccctaga 300
aagggatcc 309

<210> 78
<211> 103
<212> PRT
<213> Artificial Sequence

<220>

<223> Artificial olivetolic acid cyclase (OAC)

<400> 78

Met Ala Val Lys His Leu Ile Val Leu Lys Phe Lys Asp Glu Ile Thr
1 5 10 15

Glu Ala Gln Lys Glu Glu Phe Phe Lys Thr Tyr Val Asn Leu Val Asn
20 25 30

Ile Ile Pro Ala Met Lys Asp Val Tyr Trp Gly Lys Asp Val Thr Gln
35 40 45

Lys Asn Lys Glu Glu Gly Tyr Thr His Ile Val Glu Val Thr Phe Glu
50 55 60

Ser Val Glu Thr Ile Gln Asp Tyr Ile Ile His Pro Ala His Val Gly
65 70 75 80

Phe Gly Asp Val Tyr Arg Ser Phe Trp Glu Lys Leu Leu Ile Phe Asp
85 90 95

Tyr Thr Pro Arg Lys Gly Ser
100

<210> 79

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion tetraketide synthase-olivetolic acid cyclase (TKS-OAC)

<400> 79

atgaatcatt taagagctga aggtccagcc tccgttttgg ccatcggtac cgctaaccct 60
gaaaacattt tgttgcaaga cgaattccca gactactact tcagagtcac taagtccgaa 120
cacatgaccc aattgaagga gaagttcaga aagatttgtg acaagtccat gattagaaag 180
agaaactgtt tcttgaacga agaacacttg aagcaaaacc caagattggt tgaacatgaa 240
atgcaaaactt tggacgctag acaagacatg ttggttggtg aagtccttaa gttgggtaag 300
gatgcctgtg ctaaggccat taaagaatgg ggtcaaccta agtccaagat taccacttg 360

attttcacct ctgcctccac cactgacatg cctgggtgctg attaccactg cgctaagtta	420
ttggggtttgt ctccatccgt taagagagtt atgatgtacc aattgggttg ctacgggtgt	480
ggtactgttt taagaattgc taaggatatt gctgaaaaca acaagggtgc cagagtctta	540
gctgtctgct gtgacattat ggcttgttta ttcagaggtc catctgaatc cgacttgga	600
ttgttggttg gtcaagctat cttcggtgac ggtgctgctg ccgttattgt tgggtgctgaa	660
ccagacgaat ccgttggtga aagaccaatt tttgaattgg tttccaccgg tcaaactatt	720
ttgccaaatt ccgaaggtag catcgggtgt catatcagag aagccggttt gatcttcgac	780
ttacataagg atgtcccaat gttgatctct aacaacattg aaaagtgttt gatcgaagct	840
tttaccctaa ttggtatttc tgactggaac tctatcttct ggattacca tcctgggtgt	900
aaggctattt tggataaggt cgaggaaaaa ttgcacttga agtctgacaa gttcgttgac	960
tctagacacg tcttgtccga acatggtaat atgtcctctt ccaccgtttt attcgttatg	1020
gatgagttga gaaagagatc cttagaagaa ggtaagtcca ccaccggtga tggttttgag	1080
tgggggtgttt tgttcggttt cgggtccaggt ttgaccgtcg aaagagttgt tgttagatct	1140
gtcccaatta agtacgcagc cacaagcggg tctacgggct ccacgggctc taccggcagt	1200
gggaggagca ctgggtcaac gggatcaaca ggtagtgga gatcacacat ggttgccgtc	1260
aagcacttga tcgtttttgaa gttcaaggat gaaatcactg aagctcaaaa ggaagaattc	1320
ttcaaacct acgtcaactt agtcaatatt attccagcca tgaaggacgt ctattggggt	1380
aaggacgtta ctcaaaagaa taaggaggaa ggttatactc atatcgttga ggtcactttc	1440
gaatctgttg agactattca agactacatc atccaccag cccacgttgg tttcgggtgat	1500
gtttatcggt ctttctggga aaaattgttg atcttcgact acaccctag aaagggtaac	1560
tcgagagctt ttgattaa	1578

<210> 80

<211> 525

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion tetraketide synthase-olivetolic acid cyclase (TKS-OAC)

<400> 80

Met Asn His Leu Arg Ala Glu Gly Pro Ala Ser Val Leu Ala Ile Gly
1 5 10 15

Thr Ala Asn Pro Glu Asn Ile Leu Leu Gln Asp Glu Phe Pro Asp Tyr
20 25 30

Tyr Phe Arg Val Thr Lys Ser Glu His Met Thr Gln Leu Lys Glu Lys
35 40 45

Phe Arg Lys Ile Cys Asp Lys Ser Met Ile Arg Lys Arg Asn Cys Phe
50 55 60

Leu Asn Glu Glu His Leu Lys Gln Asn Pro Arg Leu Val Glu His Glu
65 70 75 80

Met Gln Thr Leu Asp Ala Arg Gln Asp Met Leu Val Val Glu Val Pro
85 90 95

Lys Leu Gly Lys Asp Ala Cys Ala Lys Ala Ile Lys Glu Trp Gly Gln
100 105 110

Pro Lys Ser Lys Ile Thr His Leu Ile Phe Thr Ser Ala Ser Thr Thr
115 120 125

Asp Met Pro Gly Ala Asp Tyr His Cys Ala Lys Leu Leu Gly Leu Ser
130 135 140

Pro Ser Val Lys Arg Val Met Met Tyr Gln Leu Gly Cys Tyr Gly Gly
145 150 155 160

Gly Thr Val Leu Arg Ile Ala Lys Asp Ile Ala Glu Asn Asn Lys Gly
165 170 175

Ala Arg Val Leu Ala Val Cys Cys Asp Ile Met Ala Cys Leu Phe Arg
180 185 190

Gly Pro Ser Glu Ser Asp Leu Glu Leu Leu Val Gly Gln Ala Ile Phe
195 200 205

Gly Asp Gly Ala Ala Ala Val Ile Val Gly Ala Glu Pro Asp Glu Ser
210 215 220

Val Gly Glu Arg Pro Ile Phe Glu Leu Val Ser Thr Gly Gln Thr Ile
225 230 235 240

Leu Pro Asn Ser Glu Gly Thr Ile Gly Gly His Ile Arg Glu Ala Gly
245 250 255

Leu Ile Phe Asp Leu His Lys Asp Val Pro Met Leu Ile Ser Asn Asn
260 265 270

Ile Glu Lys Cys Leu Ile Glu Ala Phe Thr Pro Ile Gly Ile Ser Asp
275 280 285

Trp Asn Ser Ile Phe Trp Ile Thr His Pro Gly Gly Lys Ala Ile Leu
290 295 300

Asp Lys Val Glu Glu Lys Leu His Leu Lys Ser Asp Lys Phe Val Asp
305 310 315 320

Ser Arg His Val Leu Ser Glu His Gly Asn Met Ser Ser Ser Thr Val
325 330 335

Leu Phe Val Met Asp Glu Leu Arg Lys Arg Ser Leu Glu Glu Gly Lys
340 345 350

Ser Thr Thr Gly Asp Gly Phe Glu Trp Gly Val Leu Phe Gly Phe Gly
355 360 365

Pro Gly Leu Thr Val Glu Arg Val Val Val Arg Ser Val Pro Ile Lys
370 375 380

Tyr Ala Ala Thr Ser Gly Ser Thr Gly Ser Thr Gly Ser Thr Gly Ser
385 390 395 400

Gly Arg Ser Thr Gly Ser Thr Gly Ser Thr Gly Ser Gly Arg Ser His
405 410 415

Met Val Ala Val Lys His Leu Ile Val Leu Lys Phe Lys Asp Glu Ile
420 425 430

Thr Glu Ala Gln Lys Glu Glu Phe Phe Lys Thr Tyr Val Asn Leu Val
435 440 445

Asn Ile Ile Pro Ala Met Lys Asp Val Tyr Trp Gly Lys Asp Val Thr
450 455 460

Gln Lys Asn Lys Glu Glu Gly Tyr Thr His Ile Val Glu Val Thr Phe
465 470 475 480

Glu Ser Val Glu Thr Ile Gln Asp Tyr Ile Ile His Pro Ala His Val
485 490 495

Gly Phe Gly Asp Val Tyr Arg Ser Phe Trp Glu Lys Leu Leu Ile Phe
500 505 510

Asp Tyr Thr Pro Arg Lys Gly Asn Ser Arg Ala Phe Asp
515 520 525

<210> 81
<211> 1185
<212> DNA
<213> Cannabis sativa

<400> 81
atgggattgt ccagcgtgtg caccttctca ttccaaacca actaccatac acttctcaat 60
ccgcacaata ataaccgaa aaccagctta ttatgttata gacacccgaa gacgcctatt 120
aagtacagtt ataacaactt tcctagcaag cattgctcta ctaaaagttt tcatctgcaa 180
aacaagtgct ctgagtcctt gagtatagca aagaatagca ttagagctgc aacgacaaat 240
caaaccgagc cgccggagtc tgataacat agtgtggcga ccaagatact aaattttggc 300
aaagcgtgtt ggaagctaca acgaccttat actattatcg cgtttacgag ttgtgcatgt 360
gggctgttcg ggaaagagct cttgcacaat acaaacttaa tcagttggag tttgatgttc 420
aaagcatttt tttttctcgt cgctatctta tgtatcgcgt catttaccac gaccataaat 480
caaatatacg atctgcatat cgatcgtatc aataagcccg acctcccact ggcctcaggt 540
gaaatttccg ttaacacggc gtggattatg agtataatcg tagcactatt tggacttatt 600
ataacatca aaatgaaggg cggtcctcta tacatttttg gatattgttt tgggattttt 660
ggaggatatag tctattccgt cccccattc agatggaaac aaaaccgtc caccgctttc 720

His Asn Thr Asn Leu Ile Ser Trp Ser Leu Met Phe Lys Ala Phe Phe
130 135 140

Phe Leu Val Ala Ile Leu Cys Ile Ala Ser Phe Thr Thr Thr Ile Asn
145 150 155 160

Gln Ile Tyr Asp Leu His Ile Asp Arg Ile Asn Lys Pro Asp Leu Pro
165 170 175

Leu Ala Ser Gly Glu Ile Ser Val Asn Thr Ala Trp Ile Met Ser Ile
180 185 190

Ile Val Ala Leu Phe Gly Leu Ile Ile Thr Ile Lys Met Lys Gly Gly
195 200 205

Pro Leu Tyr Ile Phe Gly Tyr Cys Phe Gly Ile Phe Gly Gly Ile Val
210 215 220

Tyr Ser Val Pro Pro Phe Arg Trp Lys Gln Asn Pro Ser Thr Ala Phe
225 230 235 240

Leu Leu Asn Phe Leu Ala His Ile Ile Thr Asn Phe Thr Phe Tyr Tyr
245 250 255

Ala Ser Arg Ala Ala Leu Gly Leu Pro Phe Glu Leu Arg Pro Ser Phe
260 265 270

Thr Phe Leu Leu Ala Phe Met Lys Ser Met Gly Ser Ala Leu Ala Leu
275 280 285

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

Thr Leu Ala Ser Lys Tyr Gly Ser Arg Asn Leu Thr Leu Phe Cys Ser
305 310 315 320

Gly Ile Val Leu Leu Ser Tyr Val Ala Ala Ile Leu Ala Gly Ile Ile
325 330 335

Trp Pro Gln Ala Phe Asn Ser Asn Val Met Leu Leu Ser His Ala Ile
340 345 350

Leu Ala Phe Trp Leu Ile Leu Gln Thr Arg Asp Phe Ala Leu Thr Asn
355 360 365

Tyr Asp Pro Glu Ala Gly Arg Arg Phe Tyr Glu Phe Met Trp Lys Leu
370 375 380

Tyr Tyr Ala Glu Tyr Leu Val Tyr Val Phe Ile
385 390 395

<210> 83
<211> 921
<212> DNA
<213> Streptomyces sp.

<400> 83
atgtctgagg cggcagacgt agagagagta tacgctgcta tggaggaagc ggctggatta 60
ttgggggtgg cttgtgccag agacaagata tatccgttac tgtctacttt ccaggacact 120
cttgtagaag gagggagtgt ggtggtgttt agtatggcat caggccgtca ttcaacagag 180
ctagatttca gtatatctgt gccaacaagt cacggtgatc catacgcaac cgtagtcgag 240
aagggtcttt tcccggcaac agggcatcct gtagatgatt tgcttgccga cacacagaag 300
cacctgcccc tctccatgtt cgcaatcgat ggtgaggtga ccggaggatt taaaaagact 360
tacgctttct tcccgactga caatatgcca ggagttgccg agttgagtgc aataccatcc 420
atgccgccag cagtcgcgga gaacgccgaa ttgttcgccc gttacggctt ggacaaagtc 480
caaatgacta gtatggacta taaaaagagg caggtgaatc tatatttcag cgaactttct 540
gccccaaact tggaggcgga gagcgtttta gcccttgcta gggagttagg gctacacgtc 600
ccgaatgagt tgggtttgaa attttgtaag cgtagctttt cagtatatcc gacgctgaac 660
tgggaaactg gaaagattga caggctatgc tttgcagtga tttctaata cctacgctt 720
gtaccttcct cagacgaggg cgacatcgag aaattccaca actatgccac aaaagctccg 780
tatgcctacg tcggcgaaaa acgtactcta gtatacgggtt tgactctgag tcccaaggaa 840
gagtattaca agctaggagc gtactatcat atcactgatg tgcaacgtgg cttgctgaaa 900
gccttcgact ccttagagga c 921

<210> 84
<211> 307
<212> PRT
<213> Streptomyces sp.

<400> 84

Met Ser Glu Ala Ala Asp Val Glu Arg Val Tyr Ala Ala Met Glu Glu
1 5 10 15

Ala Ala Gly Leu Leu Gly Val Ala Cys Ala Arg Asp Lys Ile Tyr Pro
20 25 30

Leu Leu Ser Thr Phe Gln Asp Thr Leu Val Glu Gly Gly Ser Val Val
35 40 45

Val Phe Ser Met Ala Ser Gly Arg His Ser Thr Glu Leu Asp Phe Ser
50 55 60

Ile Ser Val Pro Thr Ser His Gly Asp Pro Tyr Ala Thr Val Val Glu
65 70 75 80

Lys Gly Leu Phe Pro Ala Thr Gly His Pro Val Asp Asp Leu Leu Ala
85 90 95

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

Val Thr Gly Gly Phe Lys Lys Thr Tyr Ala Phe Phe Pro Thr Asp Asn
115 120 125

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

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

Gln Met Thr Ser Met Asp Tyr Lys Lys Arg Gln Val Asn Leu Tyr Phe
165 170 175

Ser Glu Leu Ser Ala Gln Thr Leu Glu Ala Glu Ser Val Leu Ala Leu
180 185 190

Val Arg Glu Leu Gly Leu His Val Pro Asn Glu Leu Gly Leu Lys Phe
195 200 205

Cys Lys Arg Ser Phe Ser Val Tyr Pro Thr Leu Asn Trp Glu Thr Gly
210 215 220

Lys Ile Asp Arg Leu Cys Phe Ala Val Ile Ser Asn Asp Pro Thr Leu
225 230 235 240

Val Pro Ser Ser Asp Glu Gly Asp Ile Glu Lys Phe His Asn Tyr Ala
245 250 255

Thr Lys Ala Pro Tyr Ala Tyr Val Gly Glu Lys Arg Thr Leu Val Tyr
260 265 270

Gly Leu Thr Leu Ser Pro Lys Glu Glu Tyr Tyr Lys Leu Gly Ala Tyr
275 280 285

Tyr His Ile Thr Asp Val Gln Arg Gly Leu Leu Lys Ala Phe Asp Ser
290 295 300

Leu Glu Asp
305

<210> 85
<211> 1635
<212> DNA
<213> Cannabis sativa

<400> 85
atgaactgtt ccgcgttttag tttctgggtc gtgtgcaaga tcattcttctt ttttctaagc 60
ttcaacattc aaatcagcat cgcgaatcct caggagaact tcctgaagtg tttctcagaa 120
tacataccaa ataatccgc caatcctaaa tttatatata cccaacatga tcagctatac 180
atgagtgtat tgaactctac gattcagaat ctaagattca catctgatac aacgccgaaa 240
cctctagtaa tcgtgacacc gtctaattgtc tcccatattc aagcttctat cttgtgtctca 300
aagaaagtcg gtcttcaa at aaggacacgt tctggcgggc atgacgccga gggcatgtca 360
tatatcagcc aagtaccatt ttagtcgtg gatttaagaa acatgcattc tataaaaatc 420

gacgttcact cccaaacggc atgggtggaa gctggagcga cactggggga ggtgtactac	480
tggatcaatg aaaagaacga aaatTTTTcc ttccccggag gatattgtcc gacagttggg	540
gtggggggcc acttctctgg cggcgggtac ggcgctctga tgcgtaatta tggactggcc	600
gcagataaca taatcgacgc gcatttggtg aacgttgacg ggaaggTTTT ggataggaag	660
tctatgggag aggacctatt ctgggcaatt agaggcggag gaggagagaa ttttgggtatt	720
attgctgcat ggaagattaa attggttgcg gtgccgagta aaagtacat cttttccgtc	780
aagaaaaaca tggagattca cggactagtt aagctgttta ataatggca aaacatcgcc	840
tataagtacg acaaagattt ggttctgatg acgcatttca taactaagaa tataactgat	900
aatcacggca agaataagac cactgtgcac ggttatttta gttcaatatt ccatggcggc	960
gttgactccc ttgtcgattt gatgaataag agcttccctg aattgggtat caagaagaca	1020
gactgcaaag aattctcctg gattgatacg actatcttct attcaggggt cgtgaatttc	1080
aacactgcga atttcaaaaa ggagatattg ttagaccgtt ccgcgggaaa aaaaactgcg	1140
ttttctatta aactagatta tgtgaaaaaa ccgattcctg agacagccat ggttaagatt	1200
cttgaaaaat tgtatgaaga ggatgtcggg gtcggtatgt acgtccttta cccttacgga	1260
ggaatcatgg aagaaatatt cgaatctgca attcctttcc cgcatcgtgc cggattattg	1320
tatgagctat ggtacaccgc tagctgggag aagcaggaag ataacgagaa gcatatcaat	1380
tgggtgaggt ctgtgtataa ttttacaaca ccatacgtca gtcaaaaccc tagattggcc	1440
tatcttaact atcgtgatct ggacttggga aaaacaaatc cagaatcccc aaataactac	1500
actcaagccc gtatatgggg cgagaagtac ttcggaacaa atttcaatag actggtcaaa	1560
gttaagacga aagcagaccc taataatttc ttccgtaacg aacaatcaat tccccgctt	1620
ccgccacacc atcac	1635

<210> 86
 <211> 545
 <212> PRT
 <213> Cannabis sativa

<400> 86

Met	Asn	Cys	Ser	Ala	Phe	Ser	Phe	Trp	Phe	Val	Cys	Lys	Ile	Ile	Phe
1				5				10					15		

Phe Phe Leu Ser Phe Asn Ile Gln Ile Ser Ile Ala Asn Pro Gln Glu
20 25 30

Asn Phe Leu Lys Cys Phe Ser Glu Tyr Ile Pro Asn Asn Pro Ala Asn
35 40 45

Pro Lys Phe Ile Tyr Thr Gln His Asp Gln Leu Tyr Met Ser Val Leu
50 55 60

Asn Ser Thr Ile Gln Asn Leu Arg Phe Thr Ser Asp Thr Thr Pro Lys
65 70 75 80

Pro Leu Val Ile Val Thr Pro Ser Asn Val Ser His Ile Gln Ala Ser
85 90 95

Ile Leu Cys Ser Lys Lys Val Gly Leu Gln Ile Arg Thr Arg Ser Gly
100 105 110

Gly His Asp Ala Glu Gly Met Ser Tyr Ile Ser Gln Val Pro Phe Val
115 120 125

Val Val Asp Leu Arg Asn Met His Ser Ile Lys Ile Asp Val His Ser
130 135 140

Gln Thr Ala Trp Val Glu Ala Gly Ala Thr Leu Gly Glu Val Tyr Tyr
145 150 155 160

Trp Ile Asn Glu Lys Asn Glu Asn Phe Ser Phe Pro Gly Gly Tyr Cys
165 170 175

Pro Thr Val Gly Val Gly Gly His Phe Ser Gly Gly Gly Tyr Gly Ala
180 185 190

Leu Met Arg Asn Tyr Gly Leu Ala Ala Asp Asn Ile Ile Asp Ala His
195 200 205

Leu Val Asn Val Asp Gly Lys Val Leu Asp Arg Lys Ser Met Gly Glu
210 215 220

Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Glu Asn Phe Gly Ile
225 230 235 240

Ile Ala Ala Trp Lys Ile Lys Leu Val Ala Val Pro Ser Lys Ser Thr
245 250 255

Ile Phe Ser Val Lys Lys Asn Met Glu Ile His Gly Leu Val Lys Leu
260 265 270

Phe Asn Lys Trp Gln Asn Ile Ala Tyr Lys Tyr Asp Lys Asp Leu Val
275 280 285

Leu Met Thr His Phe Ile Thr Lys Asn Ile Thr Asp Asn His Gly Lys
290 295 300

Asn Lys Thr Thr Val His Gly Tyr Phe Ser Ser Ile Phe His Gly Gly
305 310 315 320

Val Asp Ser Leu Val Asp Leu Met Asn Lys Ser Phe Pro Glu Leu Gly
325 330 335

Ile Lys Lys Thr Asp Cys Lys Glu Phe Ser Trp Ile Asp Thr Thr Ile
340 345 350

Phe Tyr Ser Gly Val Val Asn Phe Asn Thr Ala Asn Phe Lys Lys Glu
355 360 365

Ile Leu Leu Asp Arg Ser Ala Gly Lys Lys Thr Ala Phe Ser Ile Lys
370 375 380

Leu Asp Tyr Val Lys Lys Pro Ile Pro Glu Thr Ala Met Val Lys Ile
385 390 395 400

Leu Glu Lys Leu Tyr Glu Glu Asp Val Gly Val Gly Met Tyr Val Leu
405 410 415

Tyr Pro Tyr Gly Gly Ile Met Glu Glu Ile Ser Glu Ser Ala Ile Pro
420 425 430

Phe Pro His Arg Ala Gly Ile Met Tyr Glu Leu Trp Tyr Thr Ala Ser
435 440 445

Trp Glu Lys Gln Glu Asp Asn Glu Lys His Ile Asn Trp Val Arg Ser
450 455 460

Val Tyr Asn Phe Thr Thr Pro Tyr Val Ser Gln Asn Pro Arg Leu Ala
465 470 475 480

Tyr Leu Asn Tyr Arg Asp Leu Asp Leu Gly Lys Thr Asn Pro Glu Ser
485 490 495

Pro Asn Asn Tyr Thr Gln Ala Arg Ile Trp Gly Glu Lys Tyr Phe Gly
500 505 510

Lys Asn Phe Asn Arg Leu Val Lys Val Lys Thr Lys Ala Asp Pro Asn
515 520 525

Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro Pro Leu Pro Pro His His
530 535 540

His
545

<210> 87
<211> 1632
<212> DNA
<213> Cannabis sativa

<400> 87
atgaaatgtt ctactttcag tttttgggtc gtgtgtaaga tcatcttttt ctttttcagc 60
ttcaatatac agacaagtat cgccaatcca agagaaaatt tcttaaaatg tttttcacag 120
tacatcccta ataacgccac taacctgaaa ttagtgtaca cccaaaataa tcctctttat 180
atgtctgttt taaactccac gatccataat ttaaggttta catcagatac gacaccaaag 240
cccttggtaa tcgtgactcc cagccacgtg agccacatac aggggaccat cctgtgctct 300
aagaaagtag gcttgcatat caggacaaga tccggtggac acgacagtga gggaatgtcc 360
tatatttcac aagtcccctt cgttatagta gatctgagga acatgaggtc cattaagatt 420
gatgtgcact caciaacggc ttgggttgaa gctggagcca cattgggaga gggtttattac 480
tgggtgaatg agaagaacga gaacctttca ttagcagcgg gatattgtcc cacggtgtgc 540
gcaggtgggc atttcggggg aggagggtac ggccctttga tgagaaatta cgggctagcg 600

gcagacaaca tcatcgacgc ccatctggtg aacgtgcatg gaaaagtact ggacagaaag	660
tcaatgggcg aggacctgtt ttgggctttg agagggggcg gtgcagagtc atttggcatc	720
atagttgcat ggaaaatcag acttgttgcc gtcccaaagt ccacaatgtt ctctgttaag	780
aaaatcatgg agatacacga attggtgaaa ttagtgaata aatggcaaaa catagcgtac	840
aagtacgaca aagacttact gctgatgaca cactttatca cccgtaatat tacagataat	900
cagggtgaaga acaaaaccgc gatccataca tatttttcat ccgtttttct aggcggtgtc	960
gattcattag tagatctgat gaacaaatct ttccccgaac ttggtatcaa aaagactgat	1020
tgacagacagt tatcatggat tgatacaata attttctatt ctggtgtcgt aaattacgat	1080
accgataatt ttaataagga aatactatta gatcgttccg ctgggcagaa tgggtgcattc	1140
aagataaaac ttgattatgt caaaaagccc attccagaga gtgtctttgt gcagatcctt	1200
gagaagttgt atgaagaaga cattggtgca gggatgtacg cgctatatcc gtacgggggt	1260
attatggacg agatttctga gagcgccata ccattcccac acagagcagg aattttatac	1320
gagttatggt atatctgctc atgggaaaaa caggaagaca acgagaagca cttaaactgg	1380
atacgtaata tctataatth tatgacccca tacgtatcaa aaaatccgcg tcttgcgtag	1440
cttaactaca gggacctgga cataggtata aacgacccaa aaaatcccaa taattacacc	1500
caagctagaa tctgggggga gaagtatttc ggtaagaact ttgaccgttt ggtaaaagtc	1560
aaaactctgg tcgatccgaa caatttcttc cgtaacgagc aatccatacc tccgctaccg	1620
agacatagac at	1632

<210> 88
 <211> 544
 <212> PRT
 <213> Cannabis sativa

<400> 88

Met	Lys	Cys	Ser	Thr	Phe	Ser	Phe	Trp	Phe	Val	Cys	Lys	Ile	Ile	Phe
1				5				10					15		

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

Asn	Phe	Leu	Lys	Cys	Phe	Ser	Gln	Tyr	Ile	Pro	Asn	Asn	Ala	Thr	Asn
		35					40				45				

Leu Lys Leu Val Tyr Thr Gln Asn Asn Pro Leu Tyr Met Ser Val Leu
50 55 60

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

Pro Leu Val Ile Val Thr Pro Ser His Val Ser His Ile Gln Gly Thr
85 90 95

Ile Leu Cys Ser Lys Lys Val Gly Leu Gln Ile Arg Thr Arg Ser Gly
100 105 110

Gly His Asp Ser Glu Gly Met Ser Tyr Ile Ser Gln Val Pro Phe Val
115 120 125

Ile Val Asp Leu Arg Asn Met Arg Ser Ile Lys Ile Asp Val His Ser
130 135 140

Gln Thr Ala Trp Val Glu Ala Gly Ala Thr Leu Gly Glu Val Tyr Tyr
145 150 155 160

Trp Val Asn Glu Lys Asn Glu Asn Leu Ser Leu Ala Ala Gly Tyr Cys
165 170 175

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

Leu Met Arg Asn Tyr Gly Leu Ala Ala Asp Asn Ile Ile Asp Ala His
195 200 205

Leu Val Asn Val His Gly Lys Val Leu Asp Arg Lys Ser Met Gly Glu
210 215 220

Asp Leu Phe Trp Ala Leu Arg Gly Gly Gly Ala Glu Ser Phe Gly Ile
225 230 235 240

Ile Val Ala Trp Lys Ile Arg Leu Val Ala Val Pro Lys Ser Thr Met
245 250 255

Phe Ser Val Lys Lys Ile Met Glu Ile His Glu Leu Val Lys Leu Val
260 265 270

Asn Lys Trp Gln Asn Ile Ala Tyr Lys Tyr Asp Lys Asp Leu Leu Leu
275 280 285

Met Thr His Phe Ile Thr Arg Asn Ile Thr Asp Asn Gln Gly Lys Asn
290 295 300

Lys Thr Ala Ile His Thr Tyr Phe Ser Ser Val Phe Leu Gly Gly Val
305 310 315 320

Asp Ser Leu Val Asp Leu Met Asn Lys Ser Phe Pro Glu Leu Gly Ile
325 330 335

Lys Lys Thr Asp Cys Arg Gln Leu Ser Trp Ile Asp Thr Ile Ile Phe
340 345 350

Tyr Ser Gly Val Val Asn Tyr Asp Thr Asp Asn Phe Asn Lys Glu Ile
355 360 365

Leu Leu Asp Arg Ser Ala Gly Gln Asn Gly Ala Phe Lys Ile Lys Leu
370 375 380

Asp Tyr Val Lys Lys Pro Ile Pro Glu Ser Val Phe Val Gln Ile Leu
385 390 395 400

Glu Lys Leu Tyr Glu Glu Asp Ile Gly Ala Gly Met Tyr Ala Leu Tyr
405 410 415

Pro Tyr Gly Gly Ile Met Asp Glu Ile Ser Glu Ser Ala Ile Pro Phe
420 425 430

Pro His Arg Ala Gly Ile Leu Tyr Glu Leu Trp Tyr Ile Cys Ser Trp
435 440 445

Glu Lys Gln Glu Asp Asn Glu Lys His Leu Asn Trp Ile Arg Asn Ile
450 455 460

Tyr Asn Phe Met Thr Pro Tyr Val Ser Lys Asn Pro Arg Leu Ala Tyr
465 470 475 480

Leu Asn Tyr Arg Asp Leu Asp Ile Gly Ile Asn Asp Pro Lys Asn Pro
485 490 495

Asn Asn Tyr Thr Gln Ala Arg Ile Trp Gly Glu Lys Tyr Phe Gly Lys
500 505 510

Asn Phe Asp Arg Leu Val Lys Val Lys Thr Leu Val Asp Pro Asn Asn
515 520 525

Phe Phe Arg Asn Glu Gln Ser Ile Pro Pro Leu Pro Arg His Arg His
530 535 540

<210> 89
<211> 2160
<212> DNA
<213> Cannabis sativa

<400> 89
atgggaaaaa actacaaaag tctggactcc gtcgtcgcgt cagacttcat tgccctaggc 60
ataacatcag aggtagcgga aaccttacac ggcagactag ccgagattgt ttgtaactac 120
ggggcggtta ctccccagac ttggatcaat atagccaatc acatattaag ccccgatttg 180
ccgtttttccc ttcaccaaatt gttgttctac ggctgctata aggacttttg accagcgccc 240
cccgcgtgga ttctgatcc ggagaaagt aaatccacga atcttggggc attactagaa 300
aaacgtggca aagaattcct aggagttaaa tataaggacc ccatatcttc cttttcacac 360
tttcaagaat tttcagttag aaaccagag gtttactgga ggacagtatt aatggatgag 420
atgaagataa gctttagtaa ggatccggag tgtattctgc gtagagatga cattaacaat 480
cctggcgga gtgaatggct gcctgggtggg tacctgaata gtgctaagaa ctgttttaaac 540
gtcaactcta ataaaaaatt gaatgataca atgattgtat ggagagacga agggaacgat 600
gacctaccat tgaacaagct gactctagat cagctacgta aacgtgtatg gttggtcggg 660
tacgcgctgg aggagatggg attagaaaaa ggatgcgcaa ttgctatcga catgcctatg 720
catgtggacg cggtagtcatt ttacttggcc attgtcctag cgggttacgt cgtcgtttca 780
attgcagaca gcttttctgc acccgaaatc agtaccgctc tgcgtttgtc taaagctaag 840
gcaatattta cccaagacca tataattaga ggcaagaagc gtataccgtt gtacagtagg 900

gtttagagg	caaagtcacc	catggctatt	gtgataccat	gctctggctc	taatatagga	960
gcggagctta	gagatggtga	catctcctgg	gattactttc	ttgaacgtgc	taaggagttt	1020
aaaaactgtg	aatttactgc	aagagagcag	cccgtggatg	catacacaaa	catattgttc	1080
tccagcggta	ctacgggaga	acctaaagca	ataccttgga	cacaagctac	acccttaaa	1140
gcggccgctg	acggatggtc	ccacctggat	atcaggaagg	gtgacgtcat	agtttggccg	1200
actaacctgg	gatggatgat	gggcccttgg	ctggttttacg	ctagccttct	gaatggggcc	1260
agcattgcat	tgtacaatgg	ctcaccgctt	gtatcaggct	tcgcgaagtt	cgtacaggac	1320
gccaaggtaa	caatgctagg	cgtagtccg	tccatagtta	ggctttggaa	gagcacgaac	1380
tgcgttagtg	gctacgattg	gagcactatt	cgttgtttca	gctcttctgg	cgaggccagc	1440
aacgttgatg	aatattttgtg	gttgatgggg	agagcgaact	acaaacctgt	tattgagatg	1500
tgcggcggaa	ctgagattgg	gggagcattc	tccgccggtt	cttttctaca	agcccaaagt	1560
ttatcctctt	ttagcagcca	gtgcatgggc	tgtacactat	acattctgga	caaaaatggt	1620
tatccgatgc	cgaaaaacaa	gcccggcatc	ggagaactgg	ccctaggacc	cgtgatgttc	1680
ggcgctagta	agacgttggt	gaatgggaat	caccacgacg	tttattttta	gggaatgcca	1740
actttgaatg	gcgaagtact	tcgtagacac	ggagacatct	ttgagttgac	ttcaaacggt	1800
tactaccacg	ctcatggacg	tgccgatgat	acgatgaaca	ttgggggaat	taaaatttca	1860
tccatagaaa	tagaacgtgt	gtgtaacgaa	gtcgatgac	gtgtattcga	gactacagcg	1920
atcgggtgcc	caccgttggg	tgggggacca	gaacaattgg	taatcttttt	tgttctgaaa	1980
gactccaacg	atacgaccat	cgacctaaat	cagctgaggc	tatcctttta	tctgggcttg	2040
cagaaaaagc	taaatccttt	attcaaagtc	actagagttg	ttcctttatc	ttcattacca	2100
agaactgcaa	caaataaaat	aatgcgtaga	gttctaaggc	agcagtttag	tcatttcgaa	2160

<210> 90
 <211> 720
 <212> PRT
 <213> Cannabis sativa

<400> 90

Met	Gly	Lys	Asn	Tyr	Lys	Ser	Leu	Asp	Ser	Val	Val	Ala	Ser	Asp	Phe
1				5				10						15	

Ile Ala Leu Gly Ile Thr Ser Glu Val Ala Glu Thr Leu His Gly Arg
20 25 30

Leu Ala Glu Ile Val Cys Asn Tyr Gly Ala Ala Thr Pro Gln Thr Trp
35 40 45

Ile Asn Ile Ala Asn His Ile Leu Ser Pro Asp Leu Pro Phe Ser Leu
50 55 60

His Gln Met Leu Phe Tyr Gly Cys Tyr Lys Asp Phe Gly Pro Ala Pro
65 70 75 80

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

Ala Leu Leu Glu Lys Arg Gly Lys Glu Phe Leu Gly Val Lys Tyr Lys
100 105 110

Asp Pro Ile Ser Ser Phe Ser His Phe Gln Glu Phe Ser Val Arg Asn
115 120 125

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

Phe Ser Lys Asp Pro Glu Cys Ile Leu Arg Arg Asp Asp Ile Asn Asn
145 150 155 160

Pro Gly Gly Ser Glu Trp Leu Pro Gly Gly Tyr Leu Asn Ser Ala Lys
165 170 175

Asn Cys Leu Asn Val Asn Ser Asn Lys Lys Leu Asn Asp Thr Met Ile
180 185 190

Val Trp Arg Asp Glu Gly Asn Asp Asp Leu Pro Leu Asn Lys Leu Thr
195 200 205

Leu Asp Gln Leu Arg Lys Arg Val Trp Leu Val Gly Tyr Ala Leu Glu
210 215 220

Glu Met Gly Leu Glu Lys Gly Cys Ala Ile Ala Ile Asp Met Pro Met
225 230 235 240

His Val Asp Ala Val Val Ile Tyr Leu Ala Ile Val Leu Ala Gly Tyr
245 250 255

Val Val Val Ser Ile Ala Asp Ser Phe Ser Ala Pro Glu Ile Ser Thr
260 265 270

Arg Leu Arg Leu Ser Lys Ala Lys Ala Ile Phe Thr Gln Asp His Ile
275 280 285

Ile Arg Gly Lys Lys Arg Ile Pro Leu Tyr Ser Arg Val Val Glu Ala
290 295 300

Lys Ser Pro Met Ala Ile Val Ile Pro Cys Ser Gly Ser Asn Ile Gly
305 310 315 320

Ala Glu Leu Arg Asp Gly Asp Ile Ser Trp Asp Tyr Phe Leu Glu Arg
325 330 335

Ala Lys Glu Phe Lys Asn Cys Glu Phe Thr Ala Arg Glu Gln Pro Val
340 345 350

Asp Ala Tyr Thr Asn Ile Leu Phe Ser Ser Gly Thr Thr Gly Glu Pro
355 360 365

Lys Ala Ile Pro Trp Thr Gln Ala Thr Pro Leu Lys Ala Ala Ala Asp
370 375 380

Gly Trp Ser His Leu Asp Ile Arg Lys Gly Asp Val Ile Val Trp Pro
385 390 395 400

Thr Asn Leu Gly Trp Met Met Gly Pro Trp Leu Val Tyr Ala Ser Leu
405 410 415

Leu Asn Gly Ala Ser Ile Ala Leu Tyr Asn Gly Ser Pro Leu Val Ser
420 425 430

Gly Phe Ala Lys Phe Val Gln Asp Ala Lys Val Thr Met Leu Gly Val
435 440 445

Val Pro Ser Ile Val Arg Ser Trp Lys Ser Thr Asn Cys Val Ser Gly
450 455 460

Tyr Asp Trp Ser Thr Ile Arg Cys Phe Ser Ser Ser Gly Glu Ala Ser
465 470 475 480

Asn Val Asp Glu Tyr Leu Trp Leu Met Gly Arg Ala Asn Tyr Lys Pro
485 490 495

Val Ile Glu Met Cys Gly Gly Thr Glu Ile Gly Gly Ala Phe Ser Ala
500 505 510

Gly Ser Phe Leu Gln Ala Gln Ser Leu Ser Ser Phe Ser Ser Gln Cys
515 520 525

Met Gly Cys Thr Leu Tyr Ile Leu Asp Lys Asn Gly Tyr Pro Met Pro
530 535 540

Lys Asn Lys Pro Gly Ile Gly Glu Leu Ala Leu Gly Pro Val Met Phe
545 550 555 560

Gly Ala Ser Lys Thr Leu Leu Asn Gly Asn His His Asp Val Tyr Phe
565 570 575

Lys Gly Met Pro Thr Leu Asn Gly Glu Val Leu Arg Arg His Gly Asp
580 585 590

Ile Phe Glu Leu Thr Ser Asn Gly Tyr Tyr His Ala His Gly Arg Ala
595 600 605

Asp Asp Thr Met Asn Ile Gly Gly Ile Lys Ile Ser Ser Ile Glu Ile
610 615 620

Glu Arg Val Cys Asn Glu Val Asp Asp Arg Val Phe Glu Thr Thr Ala
625 630 635 640

Ile Gly Val Pro Pro Leu Gly Gly Gly Pro Glu Gln Leu Val Ile Phe
645 650 655

Phe Val Leu Lys Asp Ser Asn Asp Thr Thr Ile Asp Leu Asn Gln Leu
660 665 670

Arg Leu Ser Phe Asn Leu Gly Leu Gln Lys Lys Leu Asn Pro Leu Phe
675 680 685

Lys Val Thr Arg Val Val Pro Leu Ser Ser Leu Pro Arg Thr Ala Thr
690 695 700

Asn Lys Ile Met Arg Arg Val Leu Arg Gln Gln Phe Ser His Phe Glu
705 710 715 720

<210> 91
<211> 1599
<212> DNA
<213> Cannabis sativa

<400> 91
atggaaaagt ctggttatgg tagagatggg atctacaggt ctttaagacc accattgcat 60
ttgccaaaca acaacaactt gtccatgggc agtttcttgg tcagaaactc ttcttcctac 120
ccacaaaaac cagccttgat tgactctgaa actaatcaaa tcttgtcctt ctcccacttc 180
aatccaccg ttattaaggt ttctcacggg ttcttgaact tgggtatcaa gaagaatgac 240
tggttgatct acgctccaaa ctctattcat ttcccagttt gctttttggg tattattgct 300
tctggtgcta ttgctactac ttccaacca ttatacaccg tcagtgaatt gtctaagcaa 360
gtcaaggatt ctaaccctaa gttgattatc accgttccac aattattgga aaagggtcaag 420
ggtttcaact tgccaacat tttgattggg ccagactcag aacaagaatc ctcttcagat 480
aagggtatga ccttcaacga tttgggttaac ttgggtgggt cttctgggtc tgaatttcca 540
atcggtgatg acttcaagca atctgatact gctgctttgt tgtactcttc tgggtactact 600
ggatatgtcta aagggttggt gactcacaag aactttatcg cctcttcttt gatgggtacc 660
atggaacaag acttggttgg tgaaatggat aacgttttct tgtgcttctt gccaatgttc 720
catgttttcg gtttggccat tattacctac gctcaattgc aaagaggtaa cactgttatt 780
tccgccagat tcgatttgga aaagatgttg aaggacgtcg aaaagtatgt tactcatttg 840
tggtggcctc cagttatatt ggctttgtct aaaaactcca tgggttaagtt caacttgta 900
tccatcaagt acattgggtc aggtgctgct ccattgggta aggatttgat ggaagaatgt 960
tctaaatggc catacggat agttgctcaa gggtacggta tgactgaaac ttgtggtatc 1020

gtttctatgg aagatatcag aggtggtaag agaaattctg gttcagctgg tatgttggct	1080
tcagggtgttg aagctcaa atgtttctgtt gataccttga aaccattgcc accaaatcaa	1140
ttgggtgaaa tttgggttaa gggtcctaat atgatgcaag gttacttcaa caatccacaa	1200
gctaccaagt tgaccattga taagaaaggt tgggttcata ctggtgactt gggttacttt	1260
gatgaagatg gtcacttgta ctgggacaga atcaaagaat tgattaagta caagggtttt	1320
caagtcgctc cagctgaatt ggaagggttg ttgggttctc atccagaaat attggatgcc	1380
tggattccat ttccagatgc tgaagctggg gaagttccag ttgcttattg gagatcacca	1440
aactcttcat tgactgaaaa cgacgtcaag aagttcattg ctggtcaagt tgcttctttc	1500
aagagattga gaaaggtcac cttcatcaac tctgttccaa aatctgcttc cggtgaagtc	1560
ttgagaagag aattgatcca aaaggtcaga tccaatatg	1599

<210> 92
 <211> 533
 <212> PRT
 <213> Cannabis sativa

<400> 92

Met	Glu	Lys	Ser	Gly	Tyr	Gly	Arg	Asp	Gly	Ile	Tyr	Arg	Ser	Leu	Arg
1				5					10					15	

Pro	Pro	Leu	His	Leu	Pro	Asn	Asn	Asn	Asn	Leu	Ser	Met	Val	Ser	Phe
			20					25					30		

Leu	Phe	Arg	Asn	Ser	Ser	Ser	Tyr	Pro	Gln	Lys	Pro	Ala	Leu	Ile	Asp
		35					40					45			

Ser	Glu	Thr	Asn	Gln	Ile	Leu	Ser	Phe	Ser	His	Phe	Lys	Ser	Thr	Val
	50					55					60				

Ile	Lys	Val	Ser	His	Gly	Phe	Leu	Asn	Leu	Gly	Ile	Lys	Lys	Asn	Asp
65					70					75				80	

Trp	Leu	Ile	Tyr	Ala	Pro	Asn	Ser	Ile	His	Phe	Pro	Val	Cys	Phe	Leu
				85					90					95	

Gly	Ile	Ile	Ala	Ser	Gly	Ala	Ile	Ala	Thr	Thr	Ser	Asn	Pro	Leu	Tyr
			100					105					110		

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

Ile Ile Thr Val Pro Gln Leu Leu Glu Lys Val Lys Gly Phe Asn Leu
130 135 140

Pro Thr Ile Leu Ile Gly Pro Asp Ser Glu Gln Glu Ser Ser Ser Asp
145 150 155 160

Lys Val Met Thr Phe Asn Asp Leu Val Asn Leu Gly Gly Ser Ser Gly
165 170 175

Ser Glu Phe Pro Ile Val Asp Asp Phe Lys Gln Ser Asp Thr Ala Ala
180 185 190

Leu Leu Tyr Ser Ser Gly Thr Thr Gly Met Ser Lys Gly Trp Leu Thr
195 200 205

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

Leu Val Gly Glu Met Asp Asn Val Phe Leu Cys Phe Leu Pro Met Phe
225 230 235 240

His Val Phe Gly Leu Ala Ile Ile Thr Tyr Ala Gln Leu Gln Arg Gly
245 250 255

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

Val Glu Lys Tyr Val Thr His Leu Trp Trp Pro Pro Val Ile Leu Ala
275 280 285

Leu Ser Lys Asn Ser Met Val Lys Phe Asn Leu Ser Ser Ile Lys Tyr
290 295 300

Ile Gly Ser Gly Ala Ala Pro Leu Gly Lys Asp Leu Met Glu Glu Cys
305 310 315 320

Ser Lys Trp Pro Tyr Gly Ile Val Ala Gln Gly Tyr Gly Met Thr Glu
325 330 335

Thr Cys Gly Ile Val Ser Met Glu Asp Ile Arg Gly Gly Lys Arg Asn
340 345 350

Ser Gly Ser Ala Gly Met Leu Ala Ser Gly Val Glu Ala Gln Ile Val
355 360 365

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

Trp Val Lys Gly Pro Asn Met Met Gln Gly Tyr Phe Asn Asn Pro Gln
385 390 395 400

Ala Thr Lys Leu Thr Ile Asp Lys Lys Gly Trp Val His Thr Gly Asp
405 410 415

Leu Gly Tyr Phe Asp Glu Asp Gly His Leu Tyr Trp Asp Arg Ile Lys
420 425 430

Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu Leu Glu
435 440 445

Gly Leu Leu Val Ser His Pro Glu Ile Leu Asp Ala Trp Ile Pro Phe
450 455 460

Pro Asp Ala Glu Ala Gly Glu Val Pro Val Ala Tyr Trp Arg Ser Pro
465 470 475 480

Asn Ser Ser Leu Thr Glu Asn Asp Val Lys Lys Phe Ile Ala Gly Gln
485 490 495

Val Ala Ser Phe Lys Arg Leu Arg Lys Val Thr Phe Ile Asn Ser Val
500 505 510

Pro Lys Ser Ala Ser Gly Lys Ile Leu Arg Arg Glu Leu Ile Gln Lys
515 520 525

Val Arg Ser Asn Met
530

<210> 93
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial acetoacetyl-CoA reductase (PhaB) nucleotide sequence

<400> 93
atgacgcaga gaatcgccta tgtaacgggt gggatgggtg ggataggaac cgccatatgt 60
cagagactag caaaggacgg attcagggtt gtagccggtt gcggtcctaa tagtccaaga 120
agagagaaat ggttgggaaca gcaaaaagct ctaggatttg attttatagc atcagaaggg 180
aatgttgctg actgggattc tacaaagacg gcatttgaca aagtgaaatc tgaagtcggc 240
gaggtcgatg tcctaattaa caacgccggc atcaccagag atgtggtttt caggaagatg 300
actagggctg actgggacgc cgtgatagac acaaatttga cgagcttggt caacgtcaca 360
aagcaagtaa ttgacggcat ggcagatcgt ggggtggggaa ggatagtcaa tatctccagc 420
gtcaacggtc agaaaggcca gttcggacag actaactact ccacagcgaa ggctggctta 480
cacggattca cgatggcctt ggcccaagag gtggctacta aaggggtgac tgtgaacaca 540
gtgtcaccag gatacatcgc gacggatatg gtcaaagcta ttagacaaga tgtcctggac 600
aagattgttg ccactattcc cgtaaagagg cttgggttac cagaagagat agcttcaatt 660
tgcgcttggc tatctagtga ggaatcaggg ttcagcactg gggcggactt ttcattaaac 720
ggtaggattac acatgggagg atcc 744

<210> 94
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutant acetoacetyl-CoA reductase (PhaB)

<400> 94

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

Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
20 25 30

Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln
35 40 45

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

Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly
65 70 75 80

Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val
85 90 95

Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn
100 105 110

Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala
115 120 125

Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln
130 135 140

Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu
145 150 155 160

His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val
165 170 175

Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys
180 185 190

Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val
195 200 205

Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu
210 215 220

Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn
225 230 235 240

Gly Gly Leu His Met Gly Gly Ser
245

<210> 95
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial (R)-specific enoyl-CoA hydratase (PhaJ)

<400> 95
atgtctgccc agagtctgga agtcggtcaa aaagcaagac tgtcaaaaag atttggggcg 60
gcagaggtag cggcgttcgc ggcgctgtct gaggatttta atccactgca cttagatcct 120
gcgttcgccg cgacaacagc attcgagagg cccatcgtgc acggcatgct acttgcctct 180
ttgttctcag gtctactggg tcaacagtta cctgggaaag gaagcatcta tctgggacag 240
tcattgtctt ttaagctgcc cgtcttcgtc ggcgatgagg tgacagcaga agtagaagtc 300
acagcattga gggaagacaa gcctattgcg acccttacta ctcgtatattt tactcagggc 360
ggagccttag cagtgcagagg agaagctgta gtaaaactac caggatcc 408

<210> 96
<211> 136
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutant (R)-specific enoyl-CoA hydratase (PhaJ)

<400> 96

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

Arg Phe Gly Ala Ala Glu Val Ala Ala Phe Ala Ala Leu Ser Glu Asp
20 25 30

Phe Asn Pro Leu His Leu Asp Pro Ala Phe Ala Ala Thr Thr Ala Phe
35 40 45

Glu Arg Pro Ile Val His Gly Met Leu Leu Ala Ser Leu Phe Ser Gly
50 55 60

Leu Leu Gly Gln Gln Leu Pro Gly Lys Gly Ser Ile Tyr Leu Gly Gln
65 70 75 80

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

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

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

Ala Val Val Lys Leu Pro Gly Ser
130 135

<210> 97
<211> 2233
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutated acetyl-CoA carboxylase (ACC1) (S659A, S1157A)

<400> 97

Met Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr
1 5 10 15

Glu Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe
20 25 30

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

Phe Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile
50 55 60

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

Trp Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala
85 90 95

Met Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met
100 105 110

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

Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp
130 135 140

Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro
145 150 155 160

Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro
165 170 175

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

Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val
195 200 205

Asp Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp
210 215 220

Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln
225 230 235 240

Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly
245 250 255

Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile
260 265 270

Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe
275 280 285

Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu
290 295 300

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

Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile
325 330 335

Ala Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu
340 345 350

Gly Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr
355 360 365

Ser His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu
370 375 380

Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro
385 390 395 400

Ala Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser
405 410 415

Asp Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile
420 425 430

Asp Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro
435 440 445

Ile Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro
450 455 460

Asn Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe
465 470 475 480

Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly
485 490 495

Asn Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe
500 505 510

Gly Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys
515 520 525

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile
530 535 540

Lys Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly
545 550 555 560

Trp Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp
565 570 575

Pro Thr Leu Ala Val Ile Cys Gly Ala Ala Thr Lys Ala Phe Leu Ala
580 585 590

Ser Glu Glu Ala Arg His Lys Tyr Ile Glu Ser Leu Gln Lys Gly Gln
595 600 605

Val Leu Ser Lys Asp Leu Leu Gln Thr Met Phe Pro Val Asp Phe Ile
610 615 620

His Glu Gly Lys Arg Tyr Lys Phe Thr Val Ala Lys Ser Gly Asn Asp
625 630 635 640

Arg Tyr Thr Leu Phe Ile Asn Gly Ser Lys Cys Asp Ile Ile Leu Arg
645 650 655

Gln Leu Ala Asp Gly Gly Leu Leu Ile Ala Ile Gly Gly Lys Ser His
660 665 670

Thr Ile Tyr Trp Lys Glu Glu Val Ala Ala Thr Arg Leu Ser Val Asp
675 680 685

Ser Met Thr Thr Leu Leu Glu Val Glu Asn Asp Pro Thr Gln Leu Arg
690 695 700

Thr Pro Ser Pro Gly Lys Leu Val Lys Phe Leu Val Glu Asn Gly Glu
705 710 715 720

His Ile Ile Lys Gly Gln Pro Tyr Ala Glu Ile Glu Val Met Lys Met
725 730 735

Gln Met Pro Leu Val Ser Gln Glu Asn Gly Ile Val Gln Leu Leu Lys
740 745 750

Gln Pro Gly Ser Thr Ile Val Ala Gly Asp Ile Met Ala Ile Met Thr
755 760 765

Leu Asp Asp Pro Ser Lys Val Lys His Ala Leu Pro Phe Glu Gly Met
770 775 780

Leu Pro Asp Phe Gly Ser Pro Val Ile Glu Gly Thr Lys Pro Ala Tyr
785 790 795 800

Lys Phe Lys Ser Leu Val Ser Thr Leu Glu Asn Ile Leu Lys Gly Tyr
805 810 815

Asp Asn Gln Val Ile Met Asn Ala Ser Leu Gln Gln Leu Ile Glu Val
820 825 830

Leu Arg Asn Pro Lys Leu Pro Tyr Ser Glu Trp Lys Leu His Ile Ser
835 840 845

Ala Leu His Ser Arg Leu Pro Ala Lys Leu Asp Glu Gln Met Glu Glu
850 855 860

Leu Val Ala Arg Ser Leu Arg Arg Gly Ala Val Phe Pro Ala Arg Gln
865 870 875 880

Leu Ser Lys Leu Ile Asp Met Ala Val Lys Asn Pro Glu Tyr Asn Pro
885 890 895

Asp Lys Leu Leu Gly Ala Val Val Glu Pro Leu Ala Asp Ile Ala His
900 905 910

Lys Tyr Ser Asn Gly Leu Glu Ala His Glu His Ser Ile Phe Val His
915 920 925

Phe Leu Glu Glu Tyr Tyr Glu Val Glu Lys Leu Phe Asn Gly Pro Asn
930 935 940

Val Arg Glu Glu Asn Ile Ile Leu Lys Leu Arg Asp Glu Asn Pro Lys
945 950 955 960

Asp Leu Asp Lys Val Ala Leu Thr Val Leu Ser His Ser Lys Val Ser
965 970 975

Ala Lys Asn Asn Leu Ile Leu Ala Ile Leu Lys His Tyr Gln Pro Leu
980 985 990

Cys Lys Leu Ser Ser Lys Val Ser Ala Ile Phe Ser Thr Pro Leu Gln
995 1000 1005

His Ile Val Glu Leu Glu Ser Lys Ala Thr Ala Lys Val Ala Leu
1010 1015 1020

Gln Ala Arg Glu Ile Leu Ile Gln Gly Ala Leu Pro Ser Val Lys
1025 1030 1035

Glu Arg Thr Glu Gln Ile Glu His Ile Leu Lys Ser Ser Val Val
1040 1045 1050

Lys Val Ala Tyr Gly Ser Ser Asn Pro Lys Arg Ser Glu Pro Asp
1055 1060 1065

Leu Asn Ile Leu Lys Asp Leu Ile Asp Ser Asn Tyr Val Val Phe
1070 1075 1080

Asp Val Leu Leu Gln Phe Leu Thr His Gln Asp Pro Val Val Thr
1085 1090 1095

Ala Ala Ala Ala Gln Val Tyr Ile Arg Arg Ala Tyr Arg Ala Tyr
1100 1105 1110

Thr Ile Gly Asp Ile Arg Val His Glu Gly Val Thr Val Pro Ile
1115 1120 1125

Val Glu Trp Lys Phe Gln Leu Pro Ser Ala Ala Phe Ser Thr Phe
1130 1135 1140

Pro Thr Val Lys Ser Lys Met Gly Met Asn Arg Ala Val Ser Val
1145 1150 1155

Ala Asp Leu Ser Tyr Val Ala Asn Ser Gln Ser Ser Pro Leu Arg
1160 1165 1170

Glu Gly Ile Leu Met Ala Val Asp His Leu Asp Asp Val Asp Glu
1175 1180 1185

Ile Leu Ser Gln Ser Leu Glu Val Ile Pro Arg His Gln Ser Ser
1190 1195 1200

Ser Asn Gly Pro Ala Pro Asp Arg Ser Gly Ser Ser Ala Ser Leu
1205 1210 1215

Ser Asn Val Ala Asn Val Cys Val Ala Ser Thr Glu Gly Phe Glu
1220 1225 1230

Ser Glu Glu Glu Ile Leu Val Arg Leu Arg Glu Ile Leu Asp Leu
1235 1240 1245

Asn Lys Gln Glu Leu Ile Asn Ala Ser Ile Arg Arg Ile Thr Phe
1250 1255 1260

Met Phe Gly Phe Lys Asp Gly Ser Tyr Pro Lys Tyr Tyr Thr Phe
1265 1270 1275

Asn Gly Pro Asn Tyr Asn Glu Asn Glu Thr Ile Arg His Ile Glu
1280 1285 1290

Pro Ala Leu Ala Phe Gln Leu Glu Leu Gly Arg Leu Ser Asn Phe
1295 1300 1305

Asn Ile Lys Pro Ile Phe Thr Asp Asn Arg Asn Ile His Val Tyr
1310 1315 1320

Glu Ala Val Ser Lys Thr Ser Pro Leu Asp Lys Arg Phe Phe Thr
1325 1330 1335

Arg Gly Ile Ile Arg Thr Gly His Ile Arg Asp Asp Ile Ser Ile
1340 1345 1350

Gln Glu Tyr Leu Thr Ser Glu Ala Asn Arg Leu Met Ser Asp Ile
1355 1360 1365

Leu	Asp	Asn	Leu	Glu	Val	Thr	Asp	Thr	Ser	Asn	Ser	Asp	Leu	Asn
	1370					1375					1380			
His	Ile	Phe	Ile	Asn	Phe	Ile	Ala	Val	Phe	Asp	Ile	Ser	Pro	Glu
	1385					1390					1395			
Asp	Val	Glu	Ala	Ala	Phe	Gly	Gly	Phe	Leu	Glu	Arg	Phe	Gly	Lys
	1400					1405					1410			
Arg	Leu	Leu	Arg	Leu	Arg	Val	Ser	Ser	Ala	Glu	Ile	Arg	Ile	Ile
	1415					1420					1425			
Ile	Lys	Asp	Pro	Gln	Thr	Gly	Ala	Pro	Val	Pro	Leu	Arg	Ala	Leu
	1430					1435					1440			
Ile	Asn	Asn	Val	Ser	Gly	Tyr	Val	Ile	Lys	Thr	Glu	Met	Tyr	Thr
	1445					1450					1455			
Glu	Val	Lys	Asn	Ala	Lys	Gly	Glu	Trp	Val	Phe	Lys	Ser	Leu	Gly
	1460					1465					1470			
Lys	Pro	Gly	Ser	Met	His	Leu	Arg	Pro	Ile	Ala	Thr	Pro	Tyr	Pro
	1475					1480					1485			
Val	Lys	Glu	Trp	Leu	Gln	Pro	Lys	Arg	Tyr	Lys	Ala	His	Leu	Met
	1490					1495					1500			
Gly	Thr	Thr	Tyr	Val	Tyr	Asp	Phe	Pro	Glu	Leu	Phe	Arg	Gln	Ala
	1505					1510					1515			
Ser	Ser	Ser	Gln	Trp	Lys	Asn	Phe	Ser	Ala	Asp	Val	Lys	Leu	Thr
	1520					1525					1530			
Asp	Asp	Phe	Phe	Ile	Ser	Asn	Glu	Leu	Ile	Glu	Asp	Glu	Asn	Gly
	1535					1540					1545			
Glu	Leu	Thr	Glu	Val	Glu	Arg	Glu	Pro	Gly	Ala	Asn	Ala	Ile	Gly
	1550					1555					1560			
Met	Val	Ala	Phe	Lys	Ile	Thr	Val	Lys	Thr	Pro	Glu	Tyr	Pro	Arg
	1565					1570					1575			

Gly Arg Gln Phe Val Val Val Ala Asn Asp Ile Thr Phe Lys Ile
1580 1585 1590

Gly Ser Phe Gly Pro Gln Glu Asp Glu Phe Phe Asn Lys Val Thr
1595 1600 1605

Glu Tyr Ala Arg Lys Arg Gly Ile Pro Arg Ile Tyr Leu Ala Ala
1610 1615 1620

Asn Ser Gly Ala Arg Ile Gly Met Ala Glu Glu Ile Val Pro Leu
1625 1630 1635

Phe Gln Val Ala Trp Asn Asp Ala Ala Asn Pro Asp Lys Gly Phe
1640 1645 1650

Gln Tyr Leu Tyr Leu Thr Ser Glu Gly Met Glu Thr Leu Lys Lys
1655 1660 1665

Phe Asp Lys Glu Asn Ser Val Leu Thr Glu Arg Thr Val Ile Asn
1670 1675 1680

Gly Glu Glu Arg Phe Val Ile Lys Thr Ile Ile Gly Ser Glu Asp
1685 1690 1695

Gly Leu Gly Val Glu Cys Leu Arg Gly Ser Gly Leu Ile Ala Gly
1700 1705 1710

Ala Thr Ser Arg Ala Tyr His Asp Ile Phe Thr Ile Thr Leu Val
1715 1720 1725

Thr Cys Arg Ser Val Gly Ile Gly Ala Tyr Leu Val Arg Leu Gly
1730 1735 1740

Gln Arg Ala Ile Gln Val Glu Gly Gln Pro Ile Ile Leu Thr Gly
1745 1750 1755

Ala Pro Ala Ile Asn Lys Met Leu Gly Arg Glu Val Tyr Thr Ser
1760 1765 1770

Asn Leu Gln Leu Gly Gly Thr Gln Ile Met Tyr Asn Asn Gly Val
1775 1780 1785

Ser His Leu Thr Ala Val Asp Asp Leu Ala Gly Val Glu Lys Ile
1790 1795 1800

Val Glu Trp Met Ser Tyr Val Pro Ala Lys Arg Asn Met Pro Val
1805 1810 1815

Pro Ile Leu Glu Thr Lys Asp Thr Trp Asp Arg Pro Val Asp Phe
1820 1825 1830

Thr Pro Thr Asn Asp Glu Thr Tyr Asp Val Arg Trp Met Ile Glu
1835 1840 1845

Gly Arg Glu Thr Glu Ser Gly Phe Glu Tyr Gly Leu Phe Asp Lys
1850 1855 1860

Gly Ser Phe Phe Glu Thr Leu Ser Gly Trp Ala Lys Gly Val Val
1865 1870 1875

Val Gly Arg Ala Arg Leu Gly Gly Ile Pro Leu Gly Val Ile Gly
1880 1885 1890

Val Glu Thr Arg Thr Val Glu Asn Leu Ile Pro Ala Asp Pro Ala
1895 1900 1905

Asn Pro Asn Ser Ala Glu Thr Leu Ile Gln Glu Pro Gly Gln Val
1910 1915 1920

Trp His Pro Asn Ser Ala Phe Lys Thr Ala Gln Ala Ile Asn Asp
1925 1930 1935

Phe Asn Asn Gly Glu Gln Leu Pro Met Met Ile Leu Ala Asn Trp
1940 1945 1950

Arg Gly Phe Ser Gly Gly Gln Arg Asp Met Phe Asn Glu Val Leu
1955 1960 1965

Lys Tyr Gly Ser Phe Ile Val Asp Ala Leu Val Asp Tyr Lys Gln
1970 1975 1980

Pro 1985	Ile	Ile	Ile	Tyr	Ile	Pro 1990	Pro	Thr	Gly	Glu	Leu 1995	Arg	Gly	Gly
Ser 2000	Trp	Val	Val	Val	Asp	Pro 2005	Thr	Ile	Asn	Ala	Asp 2010	Gln	Met	Glu
Met 2015	Tyr	Ala	Asp	Val	Asn	Ala 2020	Arg	Ala	Gly	Val	Leu 2025	Glu	Pro	Gln
Gly 2030	Met	Val	Gly	Ile	Lys	Phe 2035	Arg	Arg	Glu	Lys	Leu 2040	Leu	Asp	Thr
Met 2045	Asn	Arg	Leu	Asp	Asp	Lys 2050	Tyr	Arg	Glu	Leu	Arg 2055	Ser	Gln	Leu
Ser 2060	Asn	Lys	Ser	Leu	Ala	Pro 2065	Glu	Val	His	Gln	Gln 2070	Ile	Ser	Lys
Gln 2075	Leu	Ala	Asp	Arg	Glu	Arg 2080	Glu	Leu	Leu	Pro	Ile 2085	Tyr	Gly	Gln
Ile 2090	Ser	Leu	Gln	Phe	Ala	Asp 2095	Leu	His	Asp	Arg	Ser 2100	Ser	Arg	Met
Val 2105	Ala	Lys	Gly	Val	Ile	Ser 2110	Lys	Glu	Leu	Glu	Trp 2115	Thr	Glu	Ala
Arg 2120	Arg	Phe	Phe	Phe	Trp	Arg 2125	Leu	Arg	Arg	Arg	Leu 2130	Asn	Glu	Glu
Tyr 2135	Leu	Ile	Lys	Arg	Leu	Ser 2140	His	Gln	Val	Gly	Glu 2145	Ala	Ser	Arg
Leu 2150	Glu	Lys	Ile	Ala	Arg	Ile 2155	Arg	Ser	Trp	Tyr	Pro 2160	Ala	Ser	Val
Asp 2165	His	Glu	Asp	Asp	Arg	Gln 2170	Val	Ala	Thr	Trp	Ile 2175	Glu	Glu	Asn

Tyr Lys Thr Leu Asp Asp Lys Leu Lys Gly Leu Lys Leu Glu Ser
2180 2185 2190

Phe Ala Gln Asp Leu Ala Lys Lys Ile Arg Ser Asp His Asp Asn
2195 2200 2205

Ala Ile Asp Gly Leu Ser Glu Val Ile Lys Met Leu Ser Thr Asp
2210 2215 2220

Asp Lys Glu Lys Leu Leu Lys Thr Leu Lys
2225 2230

<210> 98
<211> 321
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated geranyl pyrophosphate olivetolic acid
geranyltransferase CsGOTt75

<400> 98

Met Ala Ala Thr Thr Asn Gln Thr Glu Pro Pro Glu Ser Asp Asn His
1 5 10 15

Ser Val Ala Thr Lys Ile Leu Asn Phe Gly Lys Ala Cys Trp Lys Leu
20 25 30

Gln Arg Pro Tyr Thr Ile Ile Ala Phe Thr Ser Cys Ala Cys Gly Leu
35 40 45

Phe Gly Lys Glu Leu Leu His Asn Thr Asn Leu Ile Ser Trp Ser Leu
50 55 60

Met Phe Lys Ala Phe Phe Phe Leu Val Ala Ile Leu Cys Ile Ala Ser
65 70 75 80

Phe Thr Thr Thr Ile Asn Gln Ile Tyr Asp Leu His Ile Asp Arg Ile
85 90 95

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

Ala Trp Ile Met Ser Ile Ile Val Ala Leu Phe Gly Leu Ile Ile Thr
115 120 125

Ile Lys Met Lys Gly Gly Pro Leu Tyr Ile Phe Gly Tyr Cys Phe Gly
130 135 140

Ile Phe Gly Gly Ile Val Tyr Ser Val Pro Pro Phe Arg Trp Lys Gln
145 150 155 160

Asn Pro Ser Thr Ala Phe Leu Leu Asn Phe Leu Ala His Ile Ile Thr
165 170 175

Asn Phe Thr Phe Tyr Tyr Ala Ser Arg Ala Ala Leu Gly Leu Pro Phe
180 185 190

Glu Leu Arg Pro Ser Phe Thr Phe Leu Leu Ala Phe Met Lys Ser Met
195 200 205

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

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

Leu Thr Leu Phe Cys Ser Gly Ile Val Leu Leu Ser Tyr Val Ala Ala
245 250 255

Ile Leu Ala Gly Ile Ile Trp Pro Gln Ala Phe Asn Ser Asn Val Met
260 265 270

Leu Leu Ser His Ala Ile Leu Ala Phe Trp Leu Ile Leu Gln Thr Arg
275 280 285

Asp Phe Ala Leu Thr Asn Tyr Asp Pro Glu Ala Gly Arg Arg Phe Tyr
290 295 300

Glu Phe Met Trp Lys Leu Tyr Tyr Ala Glu Tyr Leu Val Tyr Val Phe
305 310 315 320

Ile

<210> 99
<211> 363
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated geranyl pyrophosphate olivetolic acid
geranyltransferase CsGOTt33

<400> 99

Met Ser His Pro Lys Thr Pro Ile Lys Tyr Ser Tyr Asn Asn Phe Pro
1 5 10 15

Ser Lys His Cys Ser Thr Lys Ser Phe His Leu Gln Asn Lys Cys Ser
20 25 30

Glu Ser Leu Ser Ile Ala Lys Asn Ser Ile Arg Ala Ala Thr Thr Asn
35 40 45

Gln Thr Glu Pro Pro Glu Ser Asp Asn His Ser Val Ala Thr Lys Ile
50 55 60

Leu Asn Phe Gly Lys Ala Cys Trp Lys Leu Gln Arg Pro Tyr Thr Ile
65 70 75 80

Ile Ala Phe Thr Ser Cys Ala Cys Gly Leu Phe Gly Lys Glu Leu Leu
85 90 95

His Asn Thr Asn Leu Ile Ser Trp Ser Leu Met Phe Lys Ala Phe Phe
100 105 110

Phe Leu Val Ala Ile Leu Cys Ile Ala Ser Phe Thr Thr Thr Ile Asn
115 120 125

Gln Ile Tyr Asp Leu His Ile Asp Arg Ile Asn Lys Pro Asp Leu Pro
130 135 140

Leu Ala Ser Gly Glu Ile Ser Val Asn Thr Ala Trp Ile Met Ser Ile
145 150 155 160

Ile Val Ala Leu Phe Gly Leu Ile Ile Thr Ile Lys Met Lys Gly Gly
165 170 175

Pro Leu Tyr Ile Phe Gly Tyr Cys Phe Gly Ile Phe Gly Gly Ile Val
180 185 190

Tyr Ser Val Pro Pro Phe Arg Trp Lys Gln Asn Pro Ser Thr Ala Phe
195 200 205

Leu Leu Asn Phe Leu Ala His Ile Ile Thr Asn Phe Thr Phe Tyr Tyr
210 215 220

Ala Ser Arg Ala Ala Leu Gly Leu Pro Phe Glu Leu Arg Pro Ser Phe
225 230 235 240

Thr Phe Leu Leu Ala Phe Met Lys Ser Met Gly Ser Ala Leu Ala Leu
245 250 255

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

Thr Leu Ala Ser Lys Tyr Gly Ser Arg Asn Leu Thr Leu Phe Cys Ser
275 280 285

Gly Ile Val Leu Leu Ser Tyr Val Ala Ala Ile Leu Ala Gly Ile Ile
290 295 300

Trp Pro Gln Ala Phe Asn Ser Asn Val Met Leu Leu Ser His Ala Ile
305 310 315 320

Leu Ala Phe Trp Leu Ile Leu Gln Thr Arg Asp Phe Ala Leu Thr Asn
325 330 335

Tyr Asp Pro Glu Ala Gly Arg Arg Phe Tyr Glu Phe Met Trp Lys Leu
340 345 350

Tyr Tyr Ala Glu Tyr Leu Val Tyr Val Phe Ile
355 360

<210> 100

<211> 323

<212> PRT
<213> Artificial Sequence

<220>

<223> Truncated geranyl pyrophosphate olivetolic acid
geranyltransferase CsPT4t

<400> 100

Met Ser Ala Gly Ser Asp Gln Ile Glu Gly Ser Pro His His Glu Ser
1 5 10 15

Asp Asn Ser Ile Ala Thr Lys Ile Leu Asn Phe Gly His Thr Cys Trp
20 25 30

Lys Leu Gln Arg Pro Tyr Val Val Lys Gly Met Ile Ser Ile Ala Cys
35 40 45

Gly Leu Phe Gly Arg Glu Leu Phe Asn Asn Arg His Leu Phe Ser Trp
50 55 60

Gly Leu Met Trp Lys Ala Phe Phe Ala Leu Val Pro Ile Leu Ser Phe
65 70 75 80

Asn Phe Phe Ala Ala Ile Met Asn Gln Ile Tyr Asp Val Asp Ile Asp
85 90 95

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

Glu Thr Ala Trp Ile Leu Ser Ile Ile Val Ala Leu Thr Gly Leu Ile
115 120 125

Val Thr Ile Lys Leu Lys Ser Ala Pro Leu Phe Val Phe Ile Tyr Ile
130 135 140

Phe Gly Ile Phe Ala Gly Phe Ala Tyr Ser Val Pro Pro Ile Arg Trp
145 150 155 160

Lys Gln Tyr Pro Phe Thr Asn Phe Leu Ile Thr Ile Ser Ser His Val
165 170 175

Gly Leu Ala Phe Thr Ser Tyr Ser Ala Thr Thr Ser Ala Leu Gly Leu

180

185

190

Pro Phe Val Trp Arg Pro Ala Phe Ser Phe Ile Ile Ala Phe Met Thr
 195 200 205

Val Met Gly Met Thr Ile Ala Phe Ala Lys Asp Ile Ser Asp Ile Glu
 210 215 220

Gly Asp Ala Lys Tyr Gly Val Ser Thr Val Ala Thr Lys Leu Gly Ala
 225 230 235 240

Arg Asn Met Thr Phe Val Val Ser Gly Val Leu Leu Leu Asn Tyr Leu
 245 250 255

Val Ser Ile Ser Ile Gly Ile Ile Trp Pro Gln Val Phe Lys Ser Asn
 260 265 270

Ile Met Ile Leu Ser His Ala Ile Leu Ala Phe Cys Leu Ile Phe Gln
 275 280 285

Thr Arg Glu Leu Ala Leu Ala Asn Tyr Ala Ser Ala Pro Ser Arg Gln
 290 295 300

Phe Phe Glu Phe Ile Trp Leu Leu Tyr Tyr Ala Glu Tyr Phe Val Tyr
 305 310 315 320

Val Phe Ile

<210> 101

<211> 323

<212> PRT

<213> Artificial Sequence

<220>

<223> Truncated geranyl pyrophosphate olivetolic acid
 geranyltransferase CsPT7t

<400> 101

Met Ser Thr Asp Thr Ala Asn Gln Thr Glu Pro Pro Glu Ser Asn Thr
 1 5 10 15

Lys Tyr Ser Val Val Thr Lys Ile Leu Ser Phe Gly His Thr Cys Trp
20 25 30

Lys Leu Gln Arg Pro Tyr Thr Phe Ile Gly Val Ile Ser Cys Ala Cys
35 40 45

Gly Leu Phe Gly Arg Glu Leu Phe His Asn Thr Asn Leu Leu Ser Trp
50 55 60

Ser Leu Met Leu Lys Ala Phe Ser Ser Leu Met Val Ile Leu Ser Val
65 70 75 80

Asn Leu Cys Thr Asn Ile Ile Asn Gln Ile Thr Asp Leu Asp Ile Asp
85 90 95

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

Glu Thr Ala Trp Ile Met Ser Ile Ile Val Ala Leu Thr Gly Leu Ile
115 120 125

Leu Thr Ile Lys Leu Asn Cys Gly Pro Leu Phe Ile Ser Leu Tyr Cys
130 135 140

Val Ser Ile Leu Val Gly Ala Leu Tyr Ser Val Pro Pro Phe Arg Trp
145 150 155 160

Lys Gln Asn Pro Asn Thr Ala Phe Ser Ser Tyr Phe Met Gly Leu Val
165 170 175

Ile Val Asn Phe Thr Cys Tyr Tyr Ala Ser Arg Ala Ala Phe Gly Leu
180 185 190

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

Ser Met Gly Ser Ala Leu Phe Leu Cys Lys Asp Val Ser Asp Ile Glu
210 215 220

Gly Asp Ser Lys His Gly Ile Ser Thr Leu Ala Thr Arg Tyr Gly Ala
225 230 235 240

Lys Asn Ile Thr Phe Leu Cys Ser Gly Ile Val Leu Leu Thr Tyr Val
245 250 255

Ser Ala Ile Leu Ala Ala Ile Ile Trp Pro Gln Ala Phe Lys Ser Asn
260 265 270

Val Met Leu Leu Ser His Ala Thr Leu Ala Phe Trp Leu Ile Phe Gln
275 280 285

Thr Arg Glu Phe Ala Leu Thr Asn Tyr Asn Pro Glu Ala Gly Arg Lys
290 295 300

Phe Tyr Glu Phe Met Trp Lys Leu His Tyr Ala Glu Tyr Leu Val Tyr
305 310 315 320

Val Phe Ile

<210> 102
<211> 315
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated geranyl pyrophosphate olivetolic acid
geranyltransferase HlPT1Lt

<400> 102

Met Asp Arg Pro Pro Glu Ser Gly Asn Leu Ser Ala Leu Thr Asn Val
1 5 10 15

Lys Asp Phe Val Ser Val Cys Trp Glu Tyr Val Arg Pro Tyr Thr Ala
20 25 30

Lys Gly Val Ile Ile Cys Ser Ser Cys Leu Phe Gly Arg Glu Leu Leu
35 40 45

Glu Asn Pro Asn Leu Phe Ser Trp Pro Leu Ile Phe Arg Ala Leu Leu
50 55 60

Gly Met Leu Ala Ile Leu Gly Ser Cys Phe Tyr Thr Ala Gly Ile Asn

65

70

75

80

Gln Ile Phe Asp Met Asp Ile Asp Arg Ile Asn Lys Pro Asp Leu Pro
 85 90 95

Leu Val Ser Gly Arg Ile Ser Val Glu Ser Ala Trp Leu Leu Thr Leu
 100 105 110

Ser Pro Ala Ile Ile Gly Phe Ile Leu Ile Leu Lys Leu Asn Ser Gly
 115 120 125

Pro Leu Leu Thr Ser Leu Tyr Cys Leu Ala Ile Leu Ser Gly Thr Ile
 130 135 140

Tyr Ser Val Pro Pro Phe Arg Trp Lys Lys Asn Pro Ile Thr Ala Phe
 145 150 155 160

Leu Cys Ile Leu Met Ile His Ala Gly Leu Asn Phe Ser Val Tyr Tyr
 165 170 175

Ala Ser Arg Ala Ala Leu Gly Leu Ala Phe Val Trp Ser Pro Ser Phe
 180 185 190

Ser Phe Ile Thr Ala Phe Ile Thr Phe Met Thr Leu Thr Leu Ala Ser
 195 200 205

Ser Lys Asp Leu Ser Asp Ile Asn Gly Asp Arg Lys Phe Gly Val Glu
 210 215 220

Thr Phe Ala Thr Lys Leu Gly Ala Lys Asn Ile Thr Leu Leu Gly Thr
 225 230 235 240

Gly Leu Leu Leu Leu Asn Tyr Val Ala Ala Ile Ser Thr Ala Ile Ile
 245 250 255

Trp Pro Lys Ala Phe Lys Ser Asn Ile Met Leu Leu Ser His Ala Ile
 260 265 270

Leu Ala Phe Ser Leu Phe Phe Gln Ala Arg Glu Leu Asp Arg Thr Asn
 275 280 285

Tyr Thr Pro Glu Ala Cys Lys Ser Phe Tyr Glu Phe Ile Trp Ile Leu
290 295 300

Phe Ser Ala Glu Tyr Val Val Tyr Leu Phe Ile
305 310 315

<210> 103
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated geranyl pyrophosphate olivetolic acid
geranyltransferase H1PT2t

<400> 103

Met Gly His Leu Pro Arg Pro Asn Ser Leu Thr Ala Trp Ser His Gln
1 5 10 15

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

Ala Ser Trp Lys Phe Val Arg Pro Ile Pro Phe Val Ala Val Ser Ile
35 40 45

Ile Cys Thr Ser Leu Phe Gly Ala Glu Leu Leu Lys Asn Pro Asn Leu
50 55 60

Phe Ser Trp Gln Leu Met Phe Asp Ala Phe Gln Gly Leu Val Val Ile
65 70 75 80

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

Glu Ser Asp Arg Ile Asn Lys Pro Asp Leu Pro Leu Ala Ala Glu Glu
100 105 110

Met Ser Val Lys Ser Ala Trp Phe Leu Thr Ile Phe Ser Ala Val Ala
115 120 125

Ser Leu Leu Leu Met Ile Lys Leu Lys Cys Gly Leu Phe Leu Thr Cys
130 135 140

Met Tyr Cys Cys Tyr Leu Val Ile Gly Ala Met Tyr Ser Val Pro Pro
145 150 155 160

Phe Arg Trp Lys Met Asn Thr Phe Thr Ser Thr Leu Trp Asn Phe Ser
165 170 175

Glu Ile Gly Ile Gly Ile Asn Phe Leu Ile Asn Tyr Ala Ser Arg Ala
180 185 190

Thr Leu Gly Leu Pro Phe Gln Trp Arg Pro Pro Phe Thr Phe Ile Ile
195 200 205

Gly Phe Val Ser Thr Leu Ser Ile Ile Leu Ser Ile Leu Lys Asp Val
210 215 220

Pro Asp Val Glu Gly Asp Lys Lys Val Gly Met Ser Thr Leu Pro Val
225 230 235 240

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

Leu Asn Tyr Val Ala Ala Ile Gly Val Ala Ile Met Trp Pro Gln Ala
260 265 270

Phe Lys Gly Tyr Ile Met Ile Pro Ala His Ala Ile Phe Ala Ser Ala
275 280 285

Leu Ile Phe Lys Thr Trp Leu Leu Asp Lys Ala Asn Tyr Ala Lys Glu
290 295 300

Ala Ser Asp Ser Tyr Tyr His Phe Leu Trp Phe Leu Met Ile Ala Glu
305 310 315 320

Tyr Ile Leu Tyr Pro Phe Ile Ser Thr
325

<210> 104
<211> 514
<212> PRT
<213> Artificial Sequence

<220>

<223> Truncated tetrahydrocannabinolic acid synthase THCAST28

<400> 104

Met Asn Phe Leu Lys Cys Phe Ser Glu Tyr Ile Pro Asn Asn Pro Ala
1 5 10 15

Asn Pro Lys Phe Ile Tyr Thr Gln His Asp Gln Leu Tyr Met Ser Val
20 25 30

Leu Asn Ser Thr Ile Gln Asn Leu Arg Phe Thr Ser Asp Thr Thr Pro
35 40 45

Lys Pro Leu Val Ile Val Thr Pro Ser Asn Val Ser His Ile Gln Ala
50 55 60

Ser Ile Leu Cys Ser Lys Lys Val Gly Leu Gln Ile Arg Thr Arg Ser
65 70 75 80

Gly Gly His Asp Ala Glu Gly Met Ser Tyr Ile Ser Gln Val Pro Phe
85 90 95

Val Val Val Asp Leu Arg Asn Met His Ser Ile Lys Ile Asp Val His
100 105 110

Ser Gln Thr Ala Trp Val Glu Ala Gly Ala Thr Leu Gly Glu Val Tyr
115 120 125

Tyr Trp Ile Asn Glu Lys Asn Glu Asn Phe Ser Phe Pro Gly Gly Tyr
130 135 140

Cys Pro Thr Val Gly Val Gly Gly His Phe Ser Gly Gly Gly Tyr Gly
145 150 155 160

Ala Leu Met Arg Asn Tyr Gly Leu Ala Ala Asp Asn Ile Ile Asp Ala
165 170 175

His Leu Val Asn Val Asp Gly Lys Val Leu Asp Arg Lys Ser Met Gly
180 185 190

Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Gly Glu Asn Phe Gly
195 200 205

Ile Ile Ala Ala Trp Lys Ile Lys Leu Val Ala Val Pro Ser Lys Ser
210 215 220

Thr Ile Phe Ser Val Lys Lys Asn Met Glu Ile His Gly Leu Val Lys
225 230 235 240

Leu Phe Asn Lys Trp Gln Asn Ile Ala Tyr Lys Tyr Asp Lys Asp Leu
245 250 255

Val Leu Met Thr His Phe Ile Thr Lys Asn Ile Thr Asp Asn His Gly
260 265 270

Lys Asn Lys Thr Thr Val His Gly Tyr Phe Ser Ser Ile Phe His Gly
275 280 285

Gly Val Asp Ser Leu Val Asp Leu Met Asn Lys Ser Phe Pro Glu Leu
290 295 300

Gly Ile Lys Lys Thr Asp Cys Lys Glu Phe Ser Trp Ile Asp Thr Thr
305 310 315 320

Ile Phe Tyr Ser Gly Val Val Asn Phe Asn Thr Ala Asn Phe Lys Lys
325 330 335

Glu Ile Leu Leu Asp Arg Ser Ala Gly Lys Lys Thr Ala Phe Ser Ile
340 345 350

Lys Leu Asp Tyr Val Lys Lys Pro Ile Pro Glu Thr Ala Met Val Lys
355 360 365

Ile Leu Glu Lys Leu Tyr Glu Glu Asp Val Gly Val Gly Met Tyr Val
370 375 380

Leu Tyr Pro Tyr Gly Gly Ile Met Glu Glu Ile Ser Glu Ser Ala Ile
385 390 395 400

Pro Phe Pro His Arg Ala Gly Ile Met Tyr Glu Leu Trp Tyr Thr Ala
405 410 415

Ser Trp Glu Lys Gln Glu Asp Asn Glu Lys His Ile Asn Trp Val Arg
420 425 430

Ser Val Tyr Asn Phe Thr Thr Pro Tyr Val Ser Gln Asn Pro Arg Leu
435 440 445

Ala Tyr Leu Asn Tyr Arg Asp Leu Asp Leu Gly Lys Thr Asn Pro Glu
450 455 460

Ser Pro Asn Asn Tyr Thr Gln Ala Arg Ile Trp Gly Glu Lys Tyr Phe
465 470 475 480

Gly Lys Asn Phe Asn Arg Leu Val Lys Val Lys Thr Lys Ala Asp Pro
485 490 495

Asn Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro Pro Leu Pro Pro His
500 505 510

His His

<210> 105
<211> 517
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated cannabidiolic acid synthase CBDAS28*

<400> 105

Met Asn Pro Arg Glu Asn Phe Leu Lys Cys Phe Ser Gln Tyr Ile Pro
1 5 10 15

Asn Asn Ala Thr Asn Leu Lys Leu Val Tyr Thr Gln Asn Asn Pro Leu
20 25 30

Tyr Met Ser Val Leu Asn Ser Thr Ile His Asn Leu Arg Phe Thr Ser
35 40 45

Asp Thr Thr Pro Lys Pro Leu Val Ile Val Thr Pro Ser His Val Ser
50 55 60

His Ile Gln Gly Thr Ile Leu Cys Ser Lys Lys Val Gly Leu Gln Ile
65 70 75 80

Arg Thr Arg Ser Gly Gly His Asp Ser Glu Gly Met Ser Tyr Ile Ser
85 90 95

Gln Val Pro Phe Val Ile Val Asp Leu Arg Asn Met Arg Ser Ile Lys
100 105 110

Ile Asp Val His Ser Gln Thr Ala Trp Val Glu Ala Gly Ala Thr Leu
115 120 125

Gly Glu Val Tyr Tyr Trp Val Asn Glu Lys Asn Glu Asn Leu Ser Leu
130 135 140

Ala Ala Gly Tyr Cys Pro Thr Val Cys Ala Gly Gly His Phe Gly Gly
145 150 155 160

Gly Gly Tyr Gly Pro Leu Met Arg Asn Tyr Gly Leu Ala Ala Asp Asn
165 170 175

Ile Ile Asp Ala His Leu Val Asn Val His Gly Lys Val Leu Asp Arg
180 185 190

Lys Ser Met Gly Glu Asp Leu Phe Trp Ala Leu Arg Gly Gly Gly Ala
195 200 205

Glu Ser Phe Gly Ile Ile Val Ala Trp Lys Ile Arg Leu Val Ala Val
210 215 220

Pro Lys Ser Thr Met Phe Ser Val Lys Lys Ile Met Glu Ile His Glu
225 230 235 240

Leu Val Lys Leu Val Asn Lys Trp Gln Asn Ile Ala Tyr Lys Tyr Asp
245 250 255

Lys Asp Leu Leu Leu Met Thr His Phe Ile Thr Arg Asn Ile Thr Asp
260 265 270

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

Phe Leu Gly Gly Val Asp Ser Leu Val Asp Leu Met Asn Lys Ser Phe
290 295 300

Pro Glu Leu Gly Ile Lys Lys Thr Asp Cys Arg Gln Leu Ser Trp Ile
305 310 315 320

Asp Thr Ile Ile Phe Tyr Ser Gly Val Val Asn Tyr Asp Thr Asp Asn
325 330 335

Phe Asn Lys Glu Ile Leu Leu Asp Arg Ser Ala Gly Gln Asn Gly Ala
340 345 350

Phe Lys Ile Lys Leu Asp Tyr Val Lys Lys Pro Ile Pro Glu Ser Val
355 360 365

Phe Val Gln Ile Leu Glu Lys Leu Tyr Glu Glu Asp Ile Gly Ala Gly
370 375 380

Met Tyr Ala Leu Tyr Pro Tyr Gly Gly Ile Met Asp Glu Ile Ser Glu
385 390 395 400

Ser Ala Ile Pro Phe Pro His Arg Ala Gly Ile Leu Tyr Glu Leu Trp
405 410 415

Tyr Ile Cys Ser Trp Glu Lys Gln Glu Asp Asn Glu Lys His Leu Asn
420 425 430

Trp Ile Arg Asn Ile Tyr Asn Phe Met Thr Pro Tyr Val Ser Lys Asn
435 440 445

Pro Arg Leu Ala Tyr Leu Asn Tyr Arg Asp Leu Asp Ile Gly Ile Asn
450 455 460

Asp Pro Lys Asn Pro Asn Asn Tyr Thr Gln Ala Arg Ile Trp Gly Glu
465 470 475 480

Lys Tyr Phe Gly Lys Asn Phe Asp Arg Leu Val Lys Val Lys Thr Leu
485 490 495

Val Asp Pro Asn Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro Pro Leu
500 505 510

Pro Arg His Arg His
515

<210> 106
<211> 2051
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutated fatty acid synthase (FAS1, I306A, R1834K)

<400> 106

Met Asp Ala Tyr Ser Thr Arg Pro Leu Thr Leu Ser His Gly Ser Leu
1 5 10 15

Glu His Val Leu Leu Val Pro Thr Ala Ser Phe Phe Ile Ala Ser Gln
20 25 30

Leu Gln Glu Gln Phe Asn Lys Ile Leu Pro Glu Pro Thr Glu Gly Phe
35 40 45

Ala Ala Asp Asp Glu Pro Thr Thr Pro Ala Glu Leu Val Gly Lys Phe
50 55 60

Leu Gly Tyr Val Ser Ser Leu Val Glu Pro Ser Lys Val Gly Gln Phe
65 70 75 80

Asp Gln Val Leu Asn Leu Cys Leu Thr Glu Phe Glu Asn Cys Tyr Leu
85 90 95

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

Asp Thr Thr Leu Val Lys Thr Lys Glu Leu Ile Lys Asn Tyr Ile Thr
115 120 125

Ala Arg Ile Met Ala Lys Arg Pro Phe Asp Lys Lys Ser Asn Ser Ala
130 135 140

Leu Phe Arg Ala Val Gly Glu Gly Asn Ala Gln Leu Val Ala Ile Phe
145 150 155 160

Gly Gly Gln Gly Asn Thr Asp Asp Tyr Phe Glu Glu Leu Arg Asp Leu
165 170 175

Tyr Gln Thr Tyr His Val Leu Val Gly Asp Leu Ile Lys Phe Ser Ala
180 185 190

Glu Thr Leu Ser Glu Leu Ile Arg Thr Thr Leu Asp Ala Glu Lys Val
195 200 205

Phe Thr Gln Gly Leu Asn Ile Leu Glu Trp Leu Glu Asn Pro Ser Asn
210 215 220

Thr Pro Asp Lys Asp Tyr Leu Leu Ser Ile Pro Ile Ser Cys Pro Leu
225 230 235 240

Ile Gly Val Ile Gln Leu Ala His Tyr Val Val Thr Ala Lys Leu Leu
245 250 255

Gly Phe Thr Pro Gly Glu Leu Arg Ser Tyr Leu Lys Gly Ala Thr Gly
260 265 270

His Ser Gln Gly Leu Val Thr Ala Val Ala Ile Ala Glu Thr Asp Ser
275 280 285

Trp Glu Ser Phe Phe Val Ser Val Arg Lys Ala Ile Thr Val Leu Phe
290 295 300

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

Pro Ser Ile Leu Glu Asp Ser Leu Glu Asn Asn Glu Gly Val Pro Ser
325 330 335

Pro Met Leu Ser Ile Ser Asn Leu Thr Gln Glu Gln Val Gln Asp Tyr
340 345 350

Val Asn Lys Thr Asn Ser His Leu Pro Ala Gly Lys Gln Val Glu Ile
355 360 365

Ser Leu Val Asn Gly Ala Lys Asn Leu Val Val Ser Gly Pro Pro Gln
370 375 380

Ser Leu Tyr Gly Leu Asn Leu Thr Leu Arg Lys Ala Lys Ala Pro Ser
385 390 395 400

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

Ser Asn Arg Phe Leu Pro Val Ala Ser Pro Phe His Ser His Leu Leu
420 425 430

Val Pro Ala Ser Asp Leu Ile Asn Lys Asp Leu Val Lys Asn Asn Val
435 440 445

Ser Phe Asn Ala Lys Asp Ile Gln Ile Pro Val Tyr Asp Thr Phe Asp
450 455 460

Gly Ser Asp Leu Arg Val Leu Ser Gly Ser Ile Ser Glu Arg Ile Val
465 470 475 480

Asp Cys Ile Ile Arg Leu Pro Val Lys Trp Glu Thr Thr Thr Gln Phe
485 490 495

Lys Ala Thr His Ile Leu Asp Phe Gly Pro Gly Gly Ala Ser Gly Leu
500 505 510

Gly Val Leu Thr His Arg Asn Lys Asp Gly Thr Gly Val Arg Val Ile
515 520 525

Val Ala Gly Thr Leu Asp Ile Asn Pro Asp Asp Asp Tyr Gly Phe Lys
530 535 540

Gln Glu Ile Phe Asp Val Thr Ser Asn Gly Leu Lys Lys Asn Pro Asn
545 550 555 560

Trp Leu Glu Glu Tyr His Pro Lys Leu Ile Lys Asn Lys Ser Gly Lys
565 570 575

Ile Phe Val Glu Thr Lys Phe Ser Lys Leu Ile Gly Arg Pro Pro Leu
580 585 590

Leu Val Pro Gly Met Thr Pro Cys Thr Val Ser Pro Asp Phe Val Ala
595 600 605

Ala Thr Thr Asn Ala Gly Tyr Thr Ile Glu Leu Ala Gly Gly Gly Tyr
610 615 620

Phe Ser Ala Ala Gly Met Thr Ala Ala Ile Asp Ser Val Val Ser Gln
625 630 635 640

Ile Glu Lys Gly Ser Thr Phe Gly Ile Asn Leu Ile Tyr Val Asn Pro
645 650 655

Phe Met Leu Gln Trp Gly Ile Pro Leu Ile Lys Glu Leu Arg Ser Lys
660 665 670

Gly Tyr Pro Ile Gln Phe Leu Thr Ile Gly Ala Gly Val Pro Ser Leu
675 680 685

Glu Val Ala Ser Glu Tyr Ile Glu Thr Leu Gly Leu Lys Tyr Leu Gly
690 695 700

Leu Lys Pro Gly Ser Ile Asp Ala Ile Ser Gln Val Ile Asn Ile Ala
705 710 715 720

Lys Ala His Pro Asn Phe Pro Ile Ala Leu Gln Trp Thr Gly Gly Arg
725 730 735

Gly Gly Gly His His Ser Phe Glu Asp Ala His Thr Pro Met Leu Gln
740 745 750

Met Tyr Ser Lys Ile Arg Arg His Pro Asn Ile Met Leu Ile Phe Gly
755 760 765

Ser Gly Phe Gly Ser Ala Asp Asp Thr Tyr Pro Tyr Leu Thr Gly Glu
770 775 780

Trp Ser Thr Lys Phe Asp Tyr Pro Pro Met Pro Phe Asp Gly Phe Leu
785 790 795 800

Phe Gly Ser Arg Val Met Ile Ala Lys Glu Val Lys Thr Ser Pro Asp
805 810 815

Ala Lys Lys Cys Ile Ala Ala Cys Thr Gly Val Pro Asp Asp Lys Trp
820 825 830

Glu Gln Thr Tyr Lys Lys Pro Thr Gly Gly Ile Val Thr Val Arg Ser
835 840 845

Glu Met Gly Glu Pro Ile His Lys Ile Ala Thr Arg Gly Val Met Leu
850 855 860

Trp Lys Glu Phe Asp Glu Thr Ile Phe Asn Leu Pro Lys Asn Lys Leu
865 870 875 880

Val Pro Thr Leu Glu Ala Lys Arg Asp Tyr Ile Ile Ser Arg Leu Asn
885 890 895

Ala Asp Phe Gln Lys Pro Trp Phe Ala Thr Val Asn Gly Gln Ala Arg
900 905 910

Asp Leu Ala Thr Met Thr Tyr Glu Glu Val Ala Lys Arg Leu Val Glu
915 920 925

Leu Met Phe Ile Arg Ser Thr Asn Ser Trp Phe Asp Val Thr Trp Arg
930 935 940

Thr Phe Thr Gly Asp Phe Leu Arg Arg Val Glu Glu Arg Phe Thr Lys
945 950 955 960

Ser Lys Thr Leu Ser Leu Ile Gln Ser Tyr Ser Leu Leu Asp Lys Pro
965 970 975

Asp Glu Ala Ile Glu Lys Val Phe Asn Ala Tyr Pro Ala Ala Arg Glu
980 985 990

Gln Phe Leu Asn Ala Gln Asp Ile Asp His Phe Leu Ser Met Cys Gln
995 1000 1005

Asn Pro Met Gln Lys Pro Val Pro Phe Val Pro Val Leu Asp Arg
1010 1015 1020

Arg Phe Glu Ile Phe Phe Lys Lys Asp Ser Leu Trp Gln Ser Glu
1025 1030 1035

His Leu Glu Ala Val Val Asp Gln Asp Val Gln Arg Thr Cys Ile
1040 1045 1050

Leu His Gly Pro Val Ala Ala Gln Phe Thr Lys Val Ile Asp Glu
1055 1060 1065

Pro Ile Lys Ser Ile Met Asp Gly Ile His Asp Gly His Ile Lys
1070 1075 1080

Lys Leu Leu His Gln Tyr Tyr Gly Asp Asp Glu Ser Lys Ile Pro
1085 1090 1095

Ala Val Glu Tyr Phe Gly Gly Glu Ser Pro Val Asp Val Gln Ser
1100 1105 1110

Gln Val Asp Ser Ser Ser Val Ser Glu Asp Ser Ala Val Phe Lys
1115 1120 1125

Ala Thr Ser Ser Thr Asp Glu Glu Ser Trp Phe Lys Ala Leu Ala
1130 1135 1140

Gly Ser Glu Ile Asn Trp Arg His Ala Ser Phe Leu Cys Ser Phe
1145 1150 1155

Ile Thr Gln Asp Lys Met Phe Val Ser Asn Pro Ile Arg Lys Val
1160 1165 1170

Phe Lys Pro Ser Gln Gly Met Val Val Glu Ile Ser Asn Gly Asn
1175 1180 1185

Thr Ser Ser Lys Thr Val Val Thr Leu Ser Glu Pro Val Gln Gly
1190 1195 1200

Glu	Leu	Lys	Pro	Thr	Val	Ile	Leu	Lys	Leu	Leu	Lys	Glu	Asn	Ile
1205						1210					1215			
Ile	Gln	Met	Glu	Met	Ile	Glu	Asn	Arg	Thr	Met	Asp	Gly	Lys	Pro
1220						1225					1230			
Val	Ser	Leu	Pro	Leu	Leu	Tyr	Asn	Phe	Asn	Pro	Asp	Asn	Gly	Phe
1235						1240					1245			
Ala	Pro	Ile	Ser	Glu	Val	Met	Glu	Asp	Arg	Asn	Gln	Arg	Ile	Lys
1250						1255					1260			
Glu	Met	Tyr	Trp	Lys	Leu	Trp	Ile	Asp	Glu	Pro	Phe	Asn	Leu	Asp
1265						1270					1275			
Phe	Asp	Pro	Arg	Asp	Val	Ile	Lys	Gly	Lys	Asp	Phe	Glu	Ile	Thr
1280						1285					1290			
Ala	Lys	Glu	Val	Tyr	Asp	Phe	Thr	His	Ala	Val	Gly	Asn	Asn	Cys
1295						1300					1305			
Glu	Asp	Phe	Val	Ser	Arg	Pro	Asp	Arg	Thr	Met	Leu	Ala	Pro	Met
1310						1315					1320			
Asp	Phe	Ala	Ile	Val	Val	Gly	Trp	Arg	Ala	Ile	Ile	Lys	Ala	Ile
1325						1330					1335			
Phe	Pro	Asn	Thr	Val	Asp	Gly	Asp	Leu	Leu	Lys	Leu	Val	His	Leu
1340						1345					1350			
Ser	Asn	Gly	Tyr	Lys	Met	Ile	Pro	Gly	Ala	Lys	Pro	Leu	Gln	Val
1355						1360					1365			
Gly	Asp	Val	Val	Ser	Thr	Thr	Ala	Val	Ile	Glu	Ser	Val	Val	Asn
1370						1375					1380			
Gln	Pro	Thr	Gly	Lys	Ile	Val	Asp	Val	Val	Gly	Thr	Leu	Ser	Arg
1385						1390					1395			
Asn	Gly	Lys	Pro	Val	Met	Glu	Val	Thr	Ser	Ser	Phe	Phe	Tyr	Arg
1400						1405					1410			

Gly Asn Tyr Thr Asp Phe Glu Asn Thr Phe Gln Lys Thr Val Glu
1415 1420 1425

Pro Val Tyr Gln Met His Ile Lys Thr Ser Lys Asp Ile Ala Val
1430 1435 1440

Leu Arg Ser Lys Glu Trp Phe Gln Leu Asp Asp Glu Asp Phe Asp
1445 1450 1455

Leu Leu Asn Lys Thr Leu Thr Phe Glu Thr Glu Thr Glu Val Thr
1460 1465 1470

Phe Lys Asn Ala Asn Ile Phe Ser Ser Val Lys Cys Phe Gly Pro
1475 1480 1485

Ile Lys Val Glu Leu Pro Thr Lys Glu Thr Val Glu Ile Gly Ile
1490 1495 1500

Val Asp Tyr Glu Ala Gly Ala Ser His Gly Asn Pro Val Val Asp
1505 1510 1515

Phe Leu Lys Arg Asn Gly Ser Thr Leu Glu Gln Lys Val Asn Leu
1520 1525 1530

Glu Asn Pro Ile Pro Ile Ala Val Leu Asp Ser Tyr Thr Pro Ser
1535 1540 1545

Thr Asn Glu Pro Tyr Ala Arg Val Ser Gly Asp Leu Asn Pro Ile
1550 1555 1560

His Val Ser Arg His Phe Ala Ser Tyr Ala Asn Leu Pro Gly Thr
1565 1570 1575

Ile Thr His Gly Met Phe Ser Ser Ala Ser Val Arg Ala Leu Ile
1580 1585 1590

Glu Asn Trp Ala Ala Asp Ser Val Ser Ser Arg Val Arg Gly Tyr
1595 1600 1605

Thr	Cys	Gln	Phe	Val	Asp	Met	Val	Leu	Pro	Asn	Thr	Ala	Leu	Lys
1610						1615					1620			
Thr	Ser	Ile	Gln	His	Val	Gly	Met	Ile	Asn	Gly	Arg	Lys	Leu	Ile
1625						1630					1635			
Lys	Phe	Glu	Thr	Arg	Asn	Glu	Asp	Asp	Val	Val	Val	Leu	Thr	Gly
1640						1645					1650			
Glu	Ala	Glu	Ile	Glu	Gln	Pro	Val	Thr	Thr	Phe	Val	Phe	Thr	Gly
1655						1660					1665			
Gln	Gly	Ser	Gln	Glu	Gln	Gly	Met	Gly	Met	Asp	Leu	Tyr	Lys	Thr
1670						1675					1680			
Ser	Lys	Ala	Ala	Gln	Asp	Val	Trp	Asn	Arg	Ala	Asp	Asn	His	Phe
1685						1690					1695			
Lys	Asp	Thr	Tyr	Gly	Phe	Ser	Ile	Leu	Asp	Ile	Val	Ile	Asn	Asn
1700						1705					1710			
Pro	Val	Asn	Leu	Thr	Ile	His	Phe	Gly	Gly	Glu	Lys	Gly	Lys	Arg
1715						1720					1725			
Ile	Arg	Glu	Asn	Tyr	Ser	Ala	Met	Ile	Phe	Glu	Thr	Ile	Val	Asp
1730						1735					1740			
Gly	Lys	Leu	Lys	Thr	Glu	Lys	Ile	Phe	Lys	Glu	Ile	Asn	Glu	His
1745						1750					1755			
Ser	Thr	Ser	Tyr	Thr	Phe	Arg	Ser	Glu	Lys	Gly	Leu	Leu	Ser	Ala
1760						1765					1770			
Thr	Gln	Phe	Thr	Gln	Pro	Ala	Leu	Thr	Leu	Met	Glu	Lys	Ala	Ala
1775						1780					1785			
Phe	Glu	Asp	Leu	Lys	Ser	Lys	Gly	Leu	Ile	Pro	Ala	Asp	Ala	Thr
1790						1795					1800			
Phe	Ala	Gly	His	Ser	Leu	Gly	Glu	Tyr	Ala	Ala	Leu	Ala	Ser	Leu
1805						1810					1815			

Ala Asp Val Met Ser Ile Glu Ser Leu Val Glu Val Val Phe Tyr
1820 1825 1830

Phe Gly Met Thr Met Gln Val Ala Val Pro Arg Asp Glu Leu Gly
1835 1840 1845

Arg Ser Asn Tyr Gly Met Ile Ala Ile Asn Pro Gly Arg Val Ala
1850 1855 1860

Ala Ser Phe Ser Gln Glu Ala Leu Gln Tyr Val Val Glu Arg Val
1865 1870 1875

Gly Lys Arg Thr Gly Trp Leu Val Glu Ile Val Asn Tyr Asn Val
1880 1885 1890

Glu Asn Gln Gln Tyr Val Ala Ala Gly Asp Leu Arg Ala Leu Asp
1895 1900 1905

Thr Val Thr Asn Val Leu Asn Phe Ile Lys Leu Gln Lys Ile Asp
1910 1915 1920

Ile Ile Glu Leu Gln Lys Ser Leu Ser Leu Glu Glu Val Glu Gly
1925 1930 1935

His Leu Phe Glu Ile Ile Asp Glu Ala Ser Lys Lys Ser Ala Val
1940 1945 1950

Lys Pro Arg Pro Leu Lys Leu Glu Arg Gly Phe Ala Cys Ile Pro
1955 1960 1965

Leu Val Gly Ile Ser Val Pro Phe His Ser Thr Tyr Leu Met Asn
1970 1975 1980

Gly Val Lys Pro Phe Lys Ser Phe Leu Lys Lys Asn Ile Ile Lys
1985 1990 1995

Glu Asn Val Lys Val Ala Arg Leu Ala Gly Lys Tyr Ile Pro Asn
2000 2005 2010

Leu Thr Ala Lys Pro Phe Gln Val Thr Lys Glu Tyr Phe Gln Asp
2015 2020 2025

Val Tyr Asp Leu Thr Gly Ser Glu Pro Ile Lys Glu Ile Ile Asp
2030 2035 2040

Asn Trp Glu Lys Tyr Glu Gln Ser
2045 2050

<210> 107
<211> 1887
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutated fatty acid synthase (FAS2, G1250S)

<400> 107

Met Lys Pro Glu Val Glu Gln Glu Leu Ala His Ile Leu Leu Thr Glu
1 5 10 15

Leu Leu Ala Tyr Gln Phe Ala Ser Pro Val Arg Trp Ile Glu Thr Gln
20 25 30

Asp Val Phe Leu Lys Asp Phe Asn Thr Glu Arg Val Val Glu Ile Gly
35 40 45

Pro Ser Pro Thr Leu Ala Gly Met Ala Gln Arg Thr Leu Lys Asn Lys
50 55 60

Tyr Glu Ser Tyr Asp Ala Ala Leu Ser Leu His Arg Glu Ile Leu Cys
65 70 75 80

Tyr Ser Lys Asp Ala Lys Glu Ile Tyr Tyr Thr Pro Asp Pro Ser Glu
85 90 95

Leu Ala Ala Lys Glu Glu Pro Ala Lys Glu Glu Ala Pro Ala Pro Thr
100 105 110

Pro Ala Ala Ser Ala Pro Ala Pro Ala Ala Ala Pro Ala Pro Val
115 120 125

Ala Ala Ala Ala Pro Ala Ala Ala Ala Ala Glu Ile Ala Asp Glu Pro
130 135 140

Val Lys Ala Ser Leu Leu Leu His Val Leu Val Ala His Lys Leu Lys
145 150 155 160

Lys Ser Leu Asp Ser Ile Pro Met Ser Lys Thr Ile Lys Asp Leu Val
165 170 175

Gly Gly Lys Ser Thr Val Gln Asn Glu Ile Leu Gly Asp Leu Gly Lys
180 185 190

Glu Phe Gly Thr Thr Pro Glu Lys Pro Glu Glu Thr Pro Leu Glu Glu
195 200 205

Leu Ala Glu Thr Phe Gln Asp Thr Phe Ser Gly Ala Leu Gly Lys Gln
210 215 220

Ser Ser Ser Leu Leu Ser Arg Leu Ile Ser Ser Lys Met Pro Gly Gly
225 230 235 240

Phe Thr Ile Thr Val Ala Arg Lys Tyr Leu Gln Thr Arg Trp Gly Leu
245 250 255

Pro Ser Gly Arg Gln Asp Gly Val Leu Leu Val Ala Leu Ser Asn Glu
260 265 270

Pro Ala Ala Arg Leu Gly Ser Glu Ala Asp Ala Lys Ala Phe Leu Asp
275 280 285

Ser Met Ala Gln Lys Tyr Ala Ser Ile Val Gly Val Asp Leu Ser Ser
290 295 300

Ala Ala Ser Ala Ser Gly Ala Ala Gly Ala Gly Ala Ala Ala Gly Ala
305 310 315 320

Ala Met Ile Asp Ala Gly Ala Leu Glu Glu Ile Thr Lys Asp His Lys
325 330 335

Val Leu Ala Arg Gln Gln Leu Gln Val Leu Ala Arg Tyr Leu Lys Met
340 345 350

Asp Leu Asp Asn Gly Glu Arg Lys Phe Leu Lys Glu Lys Asp Thr Val
355 360 365

Ala Glu Leu Gln Ala Gln Leu Asp Tyr Leu Asn Ala Glu Leu Gly Glu
370 375 380

Phe Phe Val Asn Gly Val Ala Thr Ser Phe Ser Arg Lys Lys Ala Arg
385 390 395 400

Thr Phe Asp Ser Ser Trp Asn Trp Ala Lys Gln Ser Leu Leu Ser Leu
405 410 415

Tyr Phe Glu Ile Ile His Gly Val Leu Lys Asn Val Asp Arg Glu Val
420 425 430

Val Ser Glu Ala Ile Asn Ile Met Asn Arg Ser Asn Asp Ala Leu Ile
435 440 445

Lys Phe Met Glu Tyr His Ile Ser Asn Thr Asp Glu Thr Lys Gly Glu
450 455 460

Asn Tyr Gln Leu Val Lys Thr Leu Gly Glu Gln Leu Ile Glu Asn Cys
465 470 475 480

Lys Gln Val Leu Asp Val Asp Pro Val Tyr Lys Asp Val Ala Lys Pro
485 490 495

Thr Gly Pro Lys Thr Ala Ile Asp Lys Asn Gly Asn Ile Thr Tyr Ser
500 505 510

Glu Glu Pro Arg Glu Lys Val Arg Lys Leu Ser Gln Tyr Val Gln Glu
515 520 525

Met Ala Leu Gly Gly Pro Ile Thr Lys Glu Ser Gln Pro Thr Ile Glu
530 535 540

Glu Asp Leu Thr Arg Val Tyr Lys Ala Ile Ser Ala Gln Ala Asp Lys
545 550 555 560

Gln Asp Ile Ser Ser Ser Thr Arg Val Glu Phe Glu Lys Leu Tyr Ser
565 570 575

Asp Leu Met Lys Phe Leu Glu Ser Ser Lys Glu Ile Asp Pro Ser Gln
580 585 590

Thr Thr Gln Leu Ala Gly Met Asp Val Glu Asp Ala Leu Asp Lys Asp
595 600 605

Ser Thr Lys Glu Val Ala Ser Leu Pro Asn Lys Ser Thr Ile Ser Lys
610 615 620

Thr Val Ser Ser Thr Ile Pro Arg Glu Thr Ile Pro Phe Leu His Leu
625 630 635 640

Arg Lys Lys Thr Pro Ala Gly Asp Trp Lys Tyr Asp Arg Gln Leu Ser
645 650 655

Ser Leu Phe Leu Asp Gly Leu Glu Lys Ala Ala Phe Asn Gly Val Thr
660 665 670

Phe Lys Asp Lys Tyr Val Leu Ile Thr Gly Ala Gly Lys Gly Ser Ile
675 680 685

Gly Ala Glu Val Leu Gln Gly Leu Leu Gln Gly Gly Ala Lys Val Val
690 695 700

Val Thr Thr Ser Arg Phe Ser Lys Gln Val Thr Asp Tyr Tyr Gln Ser
705 710 715 720

Ile Tyr Ala Lys Tyr Gly Ala Lys Gly Ser Thr Leu Ile Val Val Pro
725 730 735

Phe Asn Gln Gly Ser Lys Gln Asp Val Glu Ala Leu Ile Glu Phe Ile
740 745 750

Tyr Asp Thr Glu Lys Asn Gly Gly Leu Gly Trp Asp Leu Asp Ala Ile
755 760 765

Ile Pro Phe Ala Ala Ile Pro Glu Gln Gly Ile Glu Leu Glu His Ile
770 775 780

Asp Ser Lys Ser Glu Phe Ala His Arg Ile Met Leu Thr Asn Ile Leu
785 790 795 800

Arg Met Met Gly Cys Val Lys Lys Gln Lys Ser Ala Arg Gly Ile Glu
805 810 815

Thr Arg Pro Ala Gln Val Ile Leu Pro Met Ser Pro Asn His Gly Thr
820 825 830

Phe Gly Gly Asp Gly Met Tyr Ser Glu Ser Lys Leu Ser Leu Glu Thr
835 840 845

Leu Phe Asn Arg Trp His Ser Glu Ser Trp Ala Asn Gln Leu Thr Val
850 855 860

Cys Gly Ala Ile Ile Gly Trp Thr Arg Gly Thr Gly Leu Met Ser Ala
865 870 875 880

Asn Asn Ile Ile Ala Glu Gly Ile Glu Lys Met Gly Val Arg Thr Phe
885 890 895

Ser Gln Lys Glu Met Ala Phe Asn Leu Leu Gly Leu Leu Thr Pro Glu
900 905 910

Val Val Glu Leu Cys Gln Lys Ser Pro Val Met Ala Asp Leu Asn Gly
915 920 925

Gly Leu Gln Phe Val Pro Glu Leu Lys Glu Phe Thr Ala Lys Leu Arg
930 935 940

Lys Glu Leu Val Glu Thr Ser Glu Val Arg Lys Ala Val Ser Ile Glu
945 950 955 960

Thr Ala Leu Glu His Lys Val Val Asn Gly Asn Ser Ala Asp Ala Ala
965 970 975

Tyr Ala Gln Val Glu Ile Gln Pro Arg Ala Asn Ile Gln Leu Asp Phe
980 985 990

Pro Glu Leu Lys Pro Tyr Lys Gln Val Lys Gln Ile Ala Pro Ala Glu
995 1000 1005

Leu Glu Gly Leu Leu Asp Leu Glu Arg Val Ile Val Val Thr Gly
1010 1015 1020

Phe Ala Glu Val Gly Pro Trp Gly Ser Ala Arg Thr Arg Trp Glu
1025 1030 1035

Met Glu Ala Phe Gly Glu Phe Ser Leu Glu Gly Cys Val Glu Met
1040 1045 1050

Ala Trp Ile Met Gly Phe Ile Ser Tyr His Asn Gly Asn Leu Lys
1055 1060 1065

Gly Arg Pro Tyr Thr Gly Trp Val Asp Ser Lys Thr Lys Glu Pro
1070 1075 1080

Val Asp Asp Lys Asp Val Lys Ala Lys Tyr Glu Thr Ser Ile Leu
1085 1090 1095

Glu His Ser Gly Ile Arg Leu Ile Glu Pro Glu Leu Phe Asn Gly
1100 1105 1110

Tyr Asn Pro Glu Lys Lys Glu Met Ile Gln Glu Val Ile Val Glu
1115 1120 1125

Glu Asp Leu Glu Pro Phe Glu Ala Ser Lys Glu Thr Ala Glu Gln
1130 1135 1140

Phe Lys His Gln His Gly Asp Lys Val Asp Ile Phe Glu Ile Pro
1145 1150 1155

Glu Thr Gly Glu Tyr Ser Val Lys Leu Leu Lys Gly Ala Thr Leu
1160 1165 1170

Tyr Ile Pro Lys Ala Leu Arg Phe Asp Arg Leu Val Ala Gly Gln
1175 1180 1185

Ile Pro Thr Gly Trp Asn Ala Lys Thr Tyr Gly Ile Ser Asp Asp
1190 1195 1200

Ile Ile Ser Gln Val Asp Pro Ile Thr Leu Phe Val Leu Val Ser
1205 1210 1215

Val Val Glu Ala Phe Ile Ala Ser Gly Ile Thr Asp Pro Tyr Glu
1220 1225 1230

Met Tyr Lys Tyr Val His Val Ser Glu Val Gly Asn Cys Ser Gly
1235 1240 1245

Ser Ser Met Gly Gly Val Ser Ala Leu Arg Gly Met Phe Lys Asp
1250 1255 1260

Arg Phe Lys Asp Glu Pro Val Gln Asn Asp Ile Leu Gln Glu Ser
1265 1270 1275

Phe Ile Asn Thr Met Ser Ala Trp Val Asn Met Leu Leu Ile Ser
1280 1285 1290

Ser Ser Gly Pro Ile Lys Thr Pro Val Gly Ala Cys Ala Thr Ser
1295 1300 1305

Val Glu Ser Val Asp Ile Gly Val Glu Thr Ile Leu Ser Gly Lys
1310 1315 1320

Ala Arg Ile Cys Ile Val Gly Gly Tyr Asp Asp Phe Gln Glu Glu
1325 1330 1335

Gly Ser Phe Glu Phe Gly Asn Met Lys Ala Thr Ser Asn Thr Leu
1340 1345 1350

Glu Glu Phe Glu His Gly Arg Thr Pro Ala Glu Met Ser Arg Pro
1355 1360 1365

Ala Thr Thr Thr Arg Asn Gly Phe Met Glu Ala Gln Gly Ala Gly
1370 1375 1380

Ile Gln Ile Ile Met Gln Ala Asp Leu Ala Leu Lys Met Gly Val
1385 1390 1395

Pro	Ile	Tyr	Gly	Ile	Val	Ala	Met	Ala	Ala	Thr	Ala	Thr	Asp	Lys
1400						1405					1410			
Ile	Gly	Arg	Ser	Val	Pro	Ala	Pro	Gly	Lys	Gly	Ile	Leu	Thr	Thr
1415						1420					1425			
Ala	Arg	Glu	His	His	Ser	Ser	Val	Lys	Tyr	Ala	Ser	Pro	Asn	Leu
1430						1435					1440			
Asn	Met	Lys	Tyr	Arg	Lys	Arg	Gln	Leu	Val	Thr	Arg	Glu	Ala	Gln
1445						1450					1455			
Ile	Lys	Asp	Trp	Val	Glu	Asn	Glu	Leu	Glu	Ala	Leu	Lys	Leu	Glu
1460						1465					1470			
Ala	Glu	Glu	Ile	Pro	Ser	Glu	Asp	Gln	Asn	Glu	Phe	Leu	Leu	Glu
1475						1480					1485			
Arg	Thr	Arg	Glu	Ile	His	Asn	Glu	Ala	Glu	Ser	Gln	Leu	Arg	Ala
1490						1495					1500			
Ala	Gln	Gln	Gln	Trp	Gly	Asn	Asp	Phe	Tyr	Lys	Arg	Asp	Pro	Arg
1505						1510					1515			
Ile	Ala	Pro	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Tyr	Gly	Leu	Thr	Ile
1520						1525					1530			
Asp	Asp	Leu	Gly	Val	Ala	Ser	Phe	His	Gly	Thr	Ser	Thr	Lys	Ala
1535						1540					1545			
Asn	Asp	Lys	Asn	Glu	Ser	Ala	Thr	Ile	Asn	Glu	Met	Met	Lys	His
1550						1555					1560			
Leu	Gly	Arg	Ser	Glu	Gly	Asn	Pro	Val	Ile	Gly	Val	Phe	Gln	Lys
1565						1570					1575			
Phe	Leu	Thr	Gly	His	Pro	Lys	Gly	Ala	Ala	Gly	Ala	Trp	Met	Met
1580						1585					1590			
Asn	Gly	Ala	Leu	Gln	Ile	Leu	Asn	Ser	Gly	Ile	Ile	Pro	Gly	Asn
1595						1600					1605			

Arg Asn Ala Asp Asn Val Asp Lys Ile Leu Glu Gln Phe Glu Tyr
1610 1615 1620

Val Leu Tyr Pro Ser Lys Thr Leu Lys Thr Asp Gly Val Arg Ala
1625 1630 1635

Val Ser Ile Thr Ser Phe Gly Phe Gly Gln Lys Gly Gly Gln Ala
1640 1645 1650

Ile Val Val His Pro Asp Tyr Leu Tyr Gly Ala Ile Thr Glu Asp
1655 1660 1665

Arg Tyr Asn Glu Tyr Val Ala Lys Val Ser Ala Arg Glu Lys Ser
1670 1675 1680

Ala Tyr Lys Phe Phe His Asn Gly Met Ile Tyr Asn Lys Leu Phe
1685 1690 1695

Val Ser Lys Glu His Ala Pro Tyr Thr Asp Glu Leu Glu Glu Asp
1700 1705 1710

Val Tyr Leu Asp Pro Leu Ala Arg Val Ser Lys Asp Lys Lys Ser
1715 1720 1725

Gly Ser Leu Thr Phe Asn Ser Lys Asn Ile Gln Ser Lys Asp Ser
1730 1735 1740

Tyr Ile Asn Ala Asn Thr Ile Glu Thr Ala Lys Met Ile Glu Asn
1745 1750 1755

Met Thr Lys Glu Lys Val Ser Asn Gly Gly Val Gly Val Asp Val
1760 1765 1770

Glu Leu Ile Thr Ser Ile Asn Val Glu Asn Asp Thr Phe Ile Glu
1775 1780 1785

Arg Asn Phe Thr Pro Gln Glu Ile Glu Tyr Cys Ser Ala Gln Pro
1790 1795 1800

Ser Val Gln Ser Ser Phe Ala Gly Thr Trp Ser Ala Lys Glu Ala
1805 1810 1815

Val Phe Lys Ser Leu Gly Val Lys Ser Leu Gly Gly Gly Ala Ala
1820 1825 1830

Leu Lys Asp Ile Glu Ile Val Arg Val Asn Lys Asn Ala Pro Ala
1835 1840 1845

Val Glu Leu His Gly Asn Ala Lys Lys Ala Ala Glu Glu Ala Gly
1850 1855 1860

Val Thr Asp Val Lys Val Ser Ile Ser His Asp Asp Leu Gln Ala
1865 1870 1875

Val Ala Val Ala Val Ser Thr Lys Lys
1880 1885

<210> 108
<211> 371
<212> PRT
<213> Artificial Sequence

<220>
<223> MBPtag

<400> 108

Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
1 5 10 15

Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
20 25 30

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

Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
50 55 60

His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
65 70 75 80

Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
85 90 95

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

Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
115 120 125

Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
130 135 140

Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
145 150 155 160

Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
165 170 175

Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
180 185 190

Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
195 200 205

Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
210 215 220

Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
225 230 235 240

Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
245 250 255

Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
260 265 270

Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
275 280 285

Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
290 295 300

Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
305 310 315 320

Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
325 330 335

Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
340 345 350

Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Arg
355 360 365

Ile Thr Lys
370

<210> 109
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> ProA tag

<400> 109

Met Ile Phe Asp Gly Thr Thr Met Ser Ile Ala Ile Gly Leu Leu Ser
1 5 10 15

Thr Leu Gly Ile Gly Ala Glu Ala
20

<210> 110
<211> 398
<212> PRT
<213> Cannibis sativa

<400> 110

Met Gly Leu Ser Leu Val Cys Thr Phe Ser Phe Gln Thr Asn Tyr His
1 5 10 15

Thr Leu Leu Asn Pro His Asn Lys Asn Pro Lys Asn Ser Leu Leu Ser
20 25 30

Tyr Gln His Pro Lys Thr Pro Ile Ile Lys Ser Ser Tyr Asp Asn Phe
35 40 45

Pro Ser Lys Tyr Cys Leu Thr Lys Asn Phe His Leu Leu Gly Leu Asn
50 55 60

Ser His Asn Arg Ile Ser Ser Gln Ser Arg Ser Ile Arg Ala Gly Ser
65 70 75 80

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

Thr Lys Ile Leu Asn Phe Gly His Thr Cys Trp Lys Leu Gln Arg Pro
100 105 110

Tyr Val Val Lys Gly Met Ile Ser Ile Ala Cys Gly Leu Phe Gly Arg
115 120 125

Glu Leu Phe Asn Asn Arg His Leu Phe Ser Trp Gly Leu Met Trp Lys
130 135 140

Ala Phe Phe Ala Leu Val Pro Ile Leu Ser Phe Asn Phe Phe Ala Ala
145 150 155 160

Ile Met Asn Gln Ile Tyr Asp Val Asp Ile Asp Arg Ile Asn Lys Pro
165 170 175

Asp Leu Pro Leu Val Ser Gly Glu Met Ser Ile Glu Thr Ala Trp Ile
180 185 190

Leu Ser Ile Ile Val Ala Leu Thr Gly Leu Ile Val Thr Ile Lys Leu
195 200 205

Lys Ser Ala Pro Leu Phe Val Phe Ile Tyr Ile Phe Gly Ile Phe Ala
210 215 220

Gly Phe Ala Tyr Ser Val Pro Pro Ile Arg Trp Lys Gln Tyr Pro Phe
225 230 235 240

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

245

250

255

Ser Tyr Ser Ala Thr Thr Ser Ala Leu Gly Leu Pro Phe Val Trp Arg
 260 265 270

Pro Ala Phe Ser Phe Ile Ile Ala Phe Met Thr Val Met Gly Met Thr
 275 280 285

Ile Ala Phe Ala Lys Asp Ile Ser Asp Ile Glu Gly Asp Ala Lys Tyr
 290 295 300

Gly Val Ser Thr Val Ala Thr Lys Leu Gly Ala Arg Asn Met Thr Phe
 305 310 315 320

Val Val Ser Gly Val Leu Leu Leu Asn Tyr Leu Val Ser Ile Ser Ile
 325 330 335

Gly Ile Ile Trp Pro Gln Val Phe Lys Ser Asn Ile Met Ile Leu Ser
 340 345 350

His Ala Ile Leu Ala Phe Cys Leu Ile Phe Gln Thr Arg Glu Leu Ala
 355 360 365

Leu Ala Asn Tyr Ala Ser Ala Pro Ser Arg Gln Phe Phe Glu Phe Ile
 370 375 380

Trp Leu Leu Tyr Tyr Ala Glu Tyr Phe Val Tyr Val Phe Ile
 385 390 395

<210> 111

<211> 1197

<212> DNA

<213> Cannibis sativa

<400> 111

atgggtttat ctttggtctg caccttctcc tttcaaacta actaccacac tttattgaat 60

ccacataata agaatcctaa gaactcttta ttgtcctacc aacacccaaa gactcctatt 120

atcaagtcct cttacgataa cttcccatct aagtactggt tgactaagaa tttccatttg 180

ttgggtttga attctcacia cagaatttcc tcccaatccc gttctattag agccggttct 240

gatcaaatcg aagggttcccc tcatcatgag tccgataact ccattgctac taaaatttta 300

aatttcggtc atacttggtg gaagttgcaa cgtccttacg ttgtcaaggg tatgatctct 360
attgcttggtg gtttgttcgg tagagaattg tttacaaca gacacttggt ctcttgggggt 420
ttgatgtgga aagctttctt cgctttggtc ccaattttgt ctttcaattt cttcgccgcc 480
atcatgaacc aaatctacga tgttgatata gaccgtatca acaagccaga cttaccttta 540
gtttccggtg aaatgtccat tgaaactgct tggatcttgt ctatcattgt tgccttgact 600
ggtttaattg ttactattaa gttgaagtcc gctccattgt ttgtcttcat ctacatcttc 660
ggatatcttcg ctggtttcgc ttactccgtc ccacctatta gatggaaaca atatacctttt 720
accaatttct tgatcactat ttcctctcat gttggtttgg ctttcacttc ttactctgcc 780
accacttctg ctttaggttt gcctttcggt tggcgctctg ctttctcttt cattattgct 840
ttcatgactg tcatgggtat gactattgcc tttgctaaag acatttctga tatcgaaggt 900
gatgctaagt acgggtgtct taccgttgct accaagttag gtgctagaaa tatgactttt 960
gttgtttctg gtgtcttatt gttgaactac ttggtttcta tctctattgg tatcatttgg 1020
ccacaagttt tcaagtctaa cattatgata ttgtctcatg ctattttggc tttctgtttg 1080
atctttcaaa ctcgtgaatt agccttagcc aattatgcct ctgccccatc ccgtcaattt 1140
ttcgaattca tctggttggt atactatgcc gaatacttcg tttacgtctt catttaa 1197

<210> 112
<211> 522
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated acyl activating enzyme AAE (CsAAE3 truncation)

<400> 112

Met Glu Lys Ser Gly Tyr Gly Arg Asp Gly Ile Tyr Arg Ser Leu Arg
1 5 10 15

Pro Pro Leu His Leu Pro Asn Asn Asn Asn Leu Ser Met Val Ser Phe
20 25 30

Leu Phe Arg Asn Ser Ser Ser Tyr Pro Gln Lys Pro Ala Leu Ile Asp
35 40 45

Ser Glu Thr Asn Gln Ile Leu Ser Phe Ser His Phe Lys Ser Thr Val
50 55 60

Ile Lys Val Ser His Gly Phe Leu Asn Leu Gly Ile Lys Lys Asn Asp
65 70 75 80

Trp Leu Ile Tyr Ala Pro Asn Ser Ile His Phe Pro Val Cys Phe Leu
85 90 95

Gly Ile Ile Ala Ser Gly Ala Ile Ala Thr Thr Ser Asn Pro Leu Tyr
100 105 110

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

Ile Ile Thr Val Pro Gln Leu Leu Glu Lys Val Lys Gly Phe Asn Leu
130 135 140

Pro Thr Ile Leu Ile Gly Pro Asp Ser Glu Gln Glu Ser Ser Ser Asp
145 150 155 160

Lys Val Met Thr Phe Asn Asp Leu Val Asn Leu Gly Gly Ser Ser Gly
165 170 175

Ser Glu Phe Pro Ile Val Asp Asp Phe Lys Gln Ser Asp Thr Ala Ala
180 185 190

Leu Leu Tyr Ser Ser Gly Thr Thr Gly Met Ser Lys Gly Trp Leu Thr
195 200 205

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

Leu Val Gly Glu Met Asp Asn Val Phe Leu Cys Phe Leu Pro Met Phe
225 230 235 240

His Val Phe Gly Leu Ala Ile Ile Thr Tyr Ala Gln Leu Gln Arg Gly
245 250 255

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

Val Glu Lys Tyr Val Thr His Leu Trp Trp Pro Pro Val Ile Leu Ala
275 280 285

Leu Ser Lys Asn Ser Met Val Lys Phe Asn Leu Ser Ser Ile Lys Tyr
290 295 300

Ile Gly Ser Gly Ala Ala Pro Leu Gly Lys Asp Leu Met Glu Glu Cys
305 310 315 320

Ser Lys Trp Pro Tyr Gly Ile Val Ala Gln Gly Tyr Gly Met Thr Glu
325 330 335

Thr Cys Gly Ile Val Ser Met Glu Asp Ile Arg Gly Gly Lys Arg Asn
340 345 350

Ser Gly Ser Ala Gly Met Leu Ala Ser Gly Val Glu Ala Gln Ile Val
355 360 365

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

Trp Val Lys Gly Pro Asn Met Met Gln Gly Tyr Phe Asn Asn Pro Gln
385 390 395 400

Ala Thr Lys Leu Thr Ile Asp Lys Lys Gly Trp Val His Thr Gly Asp
405 410 415

Leu Gly Tyr Phe Asp Glu Asp Gly His Leu Tyr Trp Asp Arg Ile Lys
420 425 430

Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu Leu Glu
435 440 445

Gly Leu Leu Val Ser His Pro Glu Ile Leu Asp Ala Trp Ile Pro Phe
450 455 460

Pro Asp Ala Glu Ala Gly Glu Val Pro Val Ala Tyr Trp Arg Ser Pro
465 470 475 480

Asn Ser Ser Leu Thr Glu Asn Asp Val Lys Lys Phe Ile Ala Gly Gln
485 490 495

Val Ala Ser Phe Lys Arg Leu Arg Lys Val Thr Phe Ile Asn Ser Val
500 505 510

Pro Lys Ser Ala Ser Gly Lys Ile Leu Arg
515 520

<210> 113
<211> 526
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated 3-hydroxy-3-methyl-glutaryl-CoA reductase (tHMG1)

<400> 113

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

Ala Pro Val Gln Lys Ala Ser Thr Pro Val Leu Thr Asn Lys Thr Val
20 25 30

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

Ser Gly Pro Ser Ser Ser Ser Glu Glu Asp Asp Ser Arg Asp Ile Glu
50 55 60

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

Ser Ser Gly Asn Thr Lys Gln Leu Lys Asn Lys Glu Val Ala Ala Leu
85 90 95

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

Asp Thr Thr Arg Ala Val Ala Val Arg Arg Lys Ala Leu Ser Ile Leu
115 120 125

Ala Glu Ala Pro Val Leu Ala Ser Asp Arg Leu Pro Tyr Lys Asn Tyr
130 135 140

Asp Tyr Asp Arg Val Phe Gly Ala Cys Cys Glu Asn Val Ile Gly Tyr
145 150 155 160

Met Pro Leu Pro Val Gly Val Ile Gly Pro Leu Val Ile Asp Gly Thr
165 170 175

Ser Tyr His Ile Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser
180 185 190

Ala Met Arg Gly Cys Lys Ala Ile Asn Ala Gly Gly Gly Ala Thr Thr
195 200 205

Val Leu Thr Lys Asp Gly Met Thr Arg Gly Pro Val Val Arg Phe Pro
210 215 220

Thr Leu Lys Arg Ser Gly Ala Cys Lys Ile Trp Leu Asp Ser Glu Glu
225 230 235 240

Gly Gln Asn Ala Ile Lys Lys Ala Phe Asn Ser Thr Ser Arg Phe Ala
245 250 255

Arg Leu Gln His Ile Gln Thr Cys Leu Ala Gly Asp Leu Leu Phe Met
260 265 270

Arg Phe Arg Thr Thr Thr Gly Asp Ala Met Gly Met Asn Met Ile Ser
275 280 285

Lys Gly Val Glu Tyr Ser Leu Lys Gln Met Val Glu Glu Tyr Gly Trp
290 295 300

Glu Asp Met Glu Val Val Ser Val Ser Gly Asn Tyr Cys Thr Asp Lys
305 310 315 320

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

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

Asp Val Ser Ala Leu Val Glu Leu Asn Ile Ala Lys Asn Leu Val Gly
355 360 365

Ser Ala Met Ala Gly Ser Val Gly Gly Phe Asn Ala His Ala Ala Asn
370 375 380

Leu Val Thr Ala Val Phe Leu Ala Leu Gly Gln Asp Pro Ala Gln Asn
385 390 395 400

Val Glu Ser Ser Asn Cys Ile Thr Leu Met Lys Glu Val Asp Gly Asp
405 410 415

Leu Arg Ile Ser Val Ser Met Pro Ser Ile Glu Val Gly Thr Ile Gly
420 425 430

Gly Gly Thr Val Leu Glu Pro Gln Gly Ala Met Leu Asp Leu Leu Gly
435 440 445

Val Arg Gly Pro His Ala Thr Ala Pro Gly Thr Asn Ala Arg Gln Leu
450 455 460

Ala Arg Ile Val Ala Cys Ala Val Leu Ala Gly Glu Leu Ser Leu Cys
465 470 475 480

Ala Ala Leu Ala Ala Gly His Leu Val Gln Ser His Met Thr His Asn
485 490 495

Arg Lys Pro Ala Glu Pro Thr Lys Pro Asn Asn Leu Asp Ala Thr Asp
500 505 510

Ile Asn Arg Leu Lys Asp Gly Ser Val Thr Cys Ile Lys Ser
515 520 525

<210> 114

<211> 1581

<212> DNA

<213> Artificial Sequence

<220>

<223> Truncated 3-hydroxy-3-methyl-glutaryl-CoA reductase (tHMG1)

<400> 114

atgtccgatc aattagtcaa gaccgaagtc accaagaagt ccttcaccgc cccagttcaa	60
aaagcctcca ctccagtctt aactaacaag accgttatatt ctggttccaa ggtaaagtct	120
ttatcctccg ctcaatcctc ctcttccggc ccatcttctt cttctgaaga agatgattcc	180
cgtgacattg agtccttgga taagaaaatc agacctttgg aagaattaga agctttgtta	240
tcctctggta atactaagca attgaaaaac aaggaagttg ctgctttggc tattcacggc	300
aaattacctt tgtacgcttt agagaagaag ttaggtgaca ctacccgtgc tgctgccgtt	360
agaagaaaag ctttgtctat tttagctgag gccctgttt tggtcttctga cagattacca	420
tacaagaatt acgattacga tagagttttc ggtgcctgtt gtgagaacgt tatcggttat	480
atgccattac cagtcggtgt tatcggtcca ttggttattg acggtacctc ttaccacatc	540
ccaatggcta ctactgaagg ttgttttagtc gcctccgccg tgagagggtg taaggctatc	600
aatgctgggtg gtgggtgctac taccgtcttg actaaggatg gtatgactag aggtccagtt	660
gtccggtttc caactttgaa aagatctggc gcttgtaaga tttggttgga ttctgaagaa	720
ggtcaaaatg ccattaagaa ggctttcaat tccacctcta gatttgccag attacaacat	780
attcaaacct gtttagccgg tgatttggtt ttcattgagat tcagaactac tactggtgat	840
gctatgggta tgaacatgat ctctaagggt gtcgaatatt ctttaaaaca aatgggtgaa	900
gagtatgggt gggaagacat ggaggtcgtc tctgtctctg gtaactactg tactgataag	960
aaaccagctg ctatcaactg gatcgaaggc cgtggtaagt ctgttggtgc cgaagctact	1020
attccaggtg atgttggttag aaagggttta aaatccgatg tctctgcctt gggtgagttg	1080
aacattgcta aaaacttggt tggttctgct atggctgggt ctgtcgggtg ttttaatgcc	1140
catgccgccg acttagtcac cgccgttttc ttagctttgg gtcaagatcc agctcaaaat	1200
gtcgaatcct ccaactgtat cactttgatg aaagaggtcg acggtgactt gcgtatctct	1260
gtttccatgc catctatcga agttggtact atcgggtggt gtactgtttt ggagccacaa	1320
ggtgctatgt tggacttatt ggggtgttaga ggtccacacg ccactgctcc tgggtaccaac	1380
gccagacaat tagctagaat cgttgcctgt gccgtcttag ctggtgagtt gtctttatgt	1440
gctgccttag ctgctgggtc cttgggtccaa tcccacatga ctcataacag aaagccagct	1500
gaacctacca agcctaacaa cttggatgcc accgatatta atcgtttaaa agatggttct	1560
gtcacttgca ttaagtccta a	1581

<210> 115
<211> 461
<212> PRT
<213> Saccharomyces sp.

<400> 115

Met Thr Glu Leu Lys Lys Gln Lys Thr Ala Glu Gln Lys Thr Arg Pro
1 5 10 15

Gln Asn Val Gly Ile Lys Gly Ile Gln Ile Tyr Ile Pro Thr Gln Cys
20 25 30

Val Asn Gln Ser Glu Leu Glu Lys Phe Asp Gly Val Ser Gln Gly Lys
35 40 45

Tyr Thr Ile Gly Leu Gly Gln Thr Asn Met Ser Phe Val Asn Asp Arg
50 55 60

Glu Asp Ile Tyr Ser Met Ser Leu Thr Val Leu Ser Lys Leu Ile Lys
65 70 75 80

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

Glu Thr Leu Ile Asp Lys Ser Lys Ser Val Lys Ser Val Leu Met Gln
100 105 110

Leu Phe Gly Glu Asn Thr Asp Val Glu Gly Ile Asp Thr Leu Asn Ala
115 120 125

Cys Tyr Gly Gly Thr Asn Ala Leu Phe Asn Ser Leu Asn Trp Ile Glu
130 135 140

Ser Asn Ala Trp Asp Gly Arg Asp Ala Ile Val Val Cys Gly Asp Ile
145 150 155 160

Ala Ile Tyr Asp Lys Gly Ala Ala Arg Pro Thr Gly Gly Ala Gly Thr
165 170 175

Val Ala Met Trp Ile Gly Pro Asp Ala Pro Ile Val Phe Asp Ser Val

180

185

190

Arg Ala Ser Tyr Met Glu His Ala Tyr Asp Phe Tyr Lys Pro Asp Phe
 195 200 205

Thr Ser Glu Tyr Pro Tyr Val Asp Gly His Phe Ser Leu Thr Cys Tyr
 210 215 220

Val Lys Ala Leu Asp Gln Val Tyr Lys Ser Tyr Ser Lys Lys Ala Ile
 225 230 235 240

Ser Lys Gly Leu Val Ser Asp Pro Ala Gly Ser Asp Ala Leu Asn Val
 245 250 255

Leu Lys Tyr Phe Asp Tyr Asn Val Phe His Val Pro Thr Cys Lys Leu
 260 265 270

Val Thr Lys Ser Tyr Gly Arg Leu Leu Tyr Asn Asp Phe Arg Ala Asn
 275 280 285

Pro Gln Leu Phe Pro Glu Val Asp Ala Glu Leu Ala Thr Arg Asp Tyr
 290 295 300

Asp Glu Ser Leu Thr Asp Lys Asn Ile Glu Lys Thr Phe Val Asn Val
 305 310 315 320

Ala Lys Pro Phe His Lys Glu Arg Val Ala Gln Ser Leu Ile Val Pro
 325 330 335

Thr Asn Thr Gly Asn Met Tyr Thr Ala Ser Val Tyr Ala Ala Phe Ala
 340 345 350

Ser Leu Leu Asn Tyr Val Gly Ser Asp Asp Leu Gln Gly Lys Arg Val
 355 360 365

Gly Leu Phe Ser Tyr Gly Ser Gly Leu Ala Ala Ser Leu Tyr Ser Cys
 370 375 380

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

Asn Lys Leu Ala Lys Arg Ile Thr Glu Thr Pro Lys Asp Tyr Glu Ala
405 410 415

Ala Ile Glu Leu Arg Glu Asn Ala His Leu Lys Lys Asn Phe Lys Pro
420 425 430

Gln Gly Ser Ile Glu His Leu Gln Ser Gly Val Tyr Tyr Leu Thr Asn
435 440 445

Ile Asp Asp Lys Phe Arg Arg Ser Tyr Asp Val Lys Lys
450 455 460

<210> 116
<211> 1386
<212> DNA
<213> Saccharomyces sp.

<400> 116
atgaccgaat tgaagaagca aaagactgct gaacaaaaaa cccgtccaca aaatgttggt 60
atcaagggtta ttcaaactta cattccaact caatgcgtca accaatctga attggaaaaa 120
tttgatgggtg tttctcaagg taaatacact attggtttgg gtcaaactaa tatgtccttc 180
gttaacgaca gagaagatat ttactccatg tccttgaccg tcttgtccaa attgattaag 240
tcttataata ttgacaccaa caagatcggg agattggaag ttggtactga aactttgatt 300
gataagtcta agtctgttaa gtctgtttta atgcaattgt tcggtgaaaa tactgacgtt 360
gaaggatttg acactttgaa cgcttggttac ggtggtacta atgctttatt taactctttg 420
aactggattg aatccaacgc ttgggacggg agagatgcca ttgtcgtttg tggtgacatt 480
gctatctatg acaagggtgc cgctcgacca actgggtggg ctggtaccgt tgctatgtgg 540
atcggtcctg acgccccaat cgtttttgat tctgttcgtg cttcttacat ggagcatgct 600
tacgactttt ataagccaga ctttacctcc gaatatccat acgtcgatgg tcatttctct 660
ttgacctgct acgttaaagc cttagatcaa gtctacaagt cttactccaa gaaggccatt 720
tccaagggtt tagtctccga tccagctggg tccgatgctt taaacgtttt aaagtacttc 780
gattacaacg tttttcatgt ccctacttgt aaattgggta ccaaacttta cggtagatta 840
ttgtacaacg atttcagagc taatccacaa ttatttccag aagtcgatgc tgagttggct 900
actagagatt acgacgaatc cttgaccgac aaaaatattg aaaagacttt tggttaacgtt 960

gctaagccat ttcacaaaga gagagttgcc caatctttga ttgtcccaac taatactggt	1020
aatatgtata ctgcttctgt ttacgctgcc tttgcttctt tgttgaacta tgtcggttct	1080
gacgacttac aaggtaagcg tgtcggtttg ttctcctacg gttccggttt ggctgcctct	1140
ttgtattctt gtaagattgt cggatgatgtt caacacatca tcaaggaatt ggatatacacc	1200
aataaattgg ccaagagaat cactgaaact cctaaagact atgaagctgc tatcgaattg	1260
agagaaaatg ctcatthtaaa gaaaaacttt aaaccacaag gttctattga acacttgcaa	1320
tccggtgttt actacttaac taacatcgat gacaagttcc gtagatccta cgacgtcaag	1380
aagtaa	1386

<210> 117
 <211> 568
 <212> PRT
 <213> *Zymomonas mobilis*

<400> 117

Met	Ser	Tyr	Thr	Val	Gly	Thr	Tyr	Leu	Ala	Glu	Arg	Leu	Val	Gln	Ile
1				5					10					15	

Gly	Leu	Lys	His	His	Phe	Ala	Val	Ala	Gly	Asp	Tyr	Asn	Leu	Val	Leu
			20					25					30		

Leu	Asp	Asn	Leu	Leu	Leu	Asn	Lys	Asn	Met	Glu	Gln	Val	Tyr	Cys	Cys
		35					40					45			

Asn	Glu	Leu	Asn	Cys	Gly	Phe	Ser	Ala	Glu	Gly	Tyr	Ala	Arg	Ala	Lys
	50					55					60				

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

Phe	Asp	Ala	Ile	Gly	Gly	Ala	Tyr	Ala	Glu	Asn	Leu	Pro	Val	Ile	Leu
				85					90					95	

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

His	His	Ala	Leu	Gly	Lys	Thr	Asp	Tyr	His	Tyr	Gln	Leu	Glu	Met	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115

120

125

Lys Asn Ile Thr Ala Ala Ala Glu Ala Ile Tyr Thr Pro Glu Glu Ala
 130 135 140

Pro Ala Lys Ile Asp His Val Ile Lys Thr Ala Leu Arg Glu Lys Lys
 145 150 155 160

Pro Val Tyr Leu Glu Ile Ala Cys Asn Ile Ala Ser Met Pro Cys Ala
 165 170 175

Ala Pro Gly Pro Ala Ser Ala Leu Phe Asn Asp Glu Ala Ser Asp Glu
 180 185 190

Ala Ser Leu Asn Ala Ala Val Glu Glu Thr Leu Lys Phe Ile Ala Asn
 195 200 205

Arg Asp Lys Val Ala Val Leu Val Gly Ser Lys Leu Arg Ala Ala Gly
 210 215 220

Ala Glu Glu Ala Ala Val Lys Phe Ala Asp Ala Leu Gly Gly Ala Val
 225 230 235 240

Ala Thr Met Ala Ala Ala Lys Ser Phe Phe Pro Glu Glu Asn Pro His
 245 250 255

Tyr Ile Gly Thr Ser Trp Gly Glu Val Ser Tyr Pro Gly Val Glu Lys
 260 265 270

Thr Met Lys Glu Ala Asp Ala Val Ile Ala Leu Ala Pro Val Phe Asn
 275 280 285

Asp Tyr Ser Thr Thr Gly Trp Thr Asp Ile Pro Asp Pro Lys Lys Leu
 290 295 300

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

Ser Val His Leu Lys Asp Tyr Leu Thr Arg Leu Ala Gln Lys Val Ser
 325 330 335

Lys Lys Thr Gly Ala Leu Asp Phe Phe Lys Ser Leu Asn Ala Gly Glu
340 345 350

Leu Lys Lys Ala Ala Pro Ala Asp Pro Ser Ala Pro Leu Val Asn Ala
355 360 365

Glu Ile Ala Arg Gln Val Glu Ala Leu Leu Thr Pro Asn Thr Thr Val
370 375 380

Ile Ala Glu Thr Gly Asp Ser Trp Phe Asn Ala Gln Arg Met Lys Leu
385 390 395 400

Pro Asn Gly Ala Arg Val Glu Tyr Glu Met Gln Trp Gly His Ile Gly
405 410 415

Trp Ser Val Pro Ala Ala Phe Gly Tyr Ala Val Gly Ala Pro Glu Arg
420 425 430

Arg Asn Ile Leu Met Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln
435 440 445

Glu Val Ala Gln Met Val Arg Leu Lys Leu Pro Val Ile Ile Phe Leu
450 455 460

Ile Asn Asn Tyr Gly Tyr Thr Ile Glu Val Met Ile His Asp Gly Pro
465 470 475 480

Tyr Asn Asn Ile Lys Asn Trp Asp Tyr Ala Gly Leu Met Glu Val Phe
485 490 495

Asn Gly Asn Gly Gly Tyr Asp Ser Gly Ala Gly Lys Gly Leu Lys Ala
500 505 510

Lys Thr Gly Gly Glu Leu Ala Glu Ala Ile Lys Val Ala Leu Ala Asn
515 520 525

Thr Asp Gly Pro Thr Leu Ile Glu Cys Phe Ile Gly Arg Glu Asp Cys
530 535 540

Thr Glu Glu Leu Val Lys Trp Gly Lys Arg Val Ala Ala Ala Asn Ser

545

550

555

560

Arg Lys Pro Val Asn Lys Leu Leu
565

<210> 118

<211> 1707

<212> DNA

<213> *Zymomonas mobilis*

<400> 118

atgtcctaca ccgttggtac ctacttagct gagcgtttgg tccaaatcgg tttgaagcac	60
catttcgccg ttgctggtga ttacaacttg gtcttggttag ataatttatt attgaacaag	120
aacatggaac aagtctactg ctgtaatgaa ttgaactgtg gtttctctgc tgaaggttat	180
gctagagcta aagggtgccgc tgccgctgtt gtcacttact ctgttggtgc tttgtctgcc	240
ttcgacgcta ttggtggtgc ttacgccgag aatttacctg ttattttaat ttctggtgcc	300
cctaacaata acgatcatgc tgctggtcat gttttacacc acgctttggg taaaactgac	360
taccattatc aattagagat ggccaaaaac atcaccgccg ctgccgaggc catttacact	420
ccagaagaag cccagccaa aattgatcac gtcacaaaaa ccgccttgag agagaaaaaa	480
cctgtttact tggaaatcgc ctgtaatatc gcctctatgc cttgcgccgc tcctggtcct	540
gcttccgcct tattcaacga tgaggcttct gatgaagctt ccttaaagc tgctgttgag	600
gagactttaa agttcatcgc taatagagat aaggctcgtg ttttagtcgg ttctaagttg	660
cgtgctgccg gtgccgagga agctgctgtt aaattcgccg atgctttagg tggtgctgtc	720
gccacatgg ccgccccaa atcctttttc cctgaagaaa acccacacta catcggtact	780
tcttggggtg aagtctctta cccaggtgtc gaaaagacta tgaaggaagc cgatgccgtc	840
atgccttg ccaggtttt taatgattat tccaccactg gttggactga tatcccagat	900
cctaaaaagt tagtttttagc cgagcctaga tccgttggtg ttaacggtat tagattccct	960
tccgttcact tgaaggatta cttaactaga ttgggtcaaa aggtttccaa gaagaccggt	1020
gctttggact ttttcaaact tttgaacgcc ggtgagttaa agaaggccgc ccctgctgac	1080
ccatctgctc cattgggttaa cgctgagatt gctagacaag tcgaagcttt attgacccca	1140
aacactaccg ttatcgccga aactggtgac tcttggttta atgctcaaag aatgaagtta	1200
ccaaatggtg ccagagttga gtacgaaatg caatgggggtc atatcggttg gtctgtccca	1260

gctgcttttg gttatgctgt tgggtcccct gagagaagaa acatcttgat ggttggtgac	1320
ggttccttcc aattgactgc tcaagaagtc gctcaaattg ttagattaaa attaccagtc	1380
atcatcttct tgatcaataa ctacggttac actatcgaag tcatgattca cgatggtcct	1440
tacaataata ttaagaactg ggactatgct ggtttgatgg aagtctttaa tggtaacggt	1500
ggttacgatt ccggtgctgg taagggttta aaggctaaga ctggtggtga attagctgaa	1560
gccattaagg ttgccttggc taacaccgac ggtcctactt taatcgaatg tttcattggt	1620
agagaggatt gtaccgaaga gttagttaag tggggtaaga gagttgccgc tgctaattcc	1680
cgtaagcctg tcaataaatt gttataa	1707

<210> 119
 <211> 1575
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Truncated 3-hydroxy-3-methyl-glutaryl-CoA reductase (tHMG1)

<400> 119	
atgcaattgg tgaagactga agtcaccaag aagtctttta ctgctcctgt acaaaaggct	60
tctacaccag ttttaaccaa taaaacagtc atttctggat cgaaagtcaa aagtttatca	120
tctgcgcaat cgagctcatc aggaccttca tcatctagt aggaagatga ttcccgcgat	180
attgaaagct tggataagaa aatacgtcct ttagaagaat tagaagcatt attaagtagt	240
ggaaatacaa aacaattgaa gaacaaagag gtcgctgcct tggttattca cggttaagtta	300
cctttgtacg ctttggagaa aaaattaggt gatactacga gagcggttgc ggtacgtagg	360
aaggctcttt caattttggc agaagctcct gtattagcat ctgatcgttt accatataaa	420
aattatgact acgaccgcgt atttggcgct tgttgtgaaa atgttatagg ttacatgcct	480
ttgcccgttg gtgttatagg ccccttgggt atcgatggta catcttatca tataccaatg	540
gcaactacag agggttgttt ggtagcttct gccatgcgtg gctgtaaggc aatcaatgct	600
ggcgggtggtg caacaactgt ttttaactaag gatggtatga caagaggccc agtagtccgt	660
ttcccaactt tgaaaagatc tgggtgcctgt aagatatggt tagactcaga agagggacaa	720
aacgcaatta aaaaagcttt taactctaca tcaagatttg cacgtctgca acatattcaa	780
acttgtctag caggagattt actcttcatg agatttagaa caactactgg tgacgcaatg	840

ggatatgaata tgattttctaa ggggtgtcgaa tactcattaa agcaaattggt agaagagtat	900
ggctgggaag atatggaggt tgtctccgtt tctggtaact actgtaccga caaaaaacca	960
gctgccatca actggatcga aggtcgtggt aagagtgtcg tcgcagaagc tactattcct	1020
ggatgatgttgc tcagaaaagt gttaaaaagt gatgtttccg cattggttga gttgaacatt	1080
gctaagaatt tgggttgatc tgcaatggct ggggtctgtt gtggatttaa cgcacatgca	1140
gctaatttag tgacagctgt tttcttggca ttaggacaag atcctgcaca aaatgtcgaa	1200
agttccaact gtataacatt gatgaaagaa gtggacggtg atttgagaat ttccgtatcc	1260
atgccatcca tcgaagtagg taccatcggg ggtgggtactg ttctagaacc acaaggtgcc	1320
atgttggact tattaggtgt aagaggccca catgctaccg ctcttggtac caacgcacgt	1380
caattagcaa gaatagttgc ctgtgccgtc ttggcaggtg aattatcctt atgtgctgcc	1440
ctagcagccg gccatttggg tcaaagtcac atgaccaca acaggaaacc tgctgaacca	1500
acaaaacctt acaatttggg cgccactgat ataaatcgtt tgaaagatgg gtccgtcacc	1560
tgcatataat cctaa	1575

<210> 120
 <211> 1387
 <212> DNA
 <213> Saccharomyces sp.

<400> 120	
atgactgaac taaaaaaca aaagaccgct gaacaaaaaa ccagacctca aaatgtcggg	60
attaaaggta tccaaattta catcccaact caatgtgtca accaatctga gctagagaaa	120
tttgatggcg tttctcaagg taaatacaca attgggtctgg gccaaaccaa catgtctttt	180
gtcaatgaca gagaagatat ctactcgatg tccctaactg ttttgtctaa gttgatcaag	240
agttacaaca tcgacaccaa caaaattggg agattagaag tcggtactga aactctgatt	300
gacaagtcca agtctgtcaa gtctgtcttg atgcaattgt ttggtgaaaa cactgacgtc	360
gaaggatttg acacgcttaa tgcctgttac ggtgggtacca acgcgttggt caactctttg	420
aactggattg aatctaacgc atgggatggg agagacgcca ttgtagtttg cggtgatatt	480
gccatctacg ataagggtgc cgcaagacca accggtgggt cgggtactgt tgctatgtgg	540
atcggtcctg atgctccaat tgtatttgac tctgtaagag cttcttacat ggaacacgcc	600

tacgattttt acaagccaga tttcaccagc gaatatcctt acgtcgatgg tcattttttca	660
ttaacttggt acgtcaaggc tcttgatcaa gtttacaaga gttattccaa gaaggctatt	720
tctaaagggt tggttagcga tcccgcgtgg tccggatgctt tgaacgtttt gaaatatttc	780
gactacaacg ttttccatgt tccaacctgt aaattgggtca caaaatcata cggtagatta	840
ctatataacg atttcagagc caatcctcaa ttgttcccag aagttgacgc cgaattagct	900
actcgcgatt atgacgaatc ttttaaccgat aagaacattg aaaaaacttt tgттаатggt	960
gctaagccat tccacaaaga gagagttgcc caatctttga ttgttccaac aaacacaggt	1020
aacatgtaca ccgcatctgt ttatgccgcc tttgcatctc tattaacta tgttggatct	1080
gacgacttac aaggcaagcg tgttgggttta ttttcttacg gttccggttt agctgcatct	1140
ctatattctt gcaaaattgt tgggtgacgtc caacatatta tcaaggaatt agatattact	1200
aacaaattag ccaagagaat caccgaaact ccaaaggatt acgaagctgc catcgaattg	1260
agagaaaatg cccatttgaa gaagaacttc aaacctcaag gttccattga gcatttgcaa	1320
agtgggtgtt actacttgac caacatcgat gacaaattta gaagatctta cgatgttaaa	1380
aaataat	1387

<210> 121
 <211> 420
 <212> PRT
 <213> Catharanthus sp.

<400> 121

Met	Leu	Phe	Ser	Arg	Gly	Leu	Tyr	Arg	Ile	Ala	Arg	Thr	Ser	Leu	Asn
1				5					10					15	

Arg	Ser	Arg	Leu	Leu	Tyr	Pro	Leu	Gln	Ser	Gln	Ser	Pro	Glu	Leu	Leu
			20					25					30		

Gln	Ser	Phe	Gln	Phe	Arg	Ser	Pro	Ile	Gly	Ser	Ser	Gln	Lys	Val	Ser
		35					40					45			

Gly	Phe	Arg	Val	Ile	Tyr	Ser	Cys	Val	Ser	Ser	Ala	Leu	Ala	Asn	Val
	50					55					60				

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

Asp Pro Phe Ser Leu Val Ala Asp Glu Leu Ser Ile Leu Ala Asn Arg
85 90 95

Leu Arg Ser Met Val Val Ala Glu Val Pro Lys Leu Ala Ser Ala Ala
100 105 110

Glu Tyr Phe Phe Lys Leu Gly Val Glu Gly Lys Arg Phe Arg Pro Thr
115 120 125

Val Leu Leu Leu Met Ala Thr Ala Ile Asp Ala Pro Ile Ser Arg Thr
130 135 140

Pro Pro Asp Thr Ser Leu Asp Thr Leu Ser Thr Glu Leu Arg Leu Arg
145 150 155 160

Gln Gln Ser Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu
165 170 175

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

Ser Leu Asn Phe Val Met Gly Asn Lys Leu Ala Val Leu Ala Gly Asp
195 200 205

Phe Leu Leu Ser Arg Ala Cys Val Ala Leu Ala Ser Leu Lys Asn Thr
210 215 220

Glu Val Val Ser Leu Leu Ala Thr Val Val Glu His Leu Val Thr Gly
225 230 235 240

Glu Thr Met Gln Met Thr Thr Thr Ser Asp Gln Arg Cys Ser Met Glu
245 250 255

Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser Asn
260 265 270

Ser Cys Lys Ala Ile Ala Leu Leu Ala Gly Gln Thr Ser Glu Val Ala
275 280 285

Met Leu Ala Tyr Glu Tyr Gly Lys Asn Leu Gly Leu Ala Phe Gln Leu
290 295 300

Ile Asp Asp Val Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly Lys
305 310 315 320

Gly Ser Leu Ser Asp Ile Arg His Gly Ile Val Thr Ala Pro Ile Leu
325 330 335

Phe Ala Ile Glu Glu Phe Pro Glu Leu Arg Ala Val Val Asp Glu Gly
340 345 350

Phe Glu Asn Pro Tyr Asn Val Asp Leu Ala Leu His Tyr Leu Gly Lys
355 360 365

Ser Arg Gly Ile Gln Arg Thr Arg Glu Leu Ala Ile Lys His Ala Asn
370 375 380

Leu Ala Ser Asp Ala Ile Asp Ser Leu Pro Val Thr Asp Asp Glu His
385 390 395 400

Val Leu Arg Ser Arg Arg Ala Leu Val Glu Leu Thr Gln Arg Val Ile
405 410 415

Thr Arg Arg Lys
420

<210> 122
<211> 1263
<212> DNA
<213> Catharanthus sp.

<400> 122
atgttattct ctcgtggttt atacagaatc gccagaactt ctttgaacag atcccgtttg 60
ttgtaccctt tacaatctca atctcctgaa ttgttacaat ctttccaatt cagatctcca 120
atcggttcct ctcaaaagggt ttccgggtttc agagttatct actcctgcgt ttcctctgct 180
ttagctaacg ttgggtcaaca agtccaaaga caatctaatt ccgttgctga agaacccttg 240
gaccatttct ccttggttgc cgatgaatta tccatttttag ctaacagatt gcgttctatg 300
gtcgtcgtg aagttccaaa gttagcctcc gccgccgaat atttcttcaa gttgggtgtc 360

gagggtaaaa gattcagacc aactgttttg ttgttaatgg ccaccgccat tgatgccccca	420
atctctagaa ccccacctga cacctcctta gatactttat ccaccgaatt gcgtttgaga	480
caacaatcta tcgccgaaat tactgaaatg attcatgtcg cttccttggt gcacgatgat	540
gttttgatg atgctgaaac tagaagaggt attggttctt taaattttgt catgggtaac	600
aaattggctg ttttggccgg tgacttctta ttatctagag cttgtgttgc cttagcttct	660
ttgaaaaaca ctgaagtcgt ctccttggtta gccactgtcg ttgaacactt agttactggt	720
gagactatgc aaatgactac cacctccgat caaagatggt ctatggaata ctacatgcaa	780
aagacctatt acaagactgc ctctttgatt tctaactcct gtaaagccat tgccttggtta	840
gctgggtcaaa cttctgaagt tgccatgttg gcttacgaat acggtaaaaa cttggggttg	900
gctttccaat tgattgatga tgttttggat ttcactggta cttctgcttc cttaggtaaa	960
ggttctttgt ctgatattcg tcacggatc gttaccgcc caatcttggt cgctattgaa	1020
gaattcccag agttaagagc tgttgttgac gaaggtttcg aaaaccctta caatgttgac	1080
ttagccttgc actacttggg taaatctaga ggtattcaac gtaccagaga attagccatt	1140
aaacatgcta acttagcctc tgacgccatt gactctttac cagtcactga tgatgagcac	1200
gtcttacgtt ccagacgtgc cttagttgaa ttgactcaaa gagttattac tagaagaaag	1260
taa	1263

<210> 123
 <211> 421
 <212> PRT
 <213> *Mangifera indica*

<400> 123

Met	Leu	Phe	Ser	Tyr	Gly	Leu	Ser	Arg	Ile	Ser	Ile	Asn	Pro	Arg	Ala
1				5					10					15	

Ser	Leu	Leu	Thr	Cys	Arg	Trp	Leu	Leu	Ser	His	Leu	Thr	Gly	Ser	Leu
			20					25					30		

Ser	Pro	Ser	Thr	Ser	Ser	His	Thr	Ile	Ser	Asp	Ser	Val	His	Lys	Val
		35					40					45			

Trp	Gly	Cys	Arg	Glu	Ala	Tyr	Thr	Trp	Ser	Val	Pro	Ala	Leu	His	Gly
	50					55					60				

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

Leu Asp Pro Phe Ser Leu Val Ala Asp Glu Leu Ser Leu Val Ala Asn
85 90 95

Arg Leu Arg Ser Met Val Val Thr Glu Val Pro Lys Leu Ala Ser Ala
100 105 110

Ala Glu Tyr Phe Phe Lys Met Gly Val Glu Gly Lys Arg Phe Arg Pro
115 120 125

Ala Val Leu Leu Leu Met Ala Thr Ala Leu Asn Val His Val Leu Glu
130 135 140

Pro Leu Pro Glu Gly Ala Gly Asp Ala Leu Met Thr Glu Leu Arg Thr
145 150 155 160

Arg Gln Gln Cys Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser
165 170 175

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

Gly Ser Leu Asn Leu Val Met Gly Asn Lys Leu Ala Val Leu Ala Gly
195 200 205

Asp Phe Leu Leu Ser Arg Ala Cys Val Ala Leu Ala Ser Leu Lys Asn
210 215 220

Thr Glu Val Val Ser Leu Leu Ala Thr Val Val Glu His Leu Val Thr
225 230 235 240

Gly Glu Thr Met Gln Met Thr Thr Ser Ser Asp Gln Arg Cys Ser Met
245 250 255

Glu Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser
260 265 270

Asn Ser Cys Lys Ala Ile Ala Leu Leu Ala Gly Gln Ser Ala Glu Val
275 280 285

Ala Met Leu Ala Phe Glu Phe Gly Lys Asn Leu Gly Leu Ala Tyr Gln
290 295 300

Leu Ile Asp Asp Val Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly
305 310 315 320

Lys Gly Ser Leu Ser Asp Ile Arg His Gly Ile Val Thr Ala Pro Ile
325 330 335

Leu Phe Ala Met Glu Glu Phe Pro Gln Leu Arg Ala Val Ile Asp Gln
340 345 350

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

Lys Ser Arg Gly Ile Gln Arg Thr Arg Glu Leu Ala Thr Asn His Ala
370 375 380

Asn Leu Ala Ala Ala Ala Ile Asp Ala Leu Pro Lys Thr Asp Asn Glu
385 390 395 400

Glu Val Arg Lys Ser Arg Arg Ala Leu Leu Asp Leu Thr Gln Arg Val
405 410 415

Ile Thr Arg Asn Lys
420

<210> 124
<211> 1266
<212> DNA
<213> Mangifera indica

<400> 124
atgttattct cttatggttt atctcgatt tctattaacc ctcgtgcctc tttattgact 60
tgtagatggg tattatccca tttgactggg tctttatctc cttccacttc ttcccatact 120
atttctgact ccgtccataa agtctggggg tgcagagaag cctatacttg gtctgtccca 180
gctttacatg gttttagaca tcaaatccac catcaatcct cttccttgat tgaagatcaa 240

ttagacccat tctccttggg cgccgatgag ttgtccttgg ttgctaaccg ttttaagatct	300
atggttgtca ctgaagtccc taaattagcc tctgccgccg aatacttttt caagatgggt	360
gtcgaaggta agcgtttcag accagctgtc ttgttggttaa tggccactgc cttaaacggt	420
catgttttgg aacctttgcc tgaagggtgct ggtgacgctt taatgaccga gttgagaacc	480
cgtcaacaat gcattgctga aatcactgag atgatccacg tcgcctcttt attgcatgac	540
gatgttttag acgacgctga tactagaaga ggtattgggt ctttgaactt ggttatgggt	600
aacaaattgg ccgttttggc cggtgatttc ttgttatccc gtgcttgcgt tgcttttagct	660
tctttgaaga aactgaagt tgtttctttg ttggccaccg tcgttgaaca cttagttact	720
ggtgagacta tgcaaatgac cacctcttct gaccaaagat gttccatgga atattacatg	780
caaaaaactt attacaaaac cgcctccttg atttctaact cctgtaaagc catcgcctta	840
ttagctggtc aatctgctga agttgccatg ttagccttcg agtttggtta gaacttgggt	900
ttagcttacc aattgatcga tgatgtcttg gattttaccg gtacctctgc ttctttgggt	960
aagggttcct tgtccgacat tagacacggt attgttaccg cccaatctt attcgctatg	1020
gaagagtttc cacaattgag agctgttatc gaccaagggt tcgagaacct atctaacgtt	1080
gacgtcgcct tagagtatct aggtaaatct agaggatatcc aacgtaccg tgaattagct	1140
actaaccatg ctaacttagc cgccgccgcc atcgatgcct tgcctaaaac cgataatgaa	1200
gaagtccgta agtccagacg tgctttatta gatttgactc aaagagtcac caccagaaac	1260
aaatag	1266

<210> 125
 <211> 328
 <212> PRT
 <213> *Mangifera indica*

<400> 125

Met	Pro	Phe	Val	Val	Pro	Arg	Arg	Asn	Arg	Ser	Leu	Ser	Val	Ser	Ala
1				5				10						15	

Val	Leu	Thr	Lys	Glu	Glu	Thr	Leu	Arg	Glu	Glu	Glu	Glu	Asp	Pro	Lys
			20					25					30		

Pro	Val	Phe	Asp	Phe	Lys	Ser	Tyr	Met	Leu	Gln	Lys	Gly	Asn	Ser	Val
			35				40					45			

Asn Gln Ala Leu Asp Ala Val Val Ser Ile Arg Glu Pro Lys Lys Ile
50 55 60

His Glu Ala Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg
65 70 75 80

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

Met Ala Met Pro Ala Ala Cys Ala Val Glu Met Ile His Thr Met Ser
100 105 110

Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Leu Arg Arg
115 120 125

Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Val Ala Val Leu
130 135 140

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

Thr Val Gly Val Leu Pro Ser Arg Val Val Lys Ala Val Gly Glu Leu
165 170 175

Ala Lys Ser Ile Gly Ile Glu Gly Leu Val Ala Gly Gln Val Val Asp
180 185 190

Ile Asn Ser Glu Gly Leu Lys Glu Val Gly Leu Asp His Leu Glu Phe
195 200 205

Ile His Gln His Lys Thr Ala Ala Leu Leu Glu Gly Ser Val Val Leu
210 215 220

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

Thr Phe Ala Arg Cys Ile Gly Leu Leu Phe Gln Val Val Asp Asp Ile
245 250 255

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

Asp Leu Val Ala Asp Lys Val Thr Tyr Pro Lys Leu Leu Gly Ile Glu
 275 280 285

Lys Ser Arg Glu Leu Ala Asp Lys Leu Asn Lys Asp Ala Gln Gln Gln
 290 295 300

Leu Ser Gly Phe Asp Gln Glu Lys Ala Ala Pro Leu Ile Ala Leu Ser
 305 310 315 320

Asn Tyr Ile Ala Tyr Arg Gln Asn
 325

<210> 126
 <211> 987
 <212> DNA
 <213> *Mangifera indica*

<400> 126
 atgccattcg ttgttcctag aagaaaccgt tctttgtccg tttccgccgt tttgaccaag 60
 gaagaaactt taagagagga agaagaagat ccaaagccag ttttcgactt caaatcttac 120
 atgttacaaa agggtaatc tgtaaatcaa gctttggatg ctgtcgtttc cattagagaa 180
 cctaagaaaa tccatgaggc tatgcgttac tctttgttgg ctggtggtaa gagagttcgt 240
 cctgttttgt gtattgccgc ctgtgaattg gtcggtggta acgaatctat ggctatgcc 300
 gccgcctgtg ctgtcgaaat gatccacact atgtccttga ttcacgatga tttgccatgt 360
 atggataatg acgatttgcg tcgtggtaaa cctaccaacc ataaagtttt cggatgaagac 420
 gtcgccgttt tggctggtga cgctttatta gctttttcct tcgagaacat ggccgtttcc 480
 actgttggtg tcttaccatc cagagttgtc aaggctgttg gtgaattggc caagtctatc 540
 ggtattgaag gtttggttgc cggatcaagtc gtcgatatta attctgaggg tttaaaagag 600
 gtcggtttag atcacttaga atttatccat caacacaaaa ccgctgcttt gttggagggt 660
 tctgttgttt tgggtgctat tttaggtggg ggttctgatg atgaagtcga aaagttgcgt 720
 accttgcta gatgtatcgg tttgttgttt caagttgttg acgatatttt ggatgtcact 780
 aagcttcca gagaattggg taagactgcc ggtaaagatt tggttgctga taaagttact 840

tatccaaagt tgtaggtat tgaaaagtct cgtgaattgg ccgataagtt aaacaaggat 900
gctcaacaac aattatccgg ttttgatcaa gagaaggctg cccctttaat cgctttgtcc 960
aattacatcg cctacagaca aaactag 987

<210> 127
<211> 321
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated geranylgeranyl pyrophosphate synthase Cs2_GPPS_NTrunc
<400> 127

Met Val Ile Ala Glu Val Pro Lys Leu Ala Ser Ala Ala Glu Tyr Phe
1 5 10 15

Phe Lys Met Gly Val Glu Gly Lys Arg Phe Arg Pro Thr Val Leu Leu
20 25 30

Leu Met Ala Thr Ala Leu Asn Val Arg Val Pro Glu Pro Leu His Asp
35 40 45

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

Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu Leu His Asp
65 70 75 80

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

Phe Val Met Gly Asn Lys Leu Ala Val Leu Ala Gly Asp Phe Leu Leu
100 105 110

Ser Arg Ala Cys Val Ala Leu Ala Ser Leu Lys Asn Thr Glu Val Val
115 120 125

Thr Leu Leu Ala Thr Val Val Glu His Leu Val Thr Gly Glu Thr Met
130 135 140

Gln Met Thr Thr Ser Ser Asp Gln Arg Cys Ser Met Asp Tyr Tyr Met

145		150		155		160									
Gln	Lys	Thr	Tyr	Tyr	Lys	Thr	Ala	Ser	Leu	Ile	Ser	Asn	Ser	Cys	Lys
				165					170					175	
Ala	Ile	Ala	Leu	Leu	Ala	Gly	Gln	Thr	Ala	Glu	Val	Ala	Ile	Leu	Ala
			180					185					190		
Phe	Asp	Tyr	Gly	Lys	Asn	Leu	Gly	Leu	Ala	Tyr	Gln	Leu	Ile	Asp	Asp
		195					200					205			
Val	Leu	Asp	Phe	Thr	Gly	Thr	Ser	Ala	Ser	Leu	Gly	Lys	Gly	Ser	Leu
	210						215				220				
Ser	Asp	Ile	Arg	His	Gly	Ile	Ile	Thr	Ala	Pro	Ile	Leu	Phe	Ala	Met
225					230					235					240
Glu	Glu	Phe	Pro	Gln	Leu	Arg	Thr	Val	Val	Glu	Gln	Gly	Phe	Glu	Asp
				245					250					255	
Ser	Ser	Asn	Val	Asp	Ile	Ala	Leu	Glu	Tyr	Leu	Gly	Lys	Ser	Arg	Gly
			260					265					270		
Ile	Gln	Lys	Thr	Arg	Glu	Leu	Ala	Val	Lys	His	Ala	Asn	Leu	Ala	Ala
		275					280					285			
Ala	Ala	Ile	Asp	Ser	Leu	Pro	Glu	Asn	Asn	Asp	Glu	Asp	Val	Thr	Lys
	290					295					300				
Ser	Arg	Arg	Ala	Leu	Leu	Asp	Leu	Thr	His	Arg	Val	Ile	Thr	Arg	Asn
305					310					315					320

Lys

<210> 128
 <211> 966
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Truncated geranylgeranyl pyrophosphate synthase Cs2_GPPS_NTrunc

<400> 128
atggtcattg ctgaagttcc taaattagcc tctgccgccg aatacttctt caagatgggt 60
gtcgagggta agagatttcg tcctaccgtt ttgttggttaa tggccaccgc cttaaacgtc 120
agagtccctg aaccattaca tgatgggtgtt gaagatgcct ctgccaccga gttgagaact 180
agacaacaat gtattgctga aatcaccgag atgattcacg ttgcctcttt gttgcacgat 240
gatgttttgg atgatgctga taccgctcgt ggtatcggtt ctttgaactt tgtcatgggt 300
aacaagttgg ctgtcttggc tgggtgatttc ttattgtctc gtgcctgcgt tgccttagcc 360
tctttaaaaa ataccgaagt tgttacttta ttggccactg ttgttgagca cttggttact 420
ggtgaaacta tgcaaagac cacctcttcc gaccaacgtt gttccatgga ctattacatg 480
caaaagacct actacaagac cgcttctttg atttccaatt cttgtaaagc cattgcctta 540
ttagctggtc aaactgctga agttgccatc ttggccttcg actacggtaa aaacttgggt 600
ttagcttacc aattgattga tgacgtttta gattttactg gtacttctgc ttctttgggt 660
aaaggttctt tatccgatat tcgtcatggt atcattaccg ctccaatctt attcgctatg 720
gaagaatttc ctcaattgcg tactgtcgtt gaacaagggt tcgaagactc ctccaacgtt 780
gacattgcct tagaatactt gggttaagtct cgtgggtattc aaaagaccgc tgaattagcc 840
gttaaacaatg ccaacttagc cgccgccgcc atcgattcct tgcctgaaaa caacgatgag 900
gatgtcacca agtcccgtcg tgctttgtta gatttaactc acagagttat taccgtaac 960
aagtaa 966

<210> 129
<211> 416
<212> PRT
<213> Quercus sp.

<400> 129
Met Leu Phe Ser Arg Ile Ser Arg Ile Arg Arg Pro Gly Ser Asn Gly
1 5 10 15
Phe Arg Trp Phe Leu Ser His Lys Thr His Leu Gln Phe Leu Asn Pro
20 25 30
Pro Ala Tyr Ser Tyr Ser Ser Thr His Lys Val Leu Gly Cys Arg Glu
35 40 45

Ile Phe Ser Trp Gly Leu Pro Ala Leu His Gly Phe Arg His Asn Ile
50 55 60

His His Gln Ser Ser Ser Ile Val Glu Glu Gln Asn Asp Pro Phe Ser
65 70 75 80

Leu Val Ala Asp Glu Leu Ser Met Val Ala Asn Arg Leu Arg Ser Met
85 90 95

Val Val Thr Glu Val Pro Lys Leu Ala Ser Ala Ala Glu Tyr Phe Phe
100 105 110

Lys Met Gly Val Glu Gly Lys Arg Phe Arg Pro Thr Val Leu Leu Leu
115 120 125

Met Ala Thr Ala Met Asn Ile Ser Ile Leu Glu Pro Ser Leu Arg Gly
130 135 140

Pro Gly Asp Ala Leu Thr Thr Glu Leu Arg Ala Arg Gln Gln Arg Ile
145 150 155 160

Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu Leu His Asp Asp
165 170 175

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

Val Met Gly Asn Lys Leu Ala Val Leu Ala Gly Asp Phe Leu Leu Ser
195 200 205

Arg Ala Cys Val Ala Leu Ala Ser Leu Lys Asn Thr Glu Val Val Ser
210 215 220

Leu Leu Ala Lys Val Val Glu His Leu Val Thr Gly Glu Thr Met Gln
225 230 235 240

Met Thr Thr Thr Cys Glu Gln Arg Cys Ser Met Glu Tyr Tyr Met Gln
245 250 255

Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser Asn Ser Cys Lys Ala
260 265 270

Ile Ala Leu Leu Gly Gly Gln Thr Ser Glu Val Ala Met Leu Ala Tyr
275 280 285

Glu Tyr Gly Lys Asn Leu Gly Leu Ala Tyr Gln Leu Ile Asp Asp Val
290 295 300

Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly Lys Gly Ser Leu Ser
305 310 315 320

Asp Ile Arg His Gly Ile Ile Thr Ala Pro Ile Leu Phe Ala Met Glu
325 330 335

Glu Phe Pro Gln Leu Arg Glu Val Val Asp Arg Gly Phe Asp Asp Pro
340 345 350

Ala Asn Val Asp Val Ala Leu Asp Tyr Leu Gly Lys Ser Arg Gly Ile
355 360 365

Gln Arg Ala Arg Glu Leu Ala Lys Lys His Ala Asn Ile Ala Ala Glu
370 375 380

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

Arg Arg Ala Leu Leu Asp Leu Thr Glu Arg Val Ile Thr Arg Thr Lys
405 410 415

<210> 130
<211> 1251
<212> DNA
<213> Quercus sp.

<400> 130
atgttggttct ctcgtatttc tcgtatccgt agaccagggtt ctaatgggttt cagatgggttc 60
ttgtcccata agactcattt acaattcttg aaccctccag cttattccta ctcttcact 120
cataagggtct tgggttgtag agaaatTTTT tcctgggggtt tacctgcctt acatgggtttc 180
agacacaaca ttcaccacca atcttcctct attgttgaag aacaaaatga ccctttctct 240

```

ttggtcgctg atgagttgtc catggttgct aacagattgc gttctatggt tgttactgaa      300
gttcctaaat tagcctccgc cgctgaatac ttttttaaaa tgggtgttga aggtaagaga      360
ttcagaccaa ctgttttatt gttgatggct accgccatga acatttccat cttagaacca      420
tctttgagag gtccaggtga cgctttgacc actgaattga gagccagaca acaaagaatt      480
gctgaaatta ccgagatgat ccacgttgct tccttgttgc acgatgacgt tttggatgac      540
gctgatacta gaagaggtat tggttcctta aactttgtca tgggtaataa attagctgtt      600
ttggctggtg attttttgtt atctcgtgcc tgtgttgctt tagcttcttt gaagaacacc      660
gaagttgtct ccttgttagc caaggtcgtc gaacacttgg ttactggtga aactatgcaa      720
atgaccacta cttgtgaaca aagatgttcc atggaatact acatgcaaaa gacttactat      780
aagaccgctt ctttaatttc caactcctgt aaagccattg ctttattagg tgggtcaaact      840
tctgaggtcg ctatgttagc ctacgaatat ggtaaaaact tgggttttagc ttaccaattg      900
attgatgatg tcttggaattt cactggtact tctgcttcct tgggtaaggg ttccttgtct      960
gatattagac atggtatcat tactgctcca attttgtttg ctatggaaga attcccacaa     1020
ttacgtgaag ttgtcgatag aggtttcgac gatcctgcc aacgtcgatgt tgccttggac     1080
tacttgggta agtctagagg tatccaaaga gccagagagt tagctaaaaa acacgctaac     1140
attgctgccg aagccatcga ctctttgcc gaatccaacg acgaggacgt cagaaagtcc     1200
cgtcgtgctt tgttggactt gaccgaaaga gtcattactc gtactaagta a              1251

```

```

<210> 131
<211> 427
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Truncated geranylgeranyl pyrophosphate synthase Pa_GPPS_Ntrunc

```

```

<400> 131

```

```

Met Tyr Thr Arg Cys Ile Leu Arg Asp Lys Tyr Ser Arg Phe Asn Leu
1           5           10          15

```

```

Arg Arg Lys Phe Phe Thr Ser Ala Lys Ser Ile Asn Ala Leu Asn Gly
          20          25          30

```

```

Leu Pro Asp Ser Gly Asn Pro Arg Gly Glu Ser Asn Gly Ile Ser Gln

```


35

40

45

Phe Glu Ile Gln Gln Val Phe Arg Cys Lys Glu Tyr Ile Trp Ile Asp
 50 55 60

Arg His Lys Phe His Asp Val Gly Phe Gln Ala His His Lys Gly Ser
 65 70 75 80

Ile Thr Asp Glu Glu Gln Val Asp Pro Phe Ser Leu Val Ala Asp Glu
 85 90 95

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

Pro Lys Leu Gly Thr Ala Ala Glu Tyr Phe Phe Lys Leu Gly Val Glu
 115 120 125

Gly Lys Arg Phe Arg Pro Met Val Leu Leu Leu Met Ala Ser Ser Leu
 130 135 140

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

Asp Glu Glu Gln Arg Leu Arg Gln Gln Arg Ile Ala Glu Ile Thr Glu
 165 170 175

Met Ile His Val Ala Ser Leu Leu His Asp Asp Val Leu Asp Asp Ala
 180 185 190

Asp Thr Arg Arg Gly Val Gly Ser Leu Asn Phe Val Met Gly Asn Lys
 195 200 205

Leu Ala Val Leu Ala Gly Asp Phe Leu Leu Ser Arg Ala Ser Val Ala
 210 215 220

Leu Ala Ser Leu Lys Asn Thr Glu Val Val Glu Leu Leu Ser Lys Val
 225 230 235 240

Leu Glu His Leu Val Thr Gly Glu Ile Met Gln Met Thr Asn Thr Asn
 245 250 255

Glu Gln Arg Cys Ser Met Glu Tyr Tyr Met Gln Lys Thr Phe Tyr Lys
260 265 270

Thr Ala Ser Leu Met Ala Asn Ser Cys Lys Ala Ile Ala Leu Ile Ala
275 280 285

Gly Gln Pro Ala Glu Val Cys Met Leu Ala Tyr Asp Tyr Gly Arg Asn
290 295 300

Leu Gly Leu Ala Tyr Gln Leu Leu Asp Asp Val Leu Asp Phe Thr Gly
305 310 315 320

Thr Thr Ala Ser Leu Gly Lys Gly Ser Leu Ser Asp Ile Arg Gln Gly
325 330 335

Ile Val Thr Ala Pro Ile Leu Phe Ala Leu Glu Glu Phe Pro Gln Leu
340 345 350

His Asp Val Ile Asn Arg Lys Phe Lys Lys Pro Gly Asp Ile Asp Leu
355 360 365

Ala Leu Glu Phe Leu Gly Lys Ser Asp Gly Ile Arg Lys Ala Lys Gln
370 375 380

Leu Ala Ala Gln His Ala Gly Leu Ala Ala Phe Ser Val Glu Ser Phe
385 390 395 400

Pro Pro Ser Glu Ser Glu Tyr Val Lys Leu Cys Arg Lys Ala Leu Ile
405 410 415

Asp Leu Ser Glu Lys Val Ile Thr Arg Thr Arg
420 425

<210> 132

<211> 1284

<212> DNA

<213> Artificial Sequence

<220>

<223> Truncated geranylgeranyl pyrophosphate synthase Pa_GPPS_N_trunc

<400> 132

atgtataccc gttgcatttt aagagacaag tattctcgtt tcaacttgag acgtaaattc	60
ttcacttccg ctaaattccat caatgccttg aatgggtttac ctgactctgg taaccctaga	120
ggatgaatcta acggtatctc ccaattcgaa attcaacaag ttttccgttg taaagaatac	180
atgttgatcg atcgtcacaa gttccacgat gttgggttttc aagctcatca caagggttcc	240
atcactgacg aggaacaagt tgaccctttt tcttttagtcg ctgatgaatt gtccatctta	300
gctaatacgtt taagatccat gatcttaacc gagattccaa agttaggtac cgctgccgaa	360
tactttttca agttgggtgt cgaaggtaag agatttagac caatgggtttt gttgttgatg	420
gcctcctctt taactattgg tatccctgaa gttgccgctg attgtttgcg taagggtttg	480
gacgaagaac aaagattacg tcaacaacgt atcgctgaaa ttactgaaat gattcatgtc	540
gcctctttgt tgcacgatga tgttttggat gacgccgata ctagacgtgg tgttggttcc	600
ttgaactttg ttatgggtaa caagttggct gtttttagccg gtgatttctt gttatctaga	660
gcttctgttg ccttagcttc tttaaagaac actgagggtt ttgagttatt gtctaagggt	720
ttggagcact tagtcactgg tgagatcatg caaatgacta acactaatga acaaagatgt	780
tctatggaat attacatgca aaagactttc tacaagaccg cctctttgat ggctaattct	840
tgtaaagcca ttgccttgat cgctgggtcaa cctgccgaag tctgcatgtt ggcctacgac	900
tacggtagaa acttgggttt agcttatcaa ttattggatg acgttttgga tttcactggt	960
accactgctt ctttaggtaa gggttcctta tccgacatca gacaaggat tgttactgcc	1020
cctattttat tcgctttgga agaattccct caattacacg acgtcatcaa ccgtaagttc	1080
aaaaaaccag gtgacatcga tttggccttg gaatttttgg gtaagtctga tggatatccgt	1140
aaagccaaac aattggctgc tcaacatgct ggttttagctg ctttttctgt cgaatccttt	1200
ccaccatctg aatccgaata cgttaagtta tgtagaaagg ctttgatcga tttgtctgaa	1260
aaggtcatta ctcgtaccag ataa	1284

<210> 133
 <211> 381
 <212> PRT
 <213> Abies grandis

<400> 133

Met	Ala	Tyr	Ser	Ala	Met	Ala	Thr	Met	Gly	Tyr	Asn	Gly	Met	Ala	Ala
1				5					10					15	

Ser Cys His Thr Leu His Pro Thr Ser Pro Leu Lys Pro Phe His Gly
20 25 30

Ala Ser Thr Ser Leu Glu Ala Phe Asn Gly Glu His Met Gly Leu Leu
35 40 45

Arg Gly Tyr Ser Lys Arg Lys Leu Ser Ser Tyr Lys Asn Pro Ala Ser
50 55 60

Arg Ser Ser Asn Ala Thr Val Ala Gln Leu Leu Asn Pro Pro Gln Lys
65 70 75 80

Gly Lys Lys Ala Val Glu Phe Asp Phe Asn Lys Tyr Met Asp Ser Lys
85 90 95

Ala Met Thr Val Asn Glu Ala Leu Asn Lys Ala Ile Pro Leu Arg Tyr
100 105 110

Pro Gln Lys Ile Tyr Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly
115 120 125

Lys Arg Val Arg Pro Val Leu Cys Ile Ala Ala Cys Glu Leu Val Gly
130 135 140

Gly Thr Glu Glu Leu Ala Ile Pro Thr Ala Cys Ala Ile Glu Met Ile
145 150 155 160

His Thr Met Ser Leu Met His Asp Asp Leu Pro Cys Ile Asp Asn Asp
165 170 175

Asp Leu Arg Arg Gly Lys Pro Thr Asn His Lys Ile Phe Gly Glu Asp
180 185 190

Thr Ala Val Thr Ala Gly Asn Ala Leu His Ser Tyr Ala Phe Glu His
195 200 205

Ile Ala Val Ser Thr Ser Lys Thr Val Gly Ala Asp Arg Ile Leu Arg
210 215 220

Met Val Ser Glu Leu Gly Arg Ala Thr Gly Ser Glu Gly Val Met Gly
225 230 235 240

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

Gln Thr Leu Glu Trp Ile His Ile His Lys Thr Ala Met Leu Leu Glu
260 265 270

Cys Ser Val Val Cys Gly Ala Ile Ile Gly Gly Ala Ser Glu Ile Val
275 280 285

Ile Glu Arg Ala Arg Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln
290 295 300

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

Lys Thr Ala Gly Lys Asp Leu Ile Ser Asp Lys Ala Thr Tyr Pro Lys
325 330 335

Leu Met Gly Leu Glu Lys Ala Lys Glu Phe Ser Asp Glu Leu Leu Asn
340 345 350

Arg Ala Lys Gly Glu Leu Ser Cys Phe Asp Pro Val Lys Ala Ala Pro
355 360 365

Leu Leu Gly Leu Ala Asp Tyr Val Ala Phe Arg Gln Asn
370 375 380

<210> 134
<211> 1146
<212> DNA
<213> Abies grandis

<400> 134
atggcttatt ctgctatggc tactatgggt tacaacggta tggctgcttc ttgtcacact 60
ttacacccaa cttctccatt gaaacctttt cacggtgctt ctacttcctt ggaagccttc 120
aatggtgaac acatgggttt gttaagaggt tattctaagc gtaagttgtc ctcttacaaa 180
aatccagctt ctcgttcctc caatgctacc gtcgctcaat tattgaacc accacaaaag 240

ggtaagaagg ctgttgaatt tgacttcaat aagtatatgg attctaaggc tatgaccgtc	300
aacgaggcctt tgaataaagc catcccattg cgttaccac aaaagatcta cgaatctatg	360
agatattctt tgttagctgg tggtaagaga gtccgtccag ttttgtgtat cgccgcttgt	420
gaattagtcg gtgggtactga ggagtttagct attccaaccg cctgtgccat cgaaatgata	480
cacaccatgt ctttgatgca cgatgatttg ccatgtatcg acaacgatga cttgagacgt	540
ggtaaaccta ccaatcataa gattttcggg gaagatactg ctgttactgc cggtaacgct	600
ttacactctt acgccttcga acatattgct gtttctactt ccaagactgt tgggtgctgat	660
agaattttga gaatggtttc tgaattaggt cgtgctactg gttccgaagg tggttatgggt	720
gggtcaaagg tcgatattgc ttctgaaggt gacccttcca ttgatttgca aacttttagaa	780
tggatccaca tccacaagac tgctatgtta ttagaatggt ctgttgtctg tgggtgccatc	840
atcgggtggg cttctgaaat tggtattgag agagccagac gttatgctcg ttgtgtcggg	900
ttattgtttc aagttgttga cgacatttta gatgttacca aatcttctga cgaattgggt	960
aaaactgctg gtaaagattt aatctccgat aaagccacct accctaagtt gatggggttg	1020
gagaaggcca aagagttttc cgatgaatta ttaaacagag ctaaagggtga attgtcttgc	1080
ttcgatccag ttaaggctgc cccattgtta ggtttggtg actacgttgc cttcagacaa	1140
aactaa	1146

<210> 135
 <211> 257
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Truncated geranylgeranyl pyrophosphate synthase Pb_GPPS_NTrunc

<400> 135

Met	Ala	Ala	Ile	Phe	Pro	Ser	Ile	Pro	Ser	Asn	Phe	Lys	Pro	Pro	Gln
1				5				10					15		

Ile	Ser	Gln	Thr	Leu	Thr	Arg	Arg	Arg	Arg	Pro	Asn	Arg	Thr	Leu	Cys
			20					25					30		

Thr	Ala	Thr	Ser	Asp	Gln	Ser	Tyr	Leu	Ser	Ala	Ser	Ser	Ala	Asp	Ile
			35				40					45			

Tyr Ser His Leu Leu Arg Ser Leu Pro Ala Thr Ile His Pro Ser Val
50 55 60

Lys Ala Pro Ile His Ser Leu Leu Ser Ser Pro Ile Pro Pro Thr Ile
65 70 75 80

Ala Pro Pro Leu Cys Leu Ala Ala Thr Glu Leu Val Gly Gly Asn Pro
85 90 95

Asn Ser Ala Ile Asn Ala Ala Cys Ala Ile His Leu Ile His Ala Val
100 105 110

Thr His Thr Arg Thr Ala Pro Pro Leu Ala Glu Phe Ser Pro Gly Val
115 120 125

Leu Leu Met Thr Gly Asp Gly Leu Leu Val Leu Ala Tyr Glu Met Leu
130 135 140

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

Glu Val Ala Arg Thr Ala Ala Ala Val Ala Ala Ala Tyr Glu Gly Gly
165 170 175

Arg Glu Gly Glu Leu Ala Ala Gly Ala Ala Ala Cys Gly Val Ile Leu
180 185 190

Gly Gly Gly Asn Glu Glu Glu Val Glu Arg Gly Arg Arg Val Gly Met
195 200 205

Phe Ala Gly Lys Met Glu Leu Val Glu Ala Glu Val Glu Leu Arg Leu
210 215 220

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

Met Arg Phe Thr Gln Ser Phe Val Asn Val Arg Asn Pro Phe Tyr Gly
245 250 255

Lys

<210> 136
 <211> 774
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Truncated geranylgeranyl pyrophosphate synthase Pb_GPPS_NTrunc

<400> 136
 atggctgcta tctttccatc cattccatcc aacttcaaac cacctcaaat ctctcaaact 60
 ttgaccagac gtagaagacc aaaccgtact ttatgtactg ccacctctga ccaatcttac 120
 ttgtccgctt cttctgccga cttttattct catttggttaa gatctttacc agctactatt 180
 catccatctg ttaaagcccc aatccattct ttattgtcct ctccaattcc tccaaccatc 240
 gctccacctt tgtgttttagc tgctaccgaa ttgggttggtg gtaaccctaa ctctgccatt 300
 aacgccgcct gtgccattca tttgattcat gctgttactc atactagaac cgctccacca 360
 ttagctgaat tttctcctgg tgttttgttg atgactggtg atggtttatt agttttggct 420
 tacgagatgt tggccagatc cccagctggt gatgccgata cttctgtccg tgttttgaag 480
 gaagtcgcta gaaccgccgc cgccgtcgcc gctgcttatg aaggtaggtg agaaggtgaa 540
 ttagctgccg gtgccgctgc ttgtggtgtc attttggttg gtggtaacga agaagaggtc 600
 gaaagaggtc gtagagtcgg tatgttcgct ggtaaaatgg aattagttga agctgaagtc 660
 gaattgagat tgggtttcga agatgctaaa gccggtgccg ttagaagatt gttggaagaa 720
 atgcgtttca cccaatcttt tgtcaacgtt agaaaccctt tttatggtaa gtaa 774

<210> 137
 <211> 420
 <212> PRT
 <213> Azadirachta indica

<400> 137

Met Leu Phe Ser Arg Gly Leu Ser Arg Ile Ser Arg Ile Pro Arg Asn
 1 5 10 15

Ser Leu Ile Gly Cys Arg Trp Leu Val Ser Tyr Arg Pro Asp Thr Ile
 20 25 30

Leu Ser Gly Ser Ser His Ser Val Gly Asp Ser Thr Gln Lys Val Leu
35 40 45

Gly Cys Arg Glu Ala Tyr Leu Trp Ser Leu Pro Ala Leu His Gly Ile
50 55 60

Arg His Gln Ile His Gln Gln Ser Ser Ser Leu Ile Glu Glu Glu Leu
65 70 75 80

Asp Pro Phe Ser Leu Val Ala Asp Glu Leu Ser Leu Val Ala Asn Arg
85 90 95

Leu Arg Ser Met Val Val Ala Glu Val Pro Lys Leu Ala Ser Ala Ala
100 105 110

Glu Tyr Phe Phe Lys Met Gly Val Glu Gly Lys Arg Phe Arg Pro Thr
115 120 125

Val Leu Leu Leu Met Ala Ser Ala Leu Asn Val Gln Val Pro Gln Pro
130 135 140

Leu Ser Asp Gly Val Gly Asp Ala Leu Thr Thr Glu Leu Arg Thr Arg
145 150 155 160

Gln Gln Cys Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu
165 170 175

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

Ser Leu Asn Phe Val Met Gly Asn Lys Leu Ala Val Leu Ala Gly Asp
195 200 205

Phe Leu Leu Ser Arg Ala Cys Val Ala Leu Ala Ser Leu Lys Asn Thr
210 215 220

Glu Val Val Ser Leu Leu Ala Thr Val Val Glu His Leu Val Thr Gly
225 230 235 240

Glu Thr Met Gln Met Thr Thr Thr Ala Glu Gln Arg Arg Ser Met Asp
245 250 255

Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser Asn
260 265 270

Ser Cys Lys Ala Ile Ala Leu Leu Ala Gly Gln Thr Thr Glu Val Ala
275 280 285

Met Leu Ala Phe Asp Tyr Gly Lys Asn Leu Gly Leu Ala Phe Gln Leu
290 295 300

Ile Asp Asp Val Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly Lys
305 310 315 320

Gly Ser Leu Ser Asp Ile Arg His Gly Ile Val Thr Ala Pro Ile Leu
325 330 335

Phe Ala Met Glu Glu Phe Pro Glu Leu Arg Lys Val Val Asp Lys Gly
340 345 350

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

Ser Arg Gly Ile Gln Arg Thr Arg Glu Leu Ala Gln Lys His Ala Asn
370 375 380

Leu Ala Thr Val Ala Leu Asp Ser Leu Pro Glu Ser Asn Asp Asp Asp
385 390 395 400

Val Lys Lys Ser Arg Arg Ala Leu Leu Asp Leu Ala Gln Arg Val Ile
405 410 415

Thr Arg Asn Lys
420

<210> 138
<211> 1263
<212> DNA
<213> Azadirachta indica

<400> 138
atgttgtttt ccagaggttt atctcgatt tccagaatcc cacgtaactc tttgatcggt

tgtagatggt tagtttctta ccgtcctgat accattttat ctggttcctc tcactccggt	120
ggtgactcta ctcaaaaggt tttaggttgt cgtgaagctt acttgtggtc tttaccagcc	180
ttgcacggta ttagacacca aattcatcaa caatcctctt ctttgattga agaagaattg	240
gatccattct ctttagttgc tgatgaattg tcttttagtcg ctaaccgttt gagatccatg	300
gtcgtcgtg aagtcccaaa attagcctcc gccgccgagt acttcttcaa gatgggtgtt	360
gagggtaaga gattccgtcc aactgtctta ttgttgatgg cctccgcctt aaacgttcaa	420
gtcccacaac ctttgtctga cgggtgttggg gatgctttga ctaccgagtt gagaactaga	480
caacaatgca ttgctgagat tactgaaatg atccatgttg cttctttgtt gcatgacgac	540
gttttggatg atgctgacac tagacgtggg atcggttctt tgaacttcgt tatgggtaac	600
aagttggctg tcttggctgg tgatttcttg ttgtccagag cctgtgttgc tttagcttcc	660
ttgaagaata ctgaggttgt ctctttgttg gccaccgttg ttgaacactt ggtcaccggt	720
gaaactatgc aaatgactac tactgctgaa caaagacgtt ccatggatta ttacatgcaa	780
aagacttact ataagaccgc ctctttgatt tccaactctt gtaaagccat tgccttgтта	840
gctgggtcaaa ctaccgaagt tgctatgttg gctttcgatt acggtaagaa tttgggttta	900
gcttttcaat tgatcgatga cgtcttggat tttactggta cctctgcttc tttaggtaaa	960
ggttccttgt ctgatattag acacggtatc gttaccgctc caattttatt cgctatggaa	1020
gaattcccag aattaagaaa gggtgttgat aagggttttg acgacccttc caacgttgac	1080
attgctttgg agtatttggg taagtctaga ggtattcaaa gaaccagaga attggctcaa	1140
aaacatgcca atttggccac cgtcgccttg gattctttac cagaatccaa cgacgacgat	1200
gttaagaagt ctcgtagagc tttattggac ttgggtcaaa gagttattac tagaaacaag	1260
taa	1263

<210> 139

<211> 513

<212> PRT

<213> Artificial Sequence

<220>

<223> Truncated geranylgeranyl pyrophosphate synthase Es_GPPS_NTrunc

<400> 139

Met Arg Arg Ser Gly Ser Ala Thr Ala Ala Ala Ala Ala Thr Leu Ala

1	5	10	15
Arg His Ala Asn Ala Cys Cys Arg Ala Arg Ser Pro Ala Leu Gly Leu	20	25	30
Leu Pro Gly Ala Ala Ala Ser Ser Ser Thr His Arg Ala Ala Leu Ser	35	40	45
Ser Asn Ser Gly His Gly Gly Asp Gly Ser Gly His Tyr Asp Ala Ala	50	55	60
Met Arg Arg Arg Glu Ser Cys Ala Ser Arg Ser Arg His Arg Trp Ser	65	70	75
Gly Gln Glu Ala Ala Ala Ala Ser Ala Thr Thr Thr Thr Ala Arg Arg	85	90	95
Ala Pro Gly Gly Val Ala Gly Ala Ser Gly Gln Gly Ser Ala Ala Gly	100	105	110
Ser Val Arg Ala Leu Ser Ser Ser Phe Leu Ala Asp Ala Val Arg Glu	115	120	125
Thr Ala Thr Asn His Cys Ile Asp Arg Val Val Asn Gly Gly Leu Asp	130	135	140
Gly Ser Val Pro Val Asp Lys Asp Thr Pro Thr Val Glu Val Gln Asp	145	150	155
Phe Val Tyr Asp Ile Asp Phe Ala Gln Arg Pro Ser Gly Ala Ser Gln	165	170	175
Ser Leu Ala Asp Gly Pro Asp Pro Phe Glu Leu Val Ser Ala Glu Leu	180	185	190
Ala Gly Leu Ser Asp Gly Ile Lys Ser Leu Ile Gly Thr Glu His Ala	195	200	205
Val Leu Asn Ala Ala Ala Lys Tyr Phe Phe Glu Leu Asp Gly Gly Lys	210	215	220

Lys Ile Arg Pro Thr Met Val Ile Leu Met Ser Gln Ala Cys Asn Ser
225 230 235 240

Asn Ser Gln Gln Val Arg Pro Asp Val Gln Pro Gly Thr Glu Leu Val
245 250 255

Asn Pro Leu Gln Leu Arg Leu Ala Glu Ile Thr Glu Met Ile His Ala
260 265 270

Ala Ser Leu Phe His Asp Asp Val Ile Asp Glu Ala Asp Thr Arg Arg
275 280 285

Gly Val Pro Ser Val Asn Lys Val Phe Gly Asn Lys Leu Ala Ile Leu
290 295 300

Ala Gly Asp Phe Leu Leu Ala Arg Ser Ser Met Ser Leu Ala Arg Leu
305 310 315 320

Arg Ser Leu Glu Ser Val Glu Leu Met Ser Ala Ala Ile Glu His Leu
325 330 335

Val Lys Gly Glu Val Leu Gln Met Arg Pro Thr Glu Asp Gly Gly Gly
340 345 350

Ala Phe Glu Tyr Tyr Val Arg Lys Asn Tyr Tyr Lys Thr Gly Ser Leu
355 360 365

Met Ala Asn Ser Cys Lys Ala Ser Ala Val Leu Gly Gln His Asp Leu
370 375 380

Glu Val Gln Glu Val Ala Phe Glu Tyr Gly Lys Arg Val Gly Leu Ala
385 390 395 400

Phe Gln Leu Val Asp Asp Ile Leu Asp Phe Glu Gly Asn Thr Phe Thr
405 410 415

Leu Gly Lys Pro Ala Leu Asn Asp Leu Arg Gln Gly Leu Ala Thr Ala
420 425 430

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

435

440

445

Ser Arg Lys Phe Arg Gly Pro Gly Asp Val Asp Glu Ala Leu Glu Leu
 450 455 460

Val His Arg Ser Asp Gly Ile Ala Arg Ala Lys Glu Val Ala Val Val
 465 470 475 480

Gln Ala Glu Lys Ala Met Ser Ala Ile Leu Thr Leu His Asp Ser Pro
 485 490 495

Ala Gln Asn Ala Leu Val Gln Leu Ala His Lys Ile Val Asn Arg Asn
 500 505 510

His

<210> 140
 <211> 1542
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Truncated geranylgeranyl pyrophosphate synthase Es_GPPS_NTrunc

<400> 140
 atgcgtagat ccggttccgc taccgccgct gccgctgcc ccttagccag acacgccaac 60
 gcctgttgta gagcccggtc ccagcttta gggttggtgc ctggtgccgc cgcttcttcc 120
 tctactcaca gagccgcctt gtcttctaata tctggtcatg gtggtgatgg ttccggtcat 180
 tacgacgctg ctatgagaag aagagaatct tgcgcttcca gatctcgtca cagatggtcc 240
 ggtcaagaag ctgccgccgc ctccgccact accaccaccg ctgctcgtgc tccaggtggt 300
 gtcgccggtg cttctggtca aggttctgct gccggttctg ttagagcctt atcctcttct 360
 tttttagccg atgccgttcg tgaaaccgct actaaccact gtatcgaccg tgttgtcaac 420
 ggtgggttgg acggttctgt ccagtcgat aaagataccc caactgtcga agttcaagac 480
 tttgtttatg atattgactt tgctcaacgt ccatccggtg cctctcaatc tttagctgac 540
 ggtccagatc cattcgagtt agtttccgct gagttggccg gtttgtctga tggatttaag 600
 tctttgattg gtaccgaaca tgctgtcttg aacgccgccg ccaaataatt cttcgaatta 660

gatggtgta aaaagatcag acctactatg gttatcttaa tgtcccaagc ttgtaactct	720
aattcccaac aagttcgtcc tgacgttcaa ccaggtagtg aattagtcaa tcctttgcaa	780
ttaagattgg ctgaaatcac cgagatgatt catgctgctt ctttattcca cgacgatgtt	840
attgatgagg ctgatactag acgtggtgtc ctttctgtta ataaagtttt cggttaacaaa	900
ttagccatct tggccggtga cttcttattg gctagatcct ctatgtcctt ggcccgttta	960
agatccttgg agtccgtcga attgatgtcc gccgctatcg aacacttggt caaagggtgaa	1020
gttttacaaa tgcgtccaac tgaggacggt ggtggtgctt tcgagtacta cgtcagaaaa	1080
aattactaca agactgggtc tttgatggct aactcctgta aggcctccgc cgtttttaggt	1140
caacacgact tagaagtcca agaggtcgct tttgaatacg gtaagagagt cggttttggt	1200
ttccaattgg ttgacgatat tttagatttt gaaggtaata ctttcacttt gggtaagcca	1260
gctttaaacg acttgagaca aggttttagcc actgcccctg tcttgtttagc tgctgaacaa	1320
caacctggtt tagctaaatt gatctccaga aagtttagag gtcctggtga tgtcgatgaa	1380
gctttggaat tgggtccacag atccgacggt attgctagag ctaaggaggt tgctgttgtc	1440
caagccgaaa aagctatgtc tgccattttg accttgcattg actccccagc tcaaaatgct	1500
ttggttcaat tggctcacia aatcgtcaat cgtaaccatt ag	1542

<210> 141
 <211> 415
 <212> PRT
 <213> Solanum sp.

<400> 141

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

Arg	Cys	Arg	Trp	Leu	Phe	Ser	Leu	Arg	Pro	Ile	Pro	Gln	Leu	His	Gln
			20					25					30		

Ser	Asn	His	Ile	His	Asp	Pro	Pro	Lys	Val	Leu	Gly	Cys	Arg	Val	Ile
		35					40					45			

His	Ser	Trp	Val	Ser	Asn	Ala	Leu	Ser	Gly	Ile	Gly	Gln	Gln	Ile	His
						55					60				

Gln Gln Ser Thr Ala Val Ala Glu Glu Gln Val Asp Pro Phe Ser Leu
65 70 75 80

Val Ala Asp Glu Leu Ser Leu Leu Thr Asn Arg Leu Arg Ser Met Val
85 90 95

Val Ala Glu Val Pro Lys Leu Ala Ser Ala Ala Glu Tyr Phe Phe Lys
100 105 110

Leu Gly Val Glu Gly Lys Arg Phe Arg Pro Thr Val Leu Leu Leu Met
115 120 125

Ala Thr Ala Leu Asn Val Gln Ile Pro Arg Ser Ala Pro Gln Val Asp
130 135 140

Val Asp Ser Phe Ser Gly Asp Leu Arg Thr Arg Gln Gln Cys Ile Ala
145 150 155 160

Glu Ile Thr Glu Met Ile His Val Ala Ser Leu Leu His Asp Asp Val
165 170 175

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

Met Gly Asn Lys Leu Ala Val Leu Ala Gly Asp Phe Leu Leu Ser Arg
195 200 205

Ala Cys Val Ala Leu Ala Ser Leu Lys Asn Thr Glu Val Val Cys Leu
210 215 220

Leu Ala Thr Val Val Glu His Leu Val Thr Gly Glu Thr Met Gln Met
225 230 235 240

Thr Thr Ser Ser Asp Glu Arg Cys Ser Met Glu Tyr Tyr Met Gln Lys
245 250 255

Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser Asn Ser Cys Lys Ala Ile
260 265 270

Ala Leu Leu Ala Gly His Ser Ala Glu Val Ser Val Leu Ala Phe Asp
275 280 285

Tyr Gly Lys Asn Leu Gly Leu Ala Phe Gln Leu Ile Asp Asp Val Leu
290 295 300

Asp Phe Thr Gly Thr Ser Ala Thr Leu Gly Lys Gly Ser Leu Ser Asp
305 310 315 320

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

Phe Pro Gln Leu Arg Thr Leu Val Asp Arg Gly Phe Asp Asp Pro Val
340 345 350

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

Arg Thr Arg Glu Leu Ala Arg Lys His Ala Ser Leu Ala Ser Ala Ala
370 375 380

Ile Asp Ser Leu Pro Glu Ser Asp Asp Glu Glu Val Gln Arg Ser Arg
385 390 395 400

Arg Ala Leu Val Glu Leu Thr His Arg Val Ile Thr Arg Thr Lys
405 410 415

<210> 142
<211> 1248
<212> DNA
<213> Solanum sp.

<400> 142
atgatctttt ccaagggttt agtctaaatc tctcgtaata gattctctcg ttgcagatgg 60
ttattctctt tgcgtccaat tcctcaatta caccaatcca atcacatcca cgaccaccca 120
aaagttttgg gttgtcgtgt cattcactct tgggttttcta atgccttgtc tggtatcggc 180
caacaaatcc atcaacaatc tactgccgtt gccgaggaac aagtcgaccc tttttctttg 240
gttgctgatg agttatcctt gttaaccaac agattgagat ccatggttgt cgctgaagtc 300
cctaagttag cctccgccgc tgagtatttc tttaagttag gtgtcgaagg taaacgtttc 360
cgtccaactg tcttgttggt gatggccact gccttaaacg tccaaattcc tcgttctgct 420

ccacaagttg acgttgactc tttttctggt gacttgagaa ctagacaaca atgtatcgct 480
 gaaattactg aaatgattca cgtcgcctct ttgttgcattg atgacgtctt agatgatgct 540
 gatactagaa gaggtattgg ttccttaaata tttgttatgg gtaataagtt ggctgttttg 600
 gctggtgatt tcttgttatc cagagcctgc gtcgccttag cctccttgaa gaacaccgaa 660
 gttgtctgtt tattggccac cgttgtcgaa catttggtta ccggtgaaac tatgcaaagt 720
 actacctcct ccgatgaaag atgttccatg gaatactaca tgcaaaaagac ctactataag 780
 actgcctctt tgatttctaa ctcttgtaaa gccattgcct tgtagccgg tcactctgct 840
 gaagtttctg tcttggcctt cgattacggg aagaacttag gtttggcttt tcaattgatc 900
 gacgatgttt tggacttcac cgggtacctc gctactttgg gtaaaggttc cttgtccgat 960
 atcagacatg gtatcgttac tgctcctatt ttgtatgcta tggaagaatt ccctcaatta 1020
 cgtactttgg ttgacagagg tttcgatgat ccagttaatg ttgagatcgc tttggattac 1080
 ttgggtaaat cccgtggtat tcaaagaact agagaattag ccagaaagca tgcctcttta 1140
 gcctctgccg ccatcgattc cttgcctgaa tccgacgatg aggaagttca aagatctcgt 1200
 agagctttgg tcgaattgac ccatagagtc attactcgta ctaagtaa 1248

<210> 143
 <211> 330
 <212> PRT
 <213> Hevea brasiliensis

<400> 143

Met Gln Phe Leu Arg Gly Leu Ser Pro Ile Ser Arg Ser Gly Leu Arg
 1 5 10 15

Leu Phe Leu Ser Arg Gln Leu Tyr Pro Phe Pro Val Ala Asn Ser Ser
 20 25 30

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

Tyr Ser Trp Ser Leu Val Asp Ser His Gly Phe Lys Gln Gln Ile His
 50 55 60

His Gln Ser Ser Phe Leu Ser Glu Glu Pro Leu Asp Pro Phe Ser Leu
 65 70 75 80

Val Ala Asp Glu Leu Ser Leu Val Ala Asn Arg Leu Arg Ala Met Leu
85 90 95

Val Ser Glu Val Pro Lys Leu Ala Ser Ala Ala Glu Tyr Phe Phe Lys
100 105 110

Met Gly Val Glu Gly Lys Arg Leu Arg Pro Thr Val Leu Leu Leu Met
115 120 125

Ala Thr Ala Leu Asn Val His Ile His Glu Pro Met Pro Asn Gly Val
130 135 140

Gly Asp Thr Leu Gly Ala Glu Leu Arg Thr Arg Gln Gln Cys Ile Ala
145 150 155 160

Glu Ile Thr Glu Met Ile His Val Ala Ser Leu Leu His Asp Asp Val
165 170 175

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

Met Gly Asn Lys Val Ala Val Leu Ala Gly Asp Phe Leu Leu Ser Arg
195 200 205

Ala Cys Val Ala Leu Ala Ser Leu Lys Asn Thr Glu Val Val Ser Leu
210 215 220

Leu Ala Thr Val Val Glu His Leu Val Thr Gly Glu Thr Met Gln Met
225 230 235 240

Thr Ser Thr Ser Glu Gln Arg Cys Ser Met Asp His Tyr Met Gln Lys
245 250 255

Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser Asp Ser Cys Lys Ala Ile
260 265 270

Ala Leu Leu Ala Gly Gln Thr Thr Glu Val Ala Met Leu Ala Phe Glu
275 280 285

Tyr Gly Lys Ser Leu Gly Leu Ala Phe Gln Leu Ile Asp Asp Val Leu
 290 295 300

Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly Lys Gly Ser Leu Ser Asp
 305 310 315 320

Ile Arg His Val Ile Arg Leu Ser Leu Ile
 325 330

<210> 144
 <211> 993
 <212> DNA
 <213> Hevea brasiliensis

<400> 144
 atgcaatttt tgagaggttt gtcccctatt tccagatccg gtttgcgttt attcttatct 60
 cgtcaattat atccattccc agtcgccaac tcctcccaat tattaggtga ctctactcaa 120
 aaggttttta acagacgtga gacttactct tggctcttgg tcgactctca cggttttaag 180
 caacaaattc atcaccaatc ctcttttttg tctgaagaac cattggatcc attctctttg 240
 gttgctgatg aattatcctt ggtcgctaac agattgcgtg ctatgttggt ttctgaagtc 300
 ccaaaattag cctccgccgc tgaatatatt ttcaagatgg gtgttgaagg taagagattg 360
 cgtccaaccg tcttggttatt aatggccact gctttaaacg ttcatatcca tgaacctatg 420
 cctaacggtg ttggtgacac tttgggtgcc gaattgagaa ctagacaaca atgcatcgct 480
 gaaatcaccg aaatgatcca tgttgcttct ttattacatg acgacgtttt agacgatgcc 540
 gataccagaa gaggtattgg ttctttgaac ttcgttatgg gtaacaaggt tgctgttttg 600
 gccggtgact ttttgttgtc cagagcttgt gttgccttag cttctttgaa gaataccgaa 660
 gtcgtttctt tattggccac cgtcgtcgaa cacttggtta ctggtgagac tatgcaaattg 720
 acctccactt ctgagcaacg ttgttccatg gatcattata tgcaaaagac ttactataag 780
 accgcttcct taatctctga ttcctgtaaa gccatgcctt tgttagctgg tcaaactacc 840
 gaggtcgcca tgttggcctt cgaatatggg aagtctttgg gtttagcttt tcaattaatc 900
 gacgatgttt tagacttcac cgggtacttct gcttccttgg gtaagggttc tttgtccgac 960
 attagacacg ttattagatt atccttaatt taa 993

<210> 145

<211> 566
<212> PRT
<213> Artificial Sequence

<220>

<223> Mutant medium-chain fatty acid CoA ligase Ec_FADK_v1

<400> 145

Met His Pro Thr Gly Pro His Leu Gly Pro Asp Val Leu Phe Arg Glu
1 5 10 15

Ser Asn Met Lys Val Thr Leu Thr Phe Asn Glu Gln Arg Arg Ala Ala
20 25 30

Tyr Arg Gln Gln Gly Leu Trp Gly Asp Ala Ser Leu Ala Asp Tyr Trp
35 40 45

Gln Gln Thr Ala Arg Ala Met Pro Asp Lys Ile Ala Val Val Asp Asn
50 55 60

His Gly Ala Ser Tyr Thr Tyr Ser Ala Leu Asp His Ala Ala Ser Cys
65 70 75 80

Leu Ala Asn Trp Met Leu Ala Lys Gly Ile Glu Ser Gly Asp Arg Ile
85 90 95

Ala Phe Gln Leu Pro Gly Trp Cys Glu Phe Thr Val Ile Tyr Leu Ala
100 105 110

Cys Leu Lys Ile Gly Ala Val Ser Val Pro Leu Leu Pro Ser Trp Arg
115 120 125

Glu Ala Glu Leu Val Trp Val Leu Asn Lys Cys Gln Ala Lys Met Phe
130 135 140

Phe Ala Pro Thr Leu Phe Lys Gln Thr Arg Pro Val Asp Leu Ile Leu
145 150 155 160

Pro Leu Gln Asn Gln Leu Pro Gln Leu Gln Gln Ile Val Gly Val Asp
165 170 175

Lys Leu Ala Pro Ala Thr Ser Ser Leu Ser Leu Ser Gln Ile Ile Ala

180

185

190

Asp Asn Thr Ser Leu Thr Thr Ala Ile Thr Thr His Gly Asp Glu Leu
 195 200 205

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

Met Leu Thr His Asn Asn Ile Leu Ala Ser Glu Arg Ala Tyr Cys Ala
 225 230 235 240

Arg Leu Asn Leu Thr Trp Gln Asp Val Phe Met Met Pro Ala Pro Leu
 245 250 255

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

Gly Ala Arg Ser Val Leu Leu Asp Ile Phe Thr Pro Asp Ala Cys Leu
 275 280 285

Ala Leu Leu Glu Gln Gln Arg Cys Thr Cys Met Leu Gly Ala Thr Pro
 290 295 300

Phe Val Tyr Asp Leu Leu Asn Val Leu Glu Lys Gln Pro Ala Asp Leu
 305 310 315 320

Ser Ala Leu Arg Phe Phe Leu Cys Gly Gly Thr Thr Ile Pro Lys Lys
 325 330 335

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

Gly Ser Thr Glu Ser Ser Pro His Ala Val Val Asn Leu Asp Asp Pro
 355 360 365

Leu Ser Arg Phe Met His Thr Asp Gly Tyr Ala Ala Ala Gly Val Glu
 370 375 380

Ile Lys Val Val Asp Asp Ala Arg Lys Thr Leu Pro Pro Gly Cys Glu
 385 390 395 400

Gly Glu Glu Ala Ser Arg Gly Pro Asn Val Phe Met Gly Tyr Phe Asp
405 410 415

Glu Pro Glu Leu Thr Ala Arg Ala Leu Asp Glu Glu Gly Trp Tyr Tyr
420 425 430

Ser Gly Asp Leu Cys Arg Met Asp Glu Ala Gly Tyr Ile Lys Ile Thr
435 440 445

Gly Arg Lys Lys Asp Ile Ile Val Arg Gly Gly Glu Asn Ile Ser Ser
450 455 460

Arg Glu Val Glu Asp Ile Leu Leu Gln His Pro Lys Ile His Asp Ala
465 470 475 480

Cys Val Val Ala Met Ser Asp Glu Arg Leu Gly Glu Arg Ser Cys Ala
485 490 495

Tyr Val Val Leu Lys Ala Pro His His Ser Leu Ser Leu Glu Glu Val
500 505 510

Val Ala Phe Phe Ser Arg Lys Arg Val Ala Lys Tyr Lys Tyr Pro Glu
515 520 525

His Ile Val Val Ile Glu Lys Leu Pro Arg Thr Thr Ser Gly Lys Ile
530 535 540

Gln Lys Phe Leu Leu Arg Lys Asp Ile Met Arg Arg Leu Thr Gln Asp
545 550 555 560

Val Cys Glu Glu Ile Glu
565

<210> 146
<211> 1701
<212> DNA
<213> Escherichia coli

<400> 146
atgcatccaa ctggtccaca cttaggtcct gatgtcttat ttagagaatc taatatgaaa 60
gtcactttga cctttaatga acaaagacgt gccgcttaca gacaacaagg tttgtggggt 120

gacgcttctt tggctgacta ctggcaacaa actgctagag ctatgccaga caagatcgcc	180
gttgtcgata accacggtgc ttcttatacc tactctgctt tggatcatgc cgcttcttgt	240
ttggctaatt ggatgttggc taagggtatc gaatctggtg atcgtattgc ttttcaattg	300
ccaggttggt gtgaatttac cgttatctac ttggcttggt tgaagattgg tgctgtttct	360
gtccccattgt tgccatcttg gagagaagcc gaattggttt gggttttgaa caaatgccaa	420
gctaagatgt tctttgctcc aaccttggtc aagcaaacta gaccagttga cttgatttta	480
cctttacaaa atcaattacc acaattgcaa caaatcgttg gtgttgacaa gttagctcca	540
gccacctcct ctttgtcctt gtcccaaatt atcgtgata atacttcttt aaccaccgct	600
atcactactc acggtgatga gttggctgct gttttgttca cttccggtac tgagggtttg	660
ccaaagggtg ttatgttgac ccacaataac attttggctt ccgaaagagc ttattgtgct	720
cgtttgaact tgacctggca agatgttttc atgatgccag ctccattggg tcatgctact	780
ggtttcttgc acggtgttac tgccccattc ttgattggtg ctagatctgt cttgttggat	840
atctttaccc cagacgcttg cttagcttta ttggaacaac aaagatgtac ctgtatgtta	900
ggtgctactc catttgttta cgatttattg aacgttttgg aaaaacaacc agctgatttg	960
tctgccttga gattcttttt gtgtggtggt actactattc caaagaaagt tgctagagaa	1020
tgccaacaaa gaggtatcaa gttgttgtcc gtctatggtt ccactgaatc ttctcctcat	1080
gctgttgtca atttagatga cccattgtct agattcatgc acaccgatgg ttacgccgct	1140
gctggtgttg agattaaggt tgtcgacgat gctagaaaga cttacctcc aggttgtgaa	1200
ggtgaagaag cctctagagg tccaaatgtc tttatgggtt acttcgacga gccagaattg	1260
actgctagag ctttagatga ggaaggttgg tattactctg gtgatttgtg tagaatggat	1320
gaagctggtt acattaaaaat cactggtaga aagaaggaca ttattgttag aggtggtgaa	1380
aatatctcct ccagagaagt tgaagatatt ttattgcaac acccaaagat tcatgatgct	1440
tgtgttgttg ctatgtccga tgagagatta ggtgaaagat cttgtgctta cgttgttttg	1500
aaggctccac atcactcttt gtctttagaa gaagtcgttg ctttcttctc tagaaagaga	1560
gtcgccaagt acaagtaccc agaacacatt gttgttatcg aaaaattgcc tagaactact	1620
tctggtaaaa ttcaaaaatt cttgttgaga aaggatatca tgagacgttt gaccgaagat	1680
gtctgtgaag aaattgaata a	1701

<210> 147
<211> 566
<212> PRT
<213> Escherichia coli

<400> 147

Met His Pro Thr Gly Pro His Leu Gly Pro Asp Val Leu Phe Arg Glu
1 5 10 15

Ser Asn Met Lys Val Thr Leu Thr Phe Asn Glu Gln Arg Arg Ala Ala
20 25 30

Tyr Arg Gln Gln Gly Leu Trp Gly Asp Ala Ser Leu Ala Asp Tyr Trp
35 40 45

Gln Gln Thr Ala Arg Ala Met Pro Asp Lys Ile Ala Val Val Asp Asn
50 55 60

His Gly Ala Ser Tyr Thr Tyr Ser Ala Leu Asp His Ala Ala Ser Cys
65 70 75 80

Leu Ala Asn Trp Met Leu Ala Lys Gly Ile Glu Ser Gly Asp Arg Ile
85 90 95

Ala Phe Gln Leu Pro Gly Trp Cys Glu Phe Thr Val Ile Tyr Leu Ala
100 105 110

Cys Leu Lys Ile Gly Ala Val Ser Val Pro Leu Leu Pro Ser Trp Arg
115 120 125

Glu Ala Glu Leu Val Trp Val Leu Asn Lys Cys Gln Ala Lys Met Phe
130 135 140

Phe Ala Pro Thr Leu Phe Lys Gln Thr Arg Pro Val Asp Leu Ile Leu
145 150 155 160

Pro Leu Gln Asn Gln Leu Pro Gln Leu Gln Gln Ile Val Gly Val Asp
165 170 175

Lys Leu Ala Pro Ala Thr Ser Ser Leu Ser Leu Ser Gln Ile Ile Ala

180

185

190

Asp Asn Thr Ser Leu Thr Thr Ala Ile Thr Thr His Gly Asp Glu Leu
 195 200 205

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

Met Leu Thr His Asn Asn Ile Leu Ala Ser Glu Arg Ala Tyr Cys Ala
 225 230 235 240

Arg Leu Asn Leu Thr Trp Gln Asp Val Phe Met Met Pro Ala Pro Leu
 245 250 255

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

Gly Ala Arg Ser Val Leu Leu Asp Ile Phe Thr Pro Asp Ala Cys Leu
 275 280 285

Ala Leu Leu Glu Gln Gln Arg Cys Thr Cys Met Leu Gly Ala Thr Pro
 290 295 300

Phe Val Tyr Asp Leu Leu Asn Val Leu Glu Lys Gln Pro Ala Asp Leu
 305 310 315 320

Ser Ala Leu Arg Phe Phe Leu Cys Gly Gly Thr Thr Ile Pro Lys Lys
 325 330 335

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

Gly Ser Thr Glu Ser Ser Pro His Ala Val Val Asn Leu Asp Asp Pro
 355 360 365

Leu Ser Arg Phe Met His Thr Asp Gly Tyr Ala Ala Ala Gly Val Glu
 370 375 380

Ile Lys Val Val Asp Asp Ala Arg Lys Thr Leu Pro Pro Gly Cys Glu
 385 390 395 400

Gly Glu Glu Ala Ser Arg Gly Pro Asn Val Phe Met Gly Tyr Phe Asp
405 410 415

Glu Pro Glu Leu Thr Ala Arg Ala Leu Asp Glu Glu Gly Trp Tyr Tyr
420 425 430

Ser Gly Asp Leu Cys Arg Met Asp Glu Ala Gly Tyr Ile Lys Ile Thr
435 440 445

Gly Arg Lys Lys Asp Ile Ile Val Arg Gly Gly Glu Asn Ile Ser Ser
450 455 460

Arg Glu Val Glu Asp Ile Leu Leu Gln His Pro Lys Ile His Asp Ala
465 470 475 480

Cys Val Val Ala Met Ser Asp Glu Arg Leu Gly Glu Arg Ser Cys Ala
485 490 495

Tyr Val Val Leu Lys Ala Pro His His Ser Leu Ser Leu Glu Glu Val
500 505 510

Val Ala Phe Phe Ser Arg Lys Arg Val Ala Lys Tyr Lys Tyr Pro Glu
515 520 525

His Ile Val Val Ile Glu Lys Leu Pro Arg Thr Thr Ser Gly Lys Ile
530 535 540

Gln Lys Phe Leu Leu Arg Lys Asp Ile Met Arg Arg Leu Thr Gln Asp
545 550 555 560

Val Cys Glu Glu Ile Glu
565

<210> 148
<211> 1701
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial medium-chain fatty acid CoA ligase Ec_FADK_v2
nucleotide sequence

<400> 148

atgcatccaa ctggctctca cttaggtcca gatgtcttat tcagagaatc taacatgaaa	60
gtcacttttaa cttttaacga acaacgtaga gctgcttata gacaacaagg tttgtgggggt	120
gatgcttcct tggctgacta ctggcaacaa actgctagag ccatgccaga taaaattgcc	180
gttggtgaca atcacggtgc ttcttacact tattctgcct tagatcacgc tgcttcctgt	240
ttagctaact ggatgttagc taagggtatt gaatccggtg atagaattgc tttccaattg	300
ccaggttgggt gcgaatttac tgtcatttat ttagcttggt taaagattgg tgccgtctcc	360
gtccctttgt tgccatcctg gagagaggcc gagttgggtt gggttttaaa caagtgtcaa	420
gctaaaatgt tctttgctcc taccttggtc aagcaaacca gaccagttga cttaatTTTg	480
ccattacaaa accaattacc acaattgcaa caaatcgtag gtgttgataa attagctcca	540
gccacttctt ctttgcctt atcccaaatt attgctgata acacttctt aactactgct	600
attactactc acggtgatga attggccgct gttttgttca cttccggtac tgaaggtttg	660
cctaaagggtg tcatgttgac tcacaacaac attttggcct ctgaaagagc ttactgtgcc	720
cgtttaaatt tgacctggca agatgtcttc atgatgcctg ctccattggg tcacgctacc	780
ggtttcttac acggtgtcac tgccccattc ttgatcggtg ctcgttctgt tttattggat	840
atctttactc cagatgcttg cttggcttta ttggaacaac aaagatgtac ctgcatgtta	900
ggtgctactc ctttctgcta tgatttattg aacgtcttag aaaaacaacc agctgattta	960
tccgctttaa gattcttttt gtgtgggtgg actactatcc caaaaaagggt cgccagagaa	1020
tgtcaacaaa gaggtattaa attattgtcc gtttatgggt ccactgaatc ttcccctcat	1080
gctgttgca atttagacga ccctttgtcc agattcatgc acactgatgg ttacgccgct	1140
gctgggtgctg aaatcaagggt tgttgatgac gctagaaaaa ctttaccacc tggttgcgaa	1200
ggtgaagagg cttccagagg tccaaacgtc tttatgggtt actttgatga accagaattg	1260
actgccagag ctttggatga ggaagggttg tattattctg gtgatttggt tagaatggat	1320
gaagccgggt acatcaagat caccggtaga aagaaagaca tcatcgttag aggtggtgaa	1380
aacatttctt ctagagaagt tgaagacatt ttgttgcaac acccaaagat ccacgacgct	1440
tgtgtcgtcg ccatgtctga cgaaagattg ggtgaacgtt cttgtgctta cgtcgtcttg	1500
aaagccccac accactctt gtctttggaa gaagtcgttg ctttttctc tcgtaagcgt	1560
gttgccaagt acaagtaccc agagcacatc gttgttattg aaaaattgcc tcgtactact	1620

tccggtaga ttcaaaagtt cttattacgt aaggacatca tgagaagatt gactcaagac 1680
gtctgcgaag aaattgaata a 1701

<210> 149
<211> 521
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated acyl activating enzyme (Cs_AAE3_Ctrunc)

<400> 149

Met Glu Lys Ser Gly Tyr Gly Arg Asp Gly Ile Tyr Arg Ser Leu Arg
1 5 10 15

Pro Pro Leu His Leu Pro Asn Asn Asn Asn Leu Ser Met Val Ser Phe
20 25 30

Leu Phe Arg Asn Ser Ser Ser Tyr Pro Gln Lys Pro Ala Leu Ile Asp
35 40 45

Ser Glu Thr Asn Gln Ile Leu Ser Phe Ser His Phe Lys Ser Thr Val
50 55 60

Ile Lys Val Ser His Gly Phe Leu Asn Leu Gly Ile Lys Lys Asn Asp
65 70 75 80

Trp Leu Ile Tyr Ala Pro Asn Ser Ile His Phe Pro Val Cys Phe Leu
85 90 95

Gly Ile Ile Ala Ser Gly Ala Ile Ala Thr Thr Ser Asn Pro Leu Tyr
100 105 110

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

Ile Ile Thr Val Pro Gln Leu Leu Glu Lys Val Lys Gly Phe Asn Leu
130 135 140

Pro Thr Ile Leu Ile Gly Pro Asp Ser Glu Gln Glu Ser Ser Ser Asp
145 150 155 160

Lys Val Met Thr Phe Asn Asp Leu Val Asn Leu Gly Gly Ser Ser Gly
165 170 175

Ser Glu Phe Pro Ile Val Asp Asp Phe Lys Gln Ser Asp Thr Ala Ala
180 185 190

Leu Leu Tyr Ser Ser Gly Thr Thr Gly Met Ser Lys Gly Trp Leu Thr
195 200 205

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

Leu Val Gly Glu Met Asp Asn Val Phe Leu Cys Phe Leu Pro Met Phe
225 230 235 240

His Val Phe Gly Leu Ala Ile Ile Thr Tyr Ala Gln Leu Gln Arg Gly
245 250 255

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

Val Glu Lys Tyr Val Thr His Leu Trp Trp Pro Pro Val Ile Leu Ala
275 280 285

Leu Ser Lys Asn Ser Met Val Lys Phe Asn Leu Ser Ser Ile Lys Tyr
290 295 300

Ile Gly Ser Gly Ala Ala Pro Leu Gly Lys Asp Leu Met Glu Glu Cys
305 310 315 320

Ser Lys Trp Pro Tyr Gly Ile Val Ala Gln Gly Tyr Gly Met Thr Glu
325 330 335

Thr Cys Gly Ile Val Ser Met Glu Asp Ile Arg Gly Gly Lys Arg Asn
340 345 350

Ser Gly Ser Ala Gly Met Leu Ala Ser Gly Val Glu Ala Gln Ile Val
355 360 365

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

Trp Val Lys Gly Pro Asn Met Met Gln Gly Tyr Phe Asn Asn Pro Gln
385 390 395 400

Ala Thr Lys Leu Thr Ile Asp Lys Lys Gly Trp Val His Thr Gly Asp
405 410 415

Leu Gly Tyr Phe Asp Glu Asp Gly His Leu Tyr Trp Asp Arg Ile Lys
420 425 430

Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu Leu Glu
435 440 445

Gly Leu Leu Val Ser His Pro Glu Ile Leu Asp Ala Trp Ile Pro Phe
450 455 460

Pro Asp Ala Glu Ala Gly Glu Val Pro Val Ala Tyr Trp Arg Ser Pro
465 470 475 480

Asn Ser Ser Leu Thr Glu Asn Asp Val Lys Lys Phe Ile Ala Gly Gln
485 490 495

Val Ala Ser Phe Lys Arg Leu Arg Lys Val Thr Phe Ile Asn Ser Val
500 505 510

Pro Lys Ser Ala Ser Gly Lys Ile Leu
515 520

<210> 150
<211> 1563
<212> DNA
<213> Artificial Sequence

<220>
<223> Truncated acyl activating enzyme (Cs_AAE3_Ctrunc)

<400> 150
atggaaaaat ctggttatgg tagagacggt atctacagat ccttgcggtcc tccattacac 60
ttgccaaaca ataataactt atctatggtt tcctttttgt tccgtaactc ttctctttac 120
ccacaaaaac ctgctttgat tgactccgaa accaatcaaa tcttgtcctt ttcccacttc 180

aaatctactg tcattaaagt ctctcacggt ttcttgaact taggtattaa gaagaacgac	240
tggttgatct acgctcctaa ttccatccac tttccagttt gtttcttggg tatcattgct	300
tctggtgcca ttgctaccac ttctaaccct ttatacactg tttctgagtt atctaagcaa	360
gttaaagatt ctaacccaaa attgattatc actgtcccac aattattaga aaaggtcaag	420
ggtttcaatt taccaaccat tttaatcggg ccagactccg aacaagagtc ttcttccgat	480
aaagttatga cttttaacga cttagttaac ttgggtgggt cttctgggtc tgagttccca	540
atcgtcgatg atttcaagca atctgacacc gccgctttat tgtattcctc tgggtactact	600
ggtatgtcta agggttgggt gactcacaaa aactttatcg cttcctcttt gatggttacc	660
atggaacaag acttggttgg tgaaatggat aacgtcttct tgtgtttttt accaatgttc	720
catgttttcg gtttagctat cactacttac gctcaattac aaagaggtaa cactgtcatc	780
tctgctcggt ttgacttaga aaagatgttg aaagacgttg aaaagtacgt tactcacttg	840
tgggtggcctc ctgttatttt agctttgtct aagaattcta tggttaaatt caacttgtcc	900
tctatcaagt acattgggtc tggtgccgct ccattaggta aggacttgat ggaagaatgt	960
tctaaatggc cttacgggat cgtcgcctcaa gggttacggta tgactgaaac ttgtgggtatc	1020
gtttctatgg aagacatcag aggtggtaag cgtaactccg gttctgctgg tatgttggct	1080
tccggtgttg aagcccaaatt tgtttctgtc gatactttga aacctttgcc acctaaccaa	1140
ttaggtgaaa tttgggttaa aggtcctaac atgatgcaag gttacttcaa taaccctcaa	1200
gctactaagt taactattga taagaagggt tgggttcata ctggtgattt gggttacttc	1260
gatgaagatg gtcatttgta ctgggataga atcaaagaat taattaagta taaaggtttc	1320
caagttgcc cagctgaatt ggaaggtttg ttggtttctc atcctgaaat tttagatgct	1380
tggattcctt tcccagacgc tgaagccggt gaagttccag ttgcttactg gagatcccct	1440
aactcttcct tgactgaaaa cgacgtcaag aagttcatcg ctggtcaagt tgcttccttt	1500
aagagattaa gaaaagtcac cttcatcaac tccgttccaa agtctgcttc cggttaagatt	1560
ttg	1563

<210> 151
 <211> 518
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Truncated cannabidiolic acid synthase Cs_CBDAS_{t28}

<400> 151

Met Ser Asn Pro Arg Glu Asn Phe Leu Lys Cys Phe Ser Gln Tyr Ile
1 5 10 15

Pro Asn Asn Ala Thr Asn Leu Lys Leu Val Tyr Thr Gln Asn Asn Pro
20 25 30

Leu Tyr Met Ser Val Leu Asn Ser Thr Ile His Asn Leu Arg Phe Thr
35 40 45

Ser Asp Thr Thr Pro Lys Pro Leu Val Ile Val Thr Pro Ser His Val
50 55 60

Ser His Ile Gln Gly Thr Ile Leu Cys Ser Lys Lys Val Gly Leu Gln
65 70 75 80

Ile Arg Thr Arg Ser Gly Gly His Asp Ser Glu Gly Met Ser Tyr Ile
85 90 95

Ser Gln Val Pro Phe Val Ile Val Asp Leu Arg Asn Met Arg Ser Ile
100 105 110

Lys Ile Asp Val His Ser Gln Thr Ala Trp Val Glu Ala Gly Ala Thr
115 120 125

Leu Gly Glu Val Tyr Tyr Trp Val Asn Glu Lys Asn Glu Asn Leu Ser
130 135 140

Leu Ala Ala Gly Tyr Cys Pro Thr Val Cys Ala Gly Gly His Phe Gly
145 150 155 160

Gly Gly Gly Tyr Gly Pro Leu Met Arg Asn Tyr Gly Leu Ala Ala Asp
165 170 175

Asn Ile Ile Asp Ala His Leu Val Asn Val His Gly Lys Val Leu Asp
180 185 190

Arg Lys Ser Met Gly Glu Asp Leu Phe Trp Ala Leu Arg Gly Gly Gly
195 200 205

Ala Glu Ser Phe Gly Ile Ile Val Ala Trp Lys Ile Arg Leu Val Ala
210 215 220

Val Pro Lys Ser Thr Met Phe Ser Val Lys Lys Ile Met Glu Ile His
225 230 235 240

Glu Leu Val Lys Leu Val Asn Lys Trp Gln Asn Ile Ala Tyr Lys Tyr
245 250 255

Asp Lys Asp Leu Leu Leu Met Thr His Phe Ile Thr Arg Asn Ile Thr
260 265 270

Asp Asn Gln Gly Lys Asn Lys Thr Ala Ile His Thr Tyr Phe Ser Ser
275 280 285

Val Phe Leu Gly Gly Val Asp Ser Leu Val Asp Leu Met Asn Lys Ser
290 295 300

Phe Pro Glu Leu Gly Ile Lys Lys Thr Asp Cys Arg Gln Leu Ser Trp
305 310 315 320

Ile Asp Thr Ile Ile Phe Tyr Ser Gly Val Val Asn Tyr Asp Thr Asp
325 330 335

Asn Phe Asn Lys Glu Ile Leu Leu Asp Arg Ser Ala Gly Gln Asn Gly
340 345 350

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

Val Phe Val Gln Ile Leu Glu Lys Leu Tyr Glu Glu Asp Ile Gly Ala
370 375 380

Gly Met Tyr Ala Leu Tyr Pro Tyr Gly Gly Ile Met Asp Glu Ile Ser
385 390 395 400

Glu Ser Ala Ile Pro Phe Pro His Arg Ala Gly Ile Leu Tyr Glu Leu
405 410 415

Trp Tyr Ile Cys Ser Trp Glu Lys Gln Glu Asp Asn Glu Lys His Leu
420 425 430

Asn Trp Ile Arg Asn Ile Tyr Asn Phe Met Thr Pro Tyr Val Ser Lys
435 440 445

Asn Pro Arg Leu Ala Tyr Leu Asn Tyr Arg Asp Leu Asp Ile Gly Ile
450 455 460

Asn Asp Pro Lys Asn Pro Asn Asn Tyr Thr Gln Ala Arg Ile Trp Gly
465 470 475 480

Glu Lys Tyr Phe Gly Lys Asn Phe Asp Arg Leu Val Lys Val Lys Thr
485 490 495

Leu Val Asp Pro Asn Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro Pro
500 505 510

Leu Pro Arg His Arg His
515

<210> 152
<211> 1557
<212> DNA
<213> Artificial Sequence

<220>
<223> Truncated cannabidiolic acid synthase Cs_CBDAS28

<400> 152
atgtctaadc caagagagaa tttcttaaag tgtttttctc aatacatccc aaacaatgct 60
actaacttaa agttggttta cactcaaaat aaccatttgt acatgtctgt cttgaactct 120
accattcaca atttgcgttt tacttctgac accacccta agccattagt tattgttacc 180
ccatcccacg tctctcacat ccaaggtact attttgtgtt ctaaaaaggt tggtttgcaa 240
attagaacta gatctgggtg tcacgactcc gagggatatgt cttacatctc tcaagttcca 300
ttcgttattg tcgacttgcg taacatgcgt tccatcaaaa tcgatgttca ctcccaaact 360
gcttgggtcg aagccggtgc cactttaggt gaggtttatt actgggtcaa tgagaagaat 420
gagaatttgt ccttggctgc tggttattgt ccaaccgtct gtgctggtgg tcattttggt 480

```

ggtggtggtt acggtccatt aatgagaaac tatggtttgg ctgccgataa cattatcgac      540
gctcacttgg ttaatgtcca cggtaaagtc ttagatagaa aatccatggg tgaggacttg      600
ttctgggctt tgagaggtgg tgggtgctgag tcctttggta tcatcgttgc ttggaaaatt      660
cgtttagttg ctgtcccaaa atctactatg ttttctgtta agaagatcat ggaaattcac      720
gagttggtta agttggttaa taagtggcaa aatattgcct acaagtatga caaagacttg      780
ttattgatga ctcaattcat cactagaaac atcaccgata accaaggtaa aaataaaact      840
gctatccata cctacttctc ctccgttttc ttgggtggtg tcgactcctt agttgatttg      900
atgaacaaat cttttcctga attaggtatc aagaagactg attgtcgtca attgtcctgg      960
attgatacca ttatctttta ctctggtgtc gtcaattacg acaccgataa tttcaataag     1020
gaaattttat tggacagatc tgccgggtcaa aacggtgctt tcaagatcaa gttggactac     1080
gttaaaaaaac caatcccaga atccgtcttt gtccaaattt tggagaagtt atacgaggaa     1140
gacatcggtg ctggtatgta tgccttatat ccatacggtg gtattatgga tgaaatttcc     1200
gaatctgcta tcccatttcc acatcgtgct ggtattttgt atgaattatg gtacatttgt     1260
tcctgggaaa agcaagaaga taacgagaag cacttgaatt ggatcagaaa tatctacaat     1320
ttcatgactc cttacgtttc taagaatcct cgtttggtt acttgaacta cagagatttg     1380
gacatcggtg ttaatgacct aaagaacca aataactata ctcaagctag aatttgggggt     1440
gaaaagtact tcggtaaaaa ctttgacaga ttggttaagg ttaagacttt agttgatcca     1500
aataacttct tcagaaatga acaatccatc ccaccattgc ctagacacag acactaa       1557

```

```

<210> 153
<211> 519
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Truncated tetrahydrocannabinolic acid synthase Cs_THCAST28

```

```

<400> 153

```

```

Met Ser Asn Pro Arg Glu Asn Phe Leu Lys Cys Phe Ser Lys His Ile
1           5           10          15

```

```

Pro Asn Asn Val Ala Asn Pro Lys Leu Val Tyr Thr Gln His Asp Gln
          20          25          30

```

Leu Tyr Met Ser Ile Leu Asn Ser Thr Ile Gln Asn Leu Arg Phe Ile
35 40 45

Ser Asp Thr Thr Pro Lys Pro Leu Val Ile Val Thr Pro Ser Asn Asn
50 55 60

Ser His Ile Gln Ala Thr Ile Leu Cys Ser Lys Lys Val Gly Leu Gln
65 70 75 80

Ile Arg Thr Arg Ser Gly Gly His Asp Ala Glu Gly Met Ser Tyr Ile
85 90 95

Ser Gln Val Pro Phe Val Val Val Asp Leu Arg Asn Met His Ser Ile
100 105 110

Lys Ile Asp Val His Ser Gln Thr Ala Trp Val Glu Ala Gly Ala Thr
115 120 125

Leu Gly Glu Val Tyr Tyr Trp Ile Asn Glu Lys Asn Glu Asn Leu Ser
130 135 140

Phe Pro Gly Gly Tyr Cys Pro Thr Val Gly Val Gly Gly His Phe Ser
145 150 155 160

Gly Gly Gly Tyr Gly Ala Leu Met Arg Asn Tyr Gly Leu Ala Ala Asp
165 170 175

Asn Ile Ile Asp Ala His Leu Val Asn Val Asp Gly Lys Val Leu Asp
180 185 190

Arg Lys Ser Met Gly Glu Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly
195 200 205

Gly Glu Asn Phe Gly Ile Ile Ala Ala Trp Lys Ile Lys Leu Val Ala
210 215 220

Val Pro Ser Lys Ser Thr Ile Phe Ser Val Lys Lys Asn Met Glu Ile
225 230 235 240

His Gly Leu Val Lys Leu Phe Asn Lys Trp Gln Asn Ile Ala Tyr Lys
245 250 255

Tyr Asp Lys Asp Leu Val Leu Met Thr His Phe Ile Thr Lys Asn Ile
260 265 270

Thr Asp Asn His Gly Lys Asn Lys Thr Thr Val His Gly Tyr Phe Ser
275 280 285

Ser Ile Phe His Gly Gly Val Asp Ser Leu Val Asp Leu Met Asn Lys
290 295 300

Ser Phe Pro Glu Leu Gly Ile Lys Lys Thr Asp Cys Lys Glu Phe Ser
305 310 315 320

Trp Ile Asp Thr Thr Ile Phe Tyr Ser Gly Val Val Asn Phe Asn Thr
325 330 335

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

Thr Ala Phe Ser Ile Lys Leu Asp Tyr Val Lys Lys Pro Ile Pro Glu
355 360 365

Thr Ala Met Val Lys Ile Leu Glu Lys Leu Tyr Glu Glu Asp Val Gly
370 375 380

Ala Gly Met Tyr Val Leu Tyr Pro Tyr Gly Gly Ile Met Glu Glu Ile
385 390 395 400

Ser Glu Ser Ala Ile Pro Phe Pro His Arg Ala Gly Ile Met Tyr Glu
405 410 415

Leu Trp Tyr Thr Ala Ser Trp Glu Lys Gln Glu Asp Asn Glu Lys His
420 425 430

Ile Asn Trp Val Arg Ser Val Tyr Asn Phe Thr Thr Pro Tyr Val Ser
435 440 445

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

Lys Thr Asn His Ala Ser Pro Asn Asn Tyr Thr Gln Ala Arg Ile Trp
 465 470 475 480

Gly Glu Lys Tyr Phe Gly Lys Asn Phe Asn Arg Leu Val Lys Val Lys
 485 490 495

Thr Lys Val Asp Pro Asn Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro
 500 505 510

Pro Leu Pro Pro His His His
 515

<210> 154
 <211> 1560
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Truncated tetrahydrocannabinolic acid synthase Cs_THCAST28

<400> 154
 atgtctaacc ctcgtgagaa cttcttgaaa tgtttctcca aacatatccc aaacaatgtc 60
 gctaacccta agttagttaa cactcaacat gatcaattat atatgtctat cttgaactct 120
 accatccaaa acttgagatt catctccgat accaccccaa aaccattggt tattgttacc 180
 ccatccaaca atttcatat tcaagctacc attttgtgct ccaaaaagggt cggtttgcaa 240
 atccgtacta gatctgggtg tcacgatgct gaaggtatgt cttacatttc ccaagtccca 300
 ttcgttggtg tcgatttaag aaatatgcac tctatcaaaa tcgacgttca ctctcaaact 360
 gcttgggttg aagccggtgc cactttaggt gaggtttact actggattaa cgaaaagaat 420
 gaaaacttat ctttccagg tggttactgt ccaactgttg gtgttggtgg tcacttctct 480
 ggtgggtggt atgggtgcctt gatgagaaac tacggtttag ctgctgataa tattatcgac 540
 gctcacttgg ttaatgtcga cggttaagggt ttggacagaa aatccatggg tgaagattta 600
 ttctgggcca ttagaggtgg tgggtgtgaa aacttcggta tcattgctgc ttggaaaatt 660
 aaattggtcg ctgtcccatc caagtctact attttctccg tcaagaaaaa catggaaatt 720
 catggttttg ttaaattatt caacaagtgg caaaacattg cttacaaata cgacaaagac 780
 ttagttttga tgaccactt cattactaaa aacattaccg acaaccatgg taaaaataaa 840

actactgttc acggttactt ctcttccatt tttcatgggtg gtgtcgactc cttggtcgat 900
 ttaatgaaca aatctttccc tgagttgggt atcaagaaga ccgactgtaa agaattctct 960
 tggatcgaca ctactatfff ctactctgggt gtcgttaact tcaacaccgc taatttcaag 1020
 aaggaaatff tattagatag atccgctgggt aaaaagaccg ctttctctat caaattagac 1080
 tacgttaaaa aaccaatccc agaaaccgct atgggtcaaaa tcttggaana attatatgaa 1140
 gaagacgttg gtgccggtat gtacgtctta tatccatatg gtgggtattat ggaagagatc 1200
 tctgaatccg ctatccctff tccacacaga gccggtatta tgtacgaatt atgggtacact 1260
 gcttcctggg agaaacaaga agataatgaa aagcacatta actggggttag atctgtttac 1320
 aacttcacta ctccatacgt ctctcaaaac ccaagattag cctacttaaa ctaccgtgat 1380
 ttggatttag gtaaaactaa tcacgcttcc ccaacaact acaccaagc tagaatttgg 1440
 ggtgagaagt actttggtaa gaacttcaac cgtttagtca aggtcaagac taaagttgat 1500
 ccaaacaatt ttttcagaaa cgaacaatct atcccacctt taccaccaca ccaccattag 1560

<210> 155
 <211> 545
 <212> PRT
 <213> Cannabis sativa

<400> 155

Met Asn Cys Ser Ala Phe Ser Phe Trp Phe Val Cys Lys Ile Ile Phe
 1 5 10 15

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

Asn Phe Leu Lys Cys Phe Ser Lys His Ile Pro Asn Asn Val Ala Asn
 35 40 45

Pro Lys Leu Val Tyr Thr Gln His Asp Gln Leu Tyr Met Ser Ile Leu
 50 55 60

Asn Ser Thr Ile Gln Asn Leu Arg Phe Ile Ser Asp Thr Thr Pro Lys
 65 70 75 80

Pro Leu Val Ile Val Thr Pro Ser Asn Asn Ser His Ile Gln Ala Thr

85

90

95

Ile Leu Cys Ser Lys Lys Val Gly Leu Gln Ile Arg Thr Arg Ser Gly
 100 105 110

Gly His Asp Ala Glu Gly Met Ser Tyr Ile Ser Gln Val Pro Phe Val
 115 120 125

Val Val Asp Leu Arg Asn Met His Ser Ile Lys Ile Asp Val His Ser
 130 135 140

Gln Thr Ala Trp Val Glu Ala Gly Ala Thr Leu Gly Glu Val Tyr Tyr
 145 150 155 160

Trp Ile Asn Glu Lys Asn Glu Asn Leu Ser Phe Pro Gly Gly Tyr Cys
 165 170 175

Pro Thr Val Gly Val Gly Gly His Phe Ser Gly Gly Gly Tyr Gly Ala
 180 185 190

Leu Met Arg Asn Tyr Gly Leu Ala Ala Asp Asn Ile Ile Asp Ala His
 195 200 205

Leu Val Asn Val Asp Gly Lys Val Leu Asp Arg Lys Ser Met Gly Glu
 210 215 220

Asp Leu Phe Trp Ala Ile Arg Gly Gly Gly Glu Asn Phe Gly Ile
 225 230 235 240

Ile Ala Ala Trp Lys Ile Lys Leu Val Ala Val Pro Ser Lys Ser Thr
 245 250 255

Ile Phe Ser Val Lys Lys Asn Met Glu Ile His Gly Leu Val Lys Leu
 260 265 270

Phe Asn Lys Trp Gln Asn Ile Ala Tyr Lys Tyr Asp Lys Asp Leu Val
 275 280 285

Leu Met Thr His Phe Ile Thr Lys Asn Ile Thr Asp Asn His Gly Lys
 290 295 300

Asn Lys Thr Thr Val His Gly Tyr Phe Ser Ser Ile Phe His Gly Gly
305 310 315 320

Val Asp Ser Leu Val Asp Leu Met Asn Lys Ser Phe Pro Glu Leu Gly
325 330 335

Ile Lys Lys Thr Asp Cys Lys Glu Phe Ser Trp Ile Asp Thr Thr Ile
340 345 350

Phe Tyr Ser Gly Val Val Asn Phe Asn Thr Ala Asn Phe Lys Lys Glu
355 360 365

Ile Leu Leu Asp Arg Ser Ala Gly Lys Lys Thr Ala Phe Ser Ile Lys
370 375 380

Leu Asp Tyr Val Lys Lys Pro Ile Pro Glu Thr Ala Met Val Lys Ile
385 390 395 400

Leu Glu Lys Leu Tyr Glu Glu Asp Val Gly Ala Gly Met Tyr Val Leu
405 410 415

Tyr Pro Tyr Gly Gly Ile Met Glu Glu Ile Ser Glu Ser Ala Ile Pro
420 425 430

Phe Pro His Arg Ala Gly Ile Met Tyr Glu Leu Trp Tyr Thr Ala Ser
435 440 445

Trp Glu Lys Gln Glu Asp Asn Glu Lys His Ile Asn Trp Val Arg Ser
450 455 460

Val Tyr Asn Phe Thr Thr Pro Tyr Val Ser Gln Asn Pro Arg Leu Ala
465 470 475 480

Tyr Leu Asn Tyr Arg Asp Leu Asp Leu Gly Lys Thr Asn His Ala Ser
485 490 495

Pro Asn Asn Tyr Thr Gln Ala Arg Ile Trp Gly Glu Lys Tyr Phe Gly
500 505 510

Lys Asn Phe Asn Arg Leu Val Lys Val Lys Thr Lys Val Asp Pro Asn

515

520

525

Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro Pro Leu Pro Pro His His
 530 535 540

His
 545

<210> 156
 <211> 1638
 <212> DNA
 <213> Cannabis sativa

<400> 156
 atgaattggt ctgctttctc tttctgggtc gtttgtaaga tcactttttt cttcttatct 60
 ttccatattc aaatctctat cgctaaccct cgtgagaact tcttgaaatg tttctccaaa 120
 catatcccaa acaatgtcgc taaccctaag ttagtttaca ctcaacatga tcaattatat 180
 atgtctatct tgaactctac catccaaaac ttgagattca tctccgatac cccccaaaa 240
 ccattgggtta ttgttacctc atccaacaat tctcatattc aagctaccat tttgtgctcc 300
 aaaaagggtc gtttgcaaat ccgtactaga tctgggtggc acgatgctga aggtatgtct 360
 tacatttccc aagtcccatt cgttggtgtc gatttaagaa atatgcactc tatcaaaatc 420
 gacgttcact ctcaaactgc ttgggttgaa gccgggtgcca ctttaggtga gggtttactac 480
 tggattaacg aaaagaatga aaacttatcc tttccagggt gttactgtcc aactgttggt 540
 gttgggtggc acttctctgg tgggtggttat ggtgccttga tgagaaacta cggttttagct 600
 gctgataata ttatcgacgc tcacttggtt aatgtcgacg gtaagggttt ggacagaaaa 660
 tccatgggtg aagatttatt ctgggccatt agagggtgtg gtggtgaaaa cttcggtatc 720
 attgctgctt ggaaaattaa attgggtcgct gtcccatcca agtctactat tttctccgtc 780
 aagaaaaaca tggaattca tgggttggtt aaattattca acaagtggca aaacattgct 840
 taaaaatacg acaaagactt agttttgatg acccattca ttactaaaaa cattaccgac 900
 aaccatggta aaaataaaac tactgttcac gggttacttct cttccatttt tcatgggtgt 960
 gtcgactcct tgggtcgattt aatgaacaaa tctttccctg agttgggtat caagaagacc 1020
 gactgtaaag aattctcttg gatcgacact actattttct actctggtgt cgtaaacttc 1080
 aacaccgcta atttcaagaa ggaaatttta ttagatagat ccgctggtaa aaagaccgct 1140

ttctctatca aattagacta cgtaaataaa ccaatcccag aaaccgctat ggtcaaaatc	1200
ttggaaaaat tatatgaaga agacgttggt gccggtatgt acgtcttata tccatatggt	1260
ggtattatgg aagagatctc tgaatccgct atcccttttc cacacagagc cggtattatg	1320
tacgaattat ggtacactgc ttcctgggag aaacaagaag ataatgaaaa gcacattaac	1380
tgggttagat ctgtttacaa cttcactact ccatacgtct ctcaaaaccc aagattagcc	1440
tacttaaaact accgtgattt ggatttaggt aaaactaatc acgcttcccc aaacaactac	1500
acccaagcta gaatttgggg tgagaagtac tttggtaaga acttcaaccg tttagtcaag	1560
gtcaagacta aagttgatcc aaacaatttt ttcagaaacg aacaatctat cccaccttta	1620
ccaccacacc accattag	1638

<210> 157
 <211> 1197
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Erg10p: acetoacetyl CoA thiolase nucleotide sequence

<400> 157	
atgtcccaa atgtttacat tgtttctact gctagaactc ctatcggttc cttccaaggt	60
tccttatctt ccaaaactgc cgtcgaattg ggtgccgttg ctttgaaagg tgcttttagct	120
aaagttccag agttagacgc ttccaaagat ttcgatgaaa ttatcttcgg taacgtttta	180
tccgctaact tgggtcaagc tccagccaga caagttgcct tggctgccgg tttgtctaata	240
cacatcggtg cttctactgt caacaaagtt tgtgcctctg ctatgaaagc tatcatttta	300
ggtgccaat ctattaaatg tggtaatgct gacgttggtg tcgctggtgg ttgtgagtc	360
atgaccaacg ccccttacta catgccagcc gccagagccg gtgccaaatt cgggtcaaaact	420
gttttggttg acggtgttga aagagatggt ttgaacgatg cctatgacgg tttggctatg	480
ggtgttcacg ctgaaaagtg tgctagagac tgggacatta ccagagaaca acaagataat	540
ttcgctattg aatcttacca aaagtcccaa aaatctcaaa aggaaggtaa gtttgacaat	600
gaaatcggtc cagttactat caagggtttt cgtggtaagc ctgatactca agtcaccaag	660
gatgaagaac cagcccgttt acacgtcgaa aagttgagat ctgccagaac cgttttccaa	720
aaagaaaacg gtaccgttac tgctgccaat gcttctccaa tcaacgatgg tgccgctgct	780

gttattttag tctctgagaa ggttttgaag gagaaaaatt tgaagccttt agccatcatt	840
aagggttggg gtgaagctgc tcaccaacca gctgatttca cttgggcccc ttcttttagct	900
gtcccaaagg ctttaaaaca cgctgggtatt gaagatatca actctgttga ctacttcgaa	960
ttcaatgaag ctttctctgt cgtcggtttg gtcaatacca aaatcttgaa gttggatcct	1020
tctaaggtta acgtttacgg tgggtgctgtc gccttaggtc accctttagg ttgttctggt	1080
gctagagttg ttgtcacctt gttgtccatt ttacaacaag aagggtgtaa gatcggtgtt	1140
gctgctatct gtaacgggtg tgggtggtgct tcttcattg tcatcgaaaa gatctag	1197

<210> 158

<211> 1191

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial mevalonate pyrophosphate decarboxylase (Sc_ERG19)
nucleotide sequence

<400> 158

atgactgtct acactgcctc cgttactgcc cctgtcaaca ttgccacctt gaagtattgg	60
ggtaaaagag atactaaatt gaacttacca actaactcct ccatttctgt cactttgtct	120
caagatgatt tgagaacctt gacttccgct gccaccgccc ctgaatttga gagagatact	180
ttgtggttaa atgggtgaacc tcattctatt gacaacgaaa gaacccaaaa ctgtttacgt	240
gacttgagac aattgcgtaa ggaaatggaa tctaaagacg cttctttacc taccttgtct	300
caatggaaat tgcatatcgt ttctgaaaat aacttccta ctgctgccgg tttggcttcc	360
tccgctgctg gttttgctgc tttagtttct gccatcgcca aattatatca attgccacaa	420
tccacttccg aaatctctag aatcgctaga aaaggttccg gttctgcttg tagatccttg	480
ttcggtggtt acgttgcttg ggaaatgggt aaagctgaag acggtcatga ttctatggcc	540
gttcaaattg ccgactcctc cgattggcct caaatgaaag cttgtgtctt ggttgtctcc	600
gatatcaaaa aggatgtctc ttctactcaa ggtatgcaat taactgttgc cacttccgaa	660
ttgttcaaag agcgtatcga acacgttggt ccaaagagat ttgaagttat gagaaaagct	720
atcgtcgaag aggacttcgc tacctttgcc aaggagacta tgatggattc taactccttc	780
cacgctactt gtttggattc ctttccacct attttctaca tgaatgacac ctccaaacgt	840

attatctctt ggtgtcacac cattaaccaa ttttatggtg aaactatcgt cgcttacact	900
ttcgatgccg gtccaaacgc tgtcttgtac tatttggtg aaaacgaatc caagttat	960
gcttttatct ataagttgtt cggttccgtc cctggttggg acaagaaatt caccactgaa	1020
caattggaag ctttcaacca ccaattcgaa tcttccaatt tcactgctag agaattagat	1080
ttggaattac aaaaggatgt cgctagagtc atcttaactc aagttggttc cggtccacaa	1140
gaaactaacg aatctttgat tgatgctaaa actggtttgc ctaaagaata a	1191

<210> 159

<211> 867

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial isopentenyl pyrophosphate isomerase Sc_IDI1 nucleotide sequence

<400> 159

atgaccgctg acaacaactc catgccacat ggtgctgtct cctcctacgc taaattagtc	60
caaaacaaa cccctgaaga cattttagaa gagttccctg aaatcattcc attgcaacaa	120
agaccaaaca ctagatcctc cgagacttct aacgatgaat ctggtgaaac ttgtttttct	180
ggtcatgatg aagaacaaat caagttgatg aacgagaatt gtattgtttt ggactgggat	240
gacaacgcta tcggtgctgg taccaaaaag gtctgtcact tgatggaaaa catcgaaaag	300
ggtttgttgc atagagcctt ttccgtcttc atcttcaacg aacaagggtga gttattattg	360
caacaaagag ccactgaaaa aatcaccttt ccagatttat ggaccaacac ctgttgctcc	420
catccattgt gtattgatga tgaattgggt ttgaaaggta agttggacga caagattaaa	480
ggtgccatca ccgccgtgt tcgtaagtta gaccatgaat tgggtatccc tgaagacgaa	540
actaagacta gaggtaaatt ccatttcttg aatcgtattc actacatggc tccttccaat	600
gaaccatggg gtgaacacga aatcgactac attttgtttt aaaaaattaa tgctaaagaa	660
aatttaaccg ttaacccaaa cgtcaacgag gttagagatt tcaagtgggt ctctccaaac	720
gatttgaaga ctatgttcgc tgacctatcc tacaagttca ctccatgggt taagatcatc	780
tgtgaaaact atttgtttta ctgggtgggag caattggacg acttatctga agttgaaaat	840
gatcgtcaaa ttcaccgtat gttgtaa	867

<210> 160
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>

<223> Artificial phosphomevalonate kinase Sc_ERG8 nucleotide sequence

<400> 160

atgtccgagt taagagcctt ctccgctcct ggtaaagcct tattagctgg tggttactta	60
gtcttggata ctaaatatga agccttcgtc gtcggtttat ctgccagaat gcatgccgtc	120
gccccatccat acggttcctt gcaagggttct gacaagtttg aggtccgtgt caagtctaaa	180
caattcaaag atgggtgaatg gttgtatcat atttctcaa aatccggttt cattccagtt	240
tctatcgggtg gttctaagaa cccattcatc gaaaaagtca tcgctaacgt tttctcttac	300
ttcaagccta atatggatga ttattgcaat agaaatttat tcgttattga tatcttctcc	360
gatgacgcct atcattccca agaagactct gttaccgagc atagaggtaa cagaagatta	420
tctttccact ctacagaat tgaagaagtt caaaaaactg gtttaggttc ttctgctggt	480
ttagtcaccg ttttaaccac tgccttggct tctttctttg tttccgactt agaaaataac	540
gtcgacaagt atcgtgaagt catccacaac ttggcccaag ttgctcattg tcaagctcaa	600
ggtaagattg gttccggttt cgatgttgct gccgccgcct acggttccat cagatataga	660
agattccctc cagctttgat ttctaactta ccagatattg gttctgctac ttatggttcc	720
aagttggctc acttggttga cgaagaagat tggaacatta ccatcaagtc caatcacttg	780
ccatctgggt taactttgtg gatgggtgat atcaagaacg gttctgaaac tgtcaaattg	840
gtccaaaagg tcaaaaattg gtacgattcc catatgccag agtctttgaa gatctatact	900
gaattggacc acgctaactc tcgtttcatg gatggtttgt ctaagttgga cagattgcat	960
gaaactcacg acgactactc tgaccaaatt ttcgagtcct tggaaagaaa cgactgcact	1020
tgtcaaaagt atccagaaat caccgagggt agagatgccg ttgctactat tagaagatcc	1080
ttcagaaaga ttaccaagga atctggtgct gatattgagc ctccagttca aacttctttg	1140
ttggatgatt gccaaacttt aaaagggtgtt ttaacttggt taattcctgg tgctgggtgt	1200
tacgacgcca tcgccgttat caccaaaca gacgtcgact taagagcca aactgccaac	1260
gacaaaagat tctccaaggt tcaatggttg gacgtcactc aagctgattg gggtgttaga	1320
aaagaaaagg acccagagac ttacttggat aaatag	1356

<210> 161
<211> 1059
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutant farnesyl pyrophosphate synthase (Erg20mut, F96W, N127W)

<400> 161
atggccttctg agaaggagat tcgtcgtgag agattcctga atgtttttcc taaattagtc 60
gaggaattga acgcttcttt gttggcttat ggtatgccta aggaagcttg tgattggtat 120
gctcactcct tgaattataa tactccaggt ggtaaattga accgtgggtt gtctgttggt 180
gacacttacg ctattttatc taacaagacc gtcgagcaat tgggtcaaga agagtatgaa 240
aaggctcgta ttttaggttg gtgtattgaa ttgttgcaag cttactgggtt ggttgccgat 300
gacatgatgg acaagtctat tactcgtcgt ggtcaacctt gctgggtataa ggtcccagag 360
gttggtgaaa ttgctatctg ggacgctttc atgttggaag ctgctatcta taaattgttg 420
aaatcccact tcagaaacga gaaatactac attgacatca ccgagttggt ccacgaagtc 480
actttccaaa ctgagttagg tcaattaatg gacttgatca ccgctccaga agacaaagtt 540
gacttgcca agttttcctt gaaaaagcac tctttcatcg ttactttcaa gactgcttat 600
tactctttct acttaccagt tgccttggct atgtacgtcg ccggtatcac tgacgaaaag 660
gacttgaagc aagctcgtga cgttttgatt ccattaggtg aatatttcca aatccaagat 720
gactacttag actgttttgg taccctgaa caaatcggtg agatcggtac tgatattcaa 780
gataacaagt gctcttgggt tatcaacaag gcttttagagt tagcctccgc cgaacaacgt 840
aaaactttag atgaaaacta cggtaaaaaa gactctgttg ctgaggccaa gtgtaagaag 900
atttttaacg atttaaaaaat cgaacaattg tatcacgaat atgaagagtc cattgctaag 960
gatttgaagg ctaaaatttc tcaagttgac gaatcccgtg gtttcaaagc tgacgttttg 1020
actgcttttt taaacaaggt ttacaagcgt tccaaataa 1059

<210> 162
<211> 1158
<212> DNA
<213> Artificial Sequence

<220>

<223> Artificial tetraketide synthase (TKS) nucleotide sequence

<400> 162

```
atgaaccatt taagagctga ggggtccagct tccgtcttgg ctatcggtac tgctaatcca      60
gagaacattt tattacaaga tgagtttcca gattactatt tccgtgttac taagtccgag      120
catatgaccc aattgaaaga aaagttccgt aaaatctgtg ataaatctat gattagaaaa      180
agaaactgct ttttaaacga agaacacttg aagcaaaacc caagattagt tgaacacgag      240
atgcaaacct tggacgctag acaagatatg ttggttgtcg aggttcctaa attgggtaaa      300
gacgcctgtg ctaaagctat caaagagtgg ggtcaaccta agtccaagat cactcactta      360
atcttcactt ccgcttccac cactgacatg cctggtgctg attaccactg tgccaagttg      420
ttgggtttgt ctcttctgt caagagagtt atgatgtacc aattaggttg ttacgggtgg      480
ggtagtgtct taagaattgc taaggacatc gctgaaaaca acaaagggtgc tagagtttta      540
gccgtttgtt gtgacatcat ggcttgttta tttcgtggtc catctgaatc tgacttggag      600
ttgttggttg gtcaagctat ttttggtgat ggtgccgctg ccgtcatcgt tggtgctgag      660
ccagatgaat ccgttggatg aagaccaatt ttcgaattag tctctactgg tcaaactatt      720
ttgccaaact ccgagggtac tatcgggtgg catattcgtg aagccggttt aatctttgat      780
ttgcacaaag acgttccaat gttgatctct aacaacatcg aaaagtgttt aattgaggct      840
tttactccaa ttggtatctc tgactggaac tctatcttct ggatcactca tccaggtgg      900
aaggctatct tggacaaggt tgaagaaaaa ttacatttaa agtccgataa attcgtcgat      960
tctcgtcatg ttttgtctga acacggtaac atgtcttcct ccactgtctt gtttgttatg     1020
gatgaattac gtaagagatc tttggaggag ggtaagtcta ctactggtga tggtttcgaa     1080
tgggggtgtt tgttcggttt cggtcctggg ttgactgttg aacgtgttgt tgttagatct     1140
gttccaatta agtactag                                     1158
```

<210> 163

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial olivetolic acid cyclase (OAC) nucleotide sequence

<400> 163

```
atggccgtca aacacttgat cgtcttaaaa ttcaaggatg aaattactga agctcaaaaa      60
```

gaagagttct tcaaaaccta tgtcaattta gtcaacatta ttcctgctat gaaggacgtt	120
tactggggta aggatgtcac ccaaaagaac aaggaagaag gttacactca cattgttgaa	180
gtcactttcg aatctgttga aactatccaa gattatatta tccaccagc tcatgtcgg	240
tttggatgatg tttacagatc tttttgggaa aaattgttga tctttgacta tactccaaga	300
aaataa	306

<210> 164
 <211> 2163
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial acyl-activating enzyme Cs_AAE1_v1 nucleotide sequence

<400> 164	
atgggtaaga attacaagtc cttagactct gttgttgctt ctgactttat tgcttttaggt	60
attacttccg aagttgctga aaccttacac ggtagattgg ctgaaattgt ttgcaactac	120
ggtgctgcta cccctcaaac ttggattaac attgctaadc atattttgtc tccagatttg	180
ccattttctt tacaccaaatt gttgttctac gggtgttaca aggatttcgg tcctgctcct	240
ccagcttgga ttcctgatcc agaaaaagtc aaatctacta acttggtgctc tttgttgga	300
aagagaggta aggagttttt ggggtgttaag tacaaggacc caatttcttc tttctctcac	360
ttccaagaat tctctgtag aaaccctgaa gtttactgga gaactgtttt gatggatgag	420
atgaagattt ctttttctaa ggaccagag tgtatcttaa gaagagacga cattaacaat	480
ccaggtggtt ctgagtgggt accaggtggt tacttgaact ctgccaaaaa ttgcttgaac	540
gttaactcta acaagaaatt gaatgacact atgattgtct ggagagatga gggtaacgat	600
gatttgcctt tgaataaatt gactttggat caattgagaa aaagagtctg gttggttggt	660
tacgctttgg aagaaatggg tttagaaaaa gggtgtgcta tcgccatcga tatgcctatg	720
cacgttgatg ctgttggtat ttatttggct attgttttag ctggttatgt tgttgtttcc	780
atcgccgact ctttctctgc tccagaaatc tccaccagat tgagattgtc taaagccaaa	840
gccattttca cccaagacca catcattaga ggtaagaagc gtattccatt gtattctcgt	900
gttgttgaag ctaaactctc tatggctatc gtcacccat gctctggttc taacatcgg	960
gctgaattaa gagacggtga tatttcttgg gactactttt tagaaagagc taaagaattc	1020

aaaaactgcg agtttactgc tagagaacaa cctgtcgacg cttatactaa tattttattc	1080
tcttctggta ctactggtga acctaaggct attccatgga cccaagctac tcctttgaaa	1140
gccgctgctg atgggtggtc ccatttagac atcagaaaag gtgatgtcat cgtctggcca	1200
actaacttag gttggatgat ggggccatgg ttagtctacg cttctttggt gaatggtgcc	1260
tctatcgctt tatataatgg ttccccctta gtctctggtt ttgctaaatt cgttcaagat	1320
gctaagggtt ccatgttagg tgttgctcct tctatcggtt gatcttgga atctactaac	1380
tgtgtttctg gttacgactg gtccactatt cgttgtttct cttcttctgg tgaagcttcc	1440
aatgtcgatg agtacttatg gttaatgggt cgtgctaact acaagccagt catcgaaatg	1500
tgcggtggta ctgaaattgg tgggtgtttt tccgctggtt cttttttaca agcccaatcc	1560
ttgtcttcct tctcctctca atgtatgggt tgtactttat atatcttaga taagaatggt	1620
taccctatgc ctaaaaacaa gccaggtatt ggtgaattag ctttgggtcc tgttatgttt	1680
ggtgcttcta aaaccttggt aaatggtaat catcacgacg tttacttcaa aggtatgcct	1740
actttgaacg gtgaggtttt gagacgtcat ggtgatattt tcgaattaac ttccaacggt	1800
tattatcacg ctcacggtag agctgatgat actatgaaca ttggtggtat taagatctct	1860
tccatcgaag ttgagagagt ttgtaacgag gttgacgac gtgttttcga aactactgct	1920
attggtgtcc ctcttttagg tgggtggtcca gaacaattgg ttatcttttt cgtcttgaag	1980
gactccaacg acaccactat cgacttaaac caattaagat tgtctttcaa cttgggtttg	2040
caaaagaagt tgaatccatt atttaagggt actcgtgtcg ttccattgtc ctccttgcca	2100
agaactgcta ccaacaagat tatgcgtaga gtcttgagac aacaattctc tcactttgag	2160
taa	2163

<210> 165
 <211> 2163
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial acyl-activating enzyme Cs_AAE1_v2 nucleotide sequence

<400> 165	
atgggtaaga actacaaatc cttagattcc gtcgtcgctt ctgatttcat cgctttgggt	60
attacttctg aagttgctga aaccttgcac ggtagattgg ctgaaattgt ctgtaactac	120

ggtgctgcta cccacaaaac ttggatcaac attgctaacc acatcttatc ccctgacttg	180
ccattctcct tacaccaaat gttgttctac ggttggtata aagatttcgg tccagctcct	240
cctgcttgga ttcctgacct agagaagggt aagtctacta atttaggtgc tttgttagag	300
aagagaggta aggaatTTTT aggtgttaag tataaagatc caatttcttc cttctctcac	360
ttccaagaat tttctgtag aaaccagaa gtttactgga gaactgtttt gatggatgaa	420
atgaagatct ctttttccaa ggaccagag tgtattttga gacgtgatga catcaacaat	480
ccagggtggt ctgagtgggt accagggtgt tacttgaact ctgccaagaa ttgtttgaac	540
gttaactcta acaaaaagtt gaacgatacc atgattgttt ggagagacga aggtaacgat	600
gatttgccat tgaataagtt aaccttggt caattgagaa aaagagtctg gttagtcggt	660
tacgctttgg aagagatggg tttggaaaag gttgtgcta tcgccatcga tatgccaatg	720
catgttgatg ctgttggtat ctatttggcc attgttttgg ctggttacgt tgttgtttcc	780
atcgctgact ctttctctgc tccagaaatt tctactagat taagattgtc taaagccaaa	840
gccattttca ctcaagacca tattattaga ggtaagaaaa gaattccatt gtattccaga	900
gttgttgaag ctaaattccc aatggccatc gtcattccat gctctgggtc taatattggt	960
gccgaattga gagacggtga tatctcttgg gactactttt tggagcgtgc taaagaattt	1020
aaaaactgcg aattcaccgc cagagaacaa ccagttgacg cctacactaa cattttgttt	1080
tcttctggta ctactggtga acctaaggct attccatgga ctcaagctac tccattgaaa	1140
gccgccgccg atggttggtc ccacttagat attagaaagg gtgatgtcat cgtctggcct	1200
actaacttgg gttggatgat gggtccttgg ttggtttacg cttccttatt gaacggtgcc	1260
tctatcgctt tatataatgg ttccccctta gtttctggtt ttgctaaatt cgttcaagat	1320
gctaaggtta ctatgttggg tgtcgtccca tccattgtcc gttcctggaa gtctaccaat	1380
tgtgtttctg gttatgattg gtctactatt cgttgttttt cttcctctgg tgaagcttct	1440
aatgtcgatg aatatttgtg gttaatgggt agagctaact acaagccagt tattgaaatg	1500
tgtggtggta ctgaaattgg tgggtctttc tctgctggtt cttttttgca agctcaatcc	1560
ttgtcttctt tctcctccca atgtatgggt tgcactttat acatcttgga caagaatggt	1620
taccctatgc caaagaataa accagggtatt ggtgaattgg ctttggtgcc agtcatgttc	1680
ggtgcttcta agactttgtt gaacggtaac catcatgacg tctacttcaa gggatatgcct	1740

accttgaacg gtgaagtttt aagacgtcac ggtgacattt tcgaattgac ttccaacggt	1800
tattatcatg ctcacggtag agctgacgac actatgaaca tcggtggtat taagatctct	1860
tctatcgaag ttgaaagagt ttgcaacgag gttgatgac gtgtcttcga aaccactgct	1920
attggtgtcc ctcttttagg tgggtggtcct gagcaattgg ttattttctt tgtcttaaag	1980
gattctaacg acaccactat tgacttaaatt caattgagat tgtccttcaa tttgggtttg	2040
caaaagaagt tgaaccatt attcaagggt actcgtgtcg ttcctttgtc ctctttgcca	2100
agaaccgcta ccaataaaat tatgagacgt gttttgcgtc aacaattctc tcactttgaa	2160
taa	2163

<210> 166
 <211> 1602
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial acyl-activating enzyme Cs_AAE3 nucleotide sequence

<400> 166	
atggaaaaat ctggttatgg tagagacggt atctacagat ccttgcgtcc tccattacac	60
ttgcaaaca ataataactt atctatggtt tcctttttgt tccgtaactc ttctcttac	120
ccacaaaaac ctgctttgat tgactccgaa accaatcaaa tcttgtcctt ttcccacttc	180
aaatctactg tcattaaagt ctctcacggt ttcttgaact taggtattaa gaagaacgac	240
tggttgatct acgctcctaa ttccatccac tttccagttt gtttcttggg tatcattgct	300
tctggtgcca ttgctaccac ttctaaccct ttatacactg tttctgagtt atctaagcaa	360
gttaaagatt ctaaccctaa attgattatc actgtcccac aattattaga aaaggtaag	420
ggtttcaatt taccaaccat tttaatcggt ccagactccg aacaagagtc ttcttccgat	480
aaagttatga cttttaacga cttagttaac ttgggtggtt cttctggttc tgagttccca	540
atcgtcgatg atttcaagca atctgacacc gccgctttat tgtattcctc tgggtactact	600
ggtatgtcta agggttggtt gactcacaaa aactttatcg cttcctcttt gatggttacc	660
atggaacaag acttggttgg tgaaatggat aacgtcttct tgtgtttttt accaatgttc	720
catgttttcg gtttagctat cattacttac gctcaattac aaagaggtaa cactgtcatc	780
tctgctcgtt ttgacttaga aaagatgttg aaagacgttg aaaagtacgt tactcacttg	840

tggtggcctc ctgttatttt agctttgtct aagaattcta tggttaaatt caacttgtcc	900
tctatcaagt acattgggtc tggtgccgct ccattaggta aggacttgat ggaagaatgt	960
tctaaatggc cttacggtat cgtcgctcaa ggttacggta tgactgaaac ttgtgggtatc	1020
gtttctatgg aagacatcag aggtggtaag cgtaactccg gttctgctgg tatgttggct	1080
tccggtgttg aagcccaaat tgtttctgtc gatactttga aacctttgcc acctaaccaa	1140
ttaggtgaaa tttgggttaa aggtcctaac atgatgcaag gttacttcaa taaccctcaa	1200
gctactaagt taactattga taagaagggt tgggttcata ctggtgattt gggttacttc	1260
gatgaagatg gtcatttgta ctgggataga atcaaagaat taattaagta taaaggtttc	1320
caagttgccc cagctgaatt ggaaggtttg ttggttttctc atcctgaaat tttagatgct	1380
tggattcctt tcccagacgc tgaagccggt gaagttccag ttgcttactg gagatcccct	1440
aactcttcct tgactgaaaa cgacgtcaag aagttcatcg ctggtcaagt tgcttccttt	1500
aagagattaa gaaaagtcac cttcatcaac tccgttccaa agtctgcttc cggtaagatt	1560
ttgagaagag aattaatcca aaaggttcgt tccaacatgt ag	1602

<210> 167
 <211> 1635
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial cannabidiolic acid synthase (CBDAS) nucleotide sequence

<400> 167	
atgaaatgtt ccaccttttc tttctggttt gtttgtaaga tcattcttctt cttcttctcc	60
ttcaacatcc aaacttccat cgctaattcca agagagaatt tcttaaagtg tttttctcaa	120
tacatcccaa acaatgctac taacttaaag ttggttttaca ctcaaaataa cccattgtac	180
atgtctgtct tgaactctac cattcacaat ttgcgtttta cttctgacac cacccttaag	240
ccattagtta ttgttacccc atcccacgtc tctcacatcc aagggtactat tttgtgttct	300
aaaaagggtg gtttgcaaat tagaactaga tctggtggtc acgactccga gggatatgtct	360
tacatctctc aagttccatt cgttattgtc gacttgcgta acatgcgttc catcaaaatc	420
gatgttcact cccaaactgc ttgggtcgaa gccggtgcc a ctttaggtga gggtttattac	480

tgggtcaatg agaagaatga gaatttgtcc ttggctgctg gttattgtcc aaccgtctgt	540
gctgggtggc attttgggtg tgggtggttac ggtccattaa tgagaaacta tggtttggct	600
gccgataaca ttatcgacgc tcacttgggtt aatgtccacg gtaaggctctt agatagaaaa	660
tccatgggtg aggacttggt ctgggctttg agagggtggg gtgctgagtc ctttgggtatc	720
atcgttgctt ggaaaattcg tttagttgct gtcccaaat ctactatggt ttctgttaag	780
aagatcatgg aaattcacga gttgggttaag ttgggttaata agtggcaaaa tattgcctac	840
aagtatgaca aagacttggt attgatgact cacttcatca ctagaacat caccgataac	900
caaggtaaaa ataaaactgc tatccatacc tacttctcct ccgttttctt ggggtgggtgc	960
gactccttag ttgatttgat gaacaaatct tttcctgaat taggtatcaa gaagactgat	1020
tgtcgtcaat tgtcctggat tgataccatt atcttttact ctgggtgtcgt caattacgac	1080
accgataatt tcaataagga aattttattg gacagatctg ccggtcaaaa cggtgctttc	1140
aagatcaagt tggactacgt taaaaaacca atcccagaat ccgtctttgt ccaaattttg	1200
gagaagttat acgaggaaga catcggtgct ggtatgtatg cttatatcc atacgggtgg	1260
attatggatg aaatttccga atctgctatc ccatttccac atcgtgctgg tattttgtat	1320
gaattatggg acatttggtc ctgggaaaag caagaagata acgagaagca cttgaattgg	1380
atcagaaata tctacaattt catgactcct tacgtttcta agaatcctcg tttggcttac	1440
ttgaactaca gagatttgga catcggtatt aatgacccaa agaaccctaa taactatact	1500
caagctagaa tttgggggtga aaagtacttc ggtaaaaact ttgacagatt ggttaagggt	1560
aagactttag ttgatccaaa taacttcttc agaaatgaac aatccatccc accattgcct	1620
agacacagac actaa	1635

<210> 168
 <211> 2235
 <212> DNA
 <213> *Saccharomyces* sp.

<400> 168	
atggccgctc cagattatgc acttaccgat ttaattgaat cggatcctcg tttcgaaagt	60
ttgaagacaa gattagccgg ttacaccaa ggctctgatg aatatattga agagctatac	120
tctcaattac cactgaccag ctacccaggg taaaaacat ttttaaagaa acaggcggtt	180
gccatttcga atccggataa tgaagctggg tttagctcga tttataggag ttctctttct	240

tctgaaaatc tagtgagctg tgtggataaa aacttaagaa ctgcatacga tcacttcatg	300
ttttctgcaa ggagatggcc tcaacgtgac tgtttaggtt caaggccaat tgataaagcc	360
acaggcacct gggaggaaac attccgtttc gagtcgtact ccacggtatc taaaagatgt	420
cataatatcg gaagtggat attgtctttg gtaaacacga aaaggaaacg tcctttggaa	480
gccaatgatt ttgttgttgc tatcttatca cacaacaacc ctgaatggat cctaacagat	540
ttggcctgtc aggctattc tctaactaac acggctttgt acgaaacatt aggtccaaac	600
acctccgagt acatattgaa ttttaaccgag gccccattc tgatTTTTgc aaaatcaaat	660
atgtatcatg tattgaagat ggtgcctgat atgaaatttg ttaatacttt ggtttgtatg	720
gatgaattaa ctcatgacga gctccgtatg ctaaataaat cgttgctacc cgtaaagtgc	780
aactctctca atgaaaaaat cacatTTTT tcatggagc aggtagaaca agttggttgc	840
tttaacaaaa ttctgcaat tccacctacc ccagattcct tgtatactat ttcgtttact	900
tctggtacta caggtttacc taaagggtg gaaatgtctc acagaaacat tgcgtctggg	960
atagcatttg ctttttctac cttcagaata ccgccagata aaagaaacca acagttatat	1020
gatatgtgtt ttttgccatt ggctcatatt tttgaaagaa tggttattgc gtatgatcta	1080
gccatcgggt ttggaatagg cttcttacat aaaccagacc caactgtatt ggtagaggat	1140
ttgaagattt tgaaacctta cgcggttgcc ctggttccta gaatattaac acggtttgaa	1200
gccggtataa aaaatgcttt ggataaatcg actgtccaga ggaacgtagc aaatactata	1260
ttggattcta aatcggccag atttaccgca agaggtggtc cagataaatc gattatgaat	1320
tttctagttt atcatcgcgt attgattgat aaaatcagag actctttagg tttgtccaat	1380
aactcgttta taattaccgg atcagctccc atatctaaag ataccttact atttttaaga	1440
agcgccttgg atattggat aagacagggc tacggcttaa ctgaaacttt tgctggtgtc	1500
tgtttaagcg aaccgtttga aaaagatgtc ggatcttgtg gtgccatagg tatttctgca	1560
gaatgtagat tgaagtctgt tccagaaatg ggttaccatg ccgacaagga tttaaaaggt	1620
gaactgcaaa ttcgtggccc acaggttttt gaaagatatt ttaaaaatcc gaatgaaact	1680
tcaaaagccg ttgaccaaga tggttggttt tccacgggag atgttgcat tatcgatgca	1740
aaaggtcgca tcagcgtcat tgatcgagtc aagaactttt tcaagctagc acatggtgaa	1800
tatattgctc cagagaaaat cgaaaatatt tatttatcat catgccccta tatcacgcaa	1860

atatttgtct ttggagatcc tttgaagaca tttttagttg gcatcgttgg tgttgatggt 1920
 gatgcagcgc aaccgatttt agctgcaaag cacccagagg tgaaaacgtg gactaaggaa 1980
 gtgctagtag aaaacttaaa tcgtaataaa aagctaagga aggaattttt aaacaaaatt 2040
 aataaatgca tcgatgggct acaaggattt gaaaaattgc acaacatcaa agtcggactt 2100
 gagcctttga ctctcgagga tgatgtttgtg acgccaactt ttaaaataaa gcgtgccaaa 2160
 gcatcaaaat tcttcaaaga tacattagac caactatacg ccgaaggttc actagtcaag 2220
 acagaaaagc tttag 2235

<210> 169
 <211> 744
 <212> PRT
 <213> Saccharomyces sp.

<400> 169

Met Ala Ala Pro Asp Tyr Ala Leu Thr Asp Leu Ile Glu Ser Asp Pro
 1 5 10 15

Arg Phe Glu Ser Leu Lys Thr Arg Leu Ala Gly Tyr Thr Lys Gly Ser
 20 25 30

Asp Glu Tyr Ile Glu Glu Leu Tyr Ser Gln Leu Pro Leu Thr Ser Tyr
 35 40 45

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

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

Ser Glu Asn Leu Val Ser Cys Val Asp Lys Asn Leu Arg Thr Ala Tyr
 85 90 95

Asp His Phe Met Phe Ser Ala Arg Arg Trp Pro Gln Arg Asp Cys Leu
 100 105 110

Gly Ser Arg Pro Ile Asp Lys Ala Thr Gly Thr Trp Glu Glu Thr Phe
 115 120 125

Arg Phe Glu Ser Tyr Ser Thr Val Ser Lys Arg Cys His Asn Ile Gly
130 135 140

Ser Gly Ile Leu Ser Leu Val Asn Thr Lys Arg Lys Arg Pro Leu Glu
145 150 155 160

Ala Asn Asp Phe Val Val Ala Ile Leu Ser His Asn Asn Pro Glu Trp
165 170 175

Ile Leu Thr Asp Leu Ala Cys Gln Ala Tyr Ser Leu Thr Asn Thr Ala
180 185 190

Leu Tyr Glu Thr Leu Gly Pro Asn Thr Ser Glu Tyr Ile Leu Asn Leu
195 200 205

Thr Glu Ala Pro Ile Leu Ile Phe Ala Lys Ser Asn Met Tyr His Val
210 215 220

Leu Lys Met Val Pro Asp Met Lys Phe Val Asn Thr Leu Val Cys Met
225 230 235 240

Asp Glu Leu Thr His Asp Glu Leu Arg Met Leu Asn Glu Ser Leu Leu
245 250 255

Pro Val Lys Cys Asn Ser Leu Asn Glu Lys Ile Thr Phe Phe Ser Leu
260 265 270

Glu Gln Val Glu Gln Val Gly Cys Phe Asn Lys Ile Pro Ala Ile Pro
275 280 285

Pro Thr Pro Asp Ser Leu Tyr Thr Ile Ser Phe Thr Ser Gly Thr Thr
290 295 300

Gly Leu Pro Lys Gly Val Glu Met Ser His Arg Asn Ile Ala Ser Gly
305 310 315 320

Ile Ala Phe Ala Phe Ser Thr Phe Arg Ile Pro Pro Asp Lys Arg Asn
325 330 335

Gln Gln Leu Tyr Asp Met Cys Phe Leu Pro Leu Ala His Ile Phe Glu

340

345

350

Arg Met Val Ile Ala Tyr Asp Leu Ala Ile Gly Phe Gly Ile Gly Phe
 355 360 365

Leu His Lys Pro Asp Pro Thr Val Leu Val Glu Asp Leu Lys Ile Leu
 370 375 380

Lys Pro Tyr Ala Val Ala Leu Val Pro Arg Ile Leu Thr Arg Phe Glu
 385 390 395 400

Ala Gly Ile Lys Asn Ala Leu Asp Lys Ser Thr Val Gln Arg Asn Val
 405 410 415

Ala Asn Thr Ile Leu Asp Ser Lys Ser Ala Arg Phe Thr Ala Arg Gly
 420 425 430

Gly Pro Asp Lys Ser Ile Met Asn Phe Leu Val Tyr His Arg Val Leu
 435 440 445

Ile Asp Lys Ile Arg Asp Ser Leu Gly Leu Ser Asn Asn Ser Phe Ile
 450 455 460

Ile Thr Gly Ser Ala Pro Ile Ser Lys Asp Thr Leu Leu Phe Leu Arg
 465 470 475 480

Ser Ala Leu Asp Ile Gly Ile Arg Gln Gly Tyr Gly Leu Thr Glu Thr
 485 490 495

Phe Ala Gly Val Cys Leu Ser Glu Pro Phe Glu Lys Asp Val Gly Ser
 500 505 510

Cys Gly Ala Ile Gly Ile Ser Ala Glu Cys Arg Leu Lys Ser Val Pro
 515 520 525

Glu Met Gly Tyr His Ala Asp Lys Asp Leu Lys Gly Glu Leu Gln Ile
 530 535 540

Arg Gly Pro Gln Val Phe Glu Arg Tyr Phe Lys Asn Pro Asn Glu Thr
 545 550 555 560

Ser Lys Ala Val Asp Gln Asp Gly Trp Phe Ser Thr Gly Asp Val Ala
565 570 575

Phe Ile Asp Ala Lys Gly Arg Ile Ser Val Ile Asp Arg Val Lys Asn
580 585 590

Phe Phe Lys Leu Ala His Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu
595 600 605

Asn Ile Tyr Leu Ser Ser Cys Pro Tyr Ile Thr Gln Ile Phe Val Phe
610 615 620

Gly Asp Pro Leu Lys Thr Phe Leu Val Gly Ile Val Gly Val Asp Val
625 630 635 640

Asp Ala Ala Gln Pro Ile Leu Ala Ala Lys His Pro Glu Val Lys Thr
645 650 655

Trp Thr Lys Glu Val Leu Val Glu Asn Leu Asn Arg Asn Lys Lys Leu
660 665 670

Arg Lys Glu Phe Leu Asn Lys Ile Asn Lys Cys Ile Asp Gly Leu Gln
675 680 685

Gly Phe Glu Lys Leu His Asn Ile Lys Val Gly Leu Glu Pro Leu Thr
690 695 700

Leu Glu Asp Asp Val Val Thr Pro Thr Phe Lys Ile Lys Arg Ala Lys
705 710 715 720

Ala Ser Lys Phe Phe Lys Asp Thr Leu Asp Gln Leu Tyr Ala Glu Gly
725 730 735

Ser Leu Val Lys Thr Glu Lys Leu
740

<210> 170
<211> 1113
<212> DNA
<213> Artificial Sequence

<220>

<223> MBPtag

<400> 170

atgaaaatcg aagagggtaa attggtcatc tggatcaatg gtgacaaagg ttacaacggt	60
ttggctgaag tcggtaaaaa attcgagaaa gacactggta ttaaggttac cgtcgaacac	120
ccagataagt tggaagaaaa atttccacaa gttgccgcta ctggtgatgg tccagacatc	180
atcttctggg cccacgacag atttggtggt tatgctcaat ctggtttggt agccgagatc	240
acccagaca aagcctttca agataaatta taccatttta cctgggatgc tgtccgttac	300
aacggtaagt tgatcgctta cccaatcgcc gttgaagctt tgtctttaat ctacaataaa	360
gacttattgc caaaccttc aaagacctgg gaagaaattc ctgccttgga taaggaatta	420
aaggctaaag gtaaactctgc cttaatgttc aacttacaag agccttactt tacttggcca	480
ttgattgctg ctgatgggtg ttatgctttt aagtacgaaa atggtaaata cgacattaaa	540
gatgttggtg ttgacaatgc cgggtgctaaa gccggtttta ctttcttagt cgacttgatc	600
aagaacaagc acatgaatgc tgacactgat tattctatcg ctgaagccgc cttcaacaag	660
ggtgaaactg ctatgactat caatggtcct tgggcctggg ctaatattga cacctccaaa	720
gtcaactacg gtgttactgt cttaccaact ttcaaaggct aaccttccaa gccatttgct	780
ggtgttttgt ctgctggtat taacgctgcc tctccaaaca aagaattggc caaggaattt	840
ttggaaaact acttgttgac tgacgaagg ttagaggctg ttaacaaaga caaaccattg	900
ggtgctgtcg ccttgaaatc ctacgaagaa gaattagcca aggatccaag aatcgccgct	960
accatggaaa atgctcaaaa aggtgaaatt atgccaaaca ttccacaaat gtccgctttt	1020
tggtagctg ttagaactgc tgttattaat gctgcttctg gtagacaaac tgtcgatgaa	1080
gctttgaagg acgctcaaac cagaatcact aag	1113

<210> 171

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> GS12 Linker

<400> 171

ggaggaggag gaggtgggtc cggaggaggt ggttct	36
---	----

<210> 172
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> GS12 Linker

<400> 172

Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 173
<211> 174
<212> DNA
<213> Artificial Sequence

<220>
<223> GB1 tag

<400> 173

atgtctgaca cttacaagtt gatcttgaac ggtaagactt tgaaaggtga aactactacc 60
gaagctgttg atgctgccac tgctgaaaag gtttttaagc aatacgccaa tgataacggt 120
gtcgacggtg aatggactta cgatgatgcc actaagactt ttaccgttac tgaa 174

<210> 174
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> GB1 tag

<400> 174

Met Ser Asp Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys Gly
1 5 10 15

Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe
20 25 30

Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp
35 40 45

Asp Ala Thr Lys Thr Phe Thr Val Thr Glu

50

55

<210> 175
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MFalpha1_1-19

<400> 175
 atgagatttc cttcaatttt tactgcagtt ttattcgcag catcctccgc attagct 57

<210> 176
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MFalpha1_1-19

<400> 176

Met	Arg	Phe	Pro	Ser	Ile	Phe	Thr	Ala	Val	Leu	Phe	Ala	Ala	Ser	Ser
1				5					10					15	

Ala Leu Ala

<210> 177
 <211> 267
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MFalpha1_1-89

<400> 177
 atgagatttc cttcaatttt tactgcagtt ttattcgcag catcctccgc attagctgct 60
 ccagtcaaca ctacaacaga agatgaaacg gcacaaattc cggctgaagc tgtcatcggt 120
 tacttagatt tagaagggga tttcgatgtt gctgttttgc cattttccaa cagcacaaat 180
 aacgggttat tgtttataaa tactactatt gccagcattg ctgctaaaga agaaggggta 240
 tctttggata aaagagaggc tgaagct 267

<210> 178

<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> MFalpha1_1-89

<400> 178

Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1 5 10 15

Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
20 25 30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu Glu Gly Asp Phe
35 40 45

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
50 55 60

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65 70 75 80

Ser Leu Asp Lys Arg Glu Ala Glu Ala
85

<210> 179
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> DasherGFP

<400> 179

atgaccgcac taacagaagg agctaaacta ttcgaaaagg agattcctta cattacagaa 60
ttagagggtg atgtcgaagg aatgaaattc attatcaagg gcgagggtac tggtgacgct 120
actaccggta cgattaaagc aaagtacatc tgtacaacag gtgaccttcc tgttccgtgg 180
gctactctgg tgagcacttt gtcttatgga gttcaatgtt ttgctaaata cccttcgcac 240
attaaagact ttttcaaaag tgcaatgcct gagggctata ctcaggagag aacaatatct 300
ttcgaaggag atgggtgtgta taagactagg gctatggtca cgtatgaaag aggatccatc 360

tacaatagag taactttaac tggatgaaaac ttcaaaaagg acggtcacat ccttagaaag	420
aatgttgcct ttcaatgccc accatccatc ttgtacattt tgccagacac agttaacaat	480
ggtatcagag ttgagtttaa ccaagcttat gacatagagg gtgtcaccga aaagttggtt	540
acaaaatgtt cacagatgaa tcgtcccctg gcaggatcag ctgccgtcca tatcccacgt	600
taccatcata tcacttatca taccaagctg tccaaagatc gtgatgagag aagggatcac	660
atgtgtttgg ttgaagtggg aaaggccgtg gatttggata cttaccaagg ttga	714

<210> 180
 <211> 237
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DasherGFP

<400> 180

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

Tyr	Ile	Thr	Glu	Leu	Glu	Gly	Asp	Val	Glu	Gly	Met	Lys	Phe	Ile	Ile
			20					25					30		

Lys	Gly	Glu	Gly	Thr	Gly	Asp	Ala	Thr	Thr	Gly	Thr	Ile	Lys	Ala	Lys
		35					40					45			

Tyr	Ile	Cys	Thr	Thr	Gly	Asp	Leu	Pro	Val	Pro	Trp	Ala	Thr	Leu	Val
	50					55					60				

Ser	Thr	Leu	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ala	Lys	Tyr	Pro	Ser	His
65					70					75					80

Ile	Lys	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Thr	Gln	Glu
			85						90					95	

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

Val	Thr	Tyr	Glu	Arg	Gly	Ser	Ile	Tyr	Asn	Arg	Val	Thr	Leu	Thr	Gly
		115					120					125			

Glu Asn Phe Lys Lys Asp Gly His Ile Leu Arg Lys Asn Val Ala Phe
130 135 140

Gln Cys Pro Pro Ser Ile Leu Tyr Ile Leu Pro Asp Thr Val Asn Asn
145 150 155 160

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

Glu Lys Leu Val Thr Lys Cys Ser Gln Met Asn Arg Pro Leu Ala Gly
180 185 190

Ser Ala Ala Val His Ile Pro Arg Tyr His His Ile Thr Tyr His Thr
195 200 205

Lys Leu Ser Lys Asp Arg Asp Glu Arg Arg Asp His Met Cys Leu Val
210 215 220

Glu Val Val Lys Ala Val Asp Leu Asp Thr Tyr Gln Gly
225 230 235

<210> 181
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> ER1 tag

<400> 181
atattagagc aacctctgaa atttgtgctt actgcggccg tcgtgctctt gacgacgtcg 60
gttctttgtt gtgtagtatt tacataa 87

<210> 182
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> ER1 tag

<400> 182
Ile Leu Glu Gln Pro Leu Lys Phe Val Leu Thr Ala Ala Val Val Leu

1 5 10 15

Leu Thr Thr Ser Val Leu Cys Cys Val Val Phe Thr
20 25

<210> 183
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> ER2 tag

<400> 183
tctacctctg aaaaccaaag taaaggtagt ggtacattgg ttgtcatatt ggccatttta 60
atgctaggtg ttgcttatta tttgttgaac gaataa 96

<210> 184
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> ER2 tag

<400> 184

Ser Thr Ser Glu Asn Gln Ser Lys Gly Ser Gly Thr Leu Val Val Ile
1 5 10 15

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

<210> 185
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> PM1 tag

<400> 185
tggtacaagg atctaaaaat gaagatgtgt ctggcttttag taatcatcat attgcttggt 60
gtaatcatcg tccccattgc tgttcacttt agtcgataa 99

<210> 186

<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> PM1 tag

<400> 186

Trp Tyr Lys Asp Leu Lys Met Lys Met Cys Leu Ala Leu Val Ile Ile
1 5 10 15

Ile Leu Leu Val Val Ile Ile Val Pro Ile Ala Val His Phe Ser Arg
20 25 30

<210> 187
<211> 108
<212> DNA
<213> Artificial Sequence

<220>
<223> VC1 tag

<400> 187
aatataaaag aaataatgtg gtggcagaag gtcaaaaata ttacgttatt aactttcact 60
attatactat ttgtaagtc tgctttcatg tttttctatc tgtggtaa 108

<210> 188
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> VC1 tag

<400> 188

Asn Ile Lys Glu Ile Met Trp Trp Gln Lys Val Lys Asn Ile Thr Leu
1 5 10 15

Leu Thr Phe Thr Ile Ile Leu Phe Val Ser Ala Ala Phe Met Phe Phe
20 25 30

Tyr Leu Trp
35

<210> 189

<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> PEX8 tag

<400> 189
tctaaattat aa

12

<210> 190
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> PEX8 tag

<400> 190

Ser Lys Leu
1

<210> 191
<211> 2103
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 191
atggttgctc aatataccgt tccagttggg aaagccgcc aatgagcatga aactgctcca 60
agaagaaatt atcaatgccg cgagaagccg ctcgtcagac cgcctaacac aaagtgttcc 120
actgtttatg agtttgttct agagtgcctt cagaagaaca aaaattcaaa tgctatgggt 180
tggagggatg ttaaggaaat tcatgaagaa tccaaatcgg ttatgaaaaa agttgatggc 240
aaggagactt cagtggaaaa gaaatggatg tattatgaac tatcgcatta tcattataat 300
tcatttgacc aattgaccga tatcatgcat gaaattgggtc gtgggttggt gaaaatagga 360
ttaaagccta atgatgatga caaattacat ctttacgcag ccactttctca caagtggatg 420
aagatgttct taggagcgca gtctcaaggt attcctgtcg tcaactgccta cgatactttg 480
ggagagaaaag ggctaattca ttctttggtg caaacggggt ctaaggccat ttttaccgat 540
aactctttat taccatcctt gatcaaacca gtgcaagccg ctcaagacgt aaaatacata 600
attcatttcg attccatcag ttctgaggac aggaggcaaa gtggtaagat ctatcaatct 660
gctcatgatg ccatcaacag aattaaagaa gttagacctg atatcaagac ctttagcttt 720

gacgacatct tgaagctagg taaagaatcc tgtaacgaaa tcgatgttca tccacctggc	780
aaggatgatac tttgttgcat catgtatacg tctggttcta caggtgagcc aaagggtgtt	840
gtcttgaaac attcaaagt tgtcgcaggt gttgggtgtg caagtttgaa tgttttgaag	900
tttgtgggca ataccgaccg tgttatctgt tttttgccac tagctcatat ttttgaattg	960
gttttcgaac tattgtcctt ttattggggg gcctgcattg gttatgccac cgtaaaaact	1020
ttaactagca gctctgtgag aaattgtcaa ggtgatttgc aagaattcaa gccacaatc	1080
atggttgggtg tcgccgctgt ttgggaaaca gtgagaaaag ggatcttaaa ccaaattgat	1140
aatttgcct tcctcacaa gaaaatcttc tggaccgctg ataatacaca gttgaacatg	1200
caacgtctcc acatccctgg tggcggcgcc ttaggaaact tggttttcaa aaaaatcaga	1260
actgccacag gtggccaatt aagatatttg ttaaaccgtg gttctccaat cagtcgggat	1320
gctcaggaat tcatcacaaa tttaatctgc cctatgctta ttggttacgg ttttaaccgag	1380
acatgcgcta gtaccacat cttggatcct gctaattttg aactcggcgt cgctggtgac	1440
ctaacagggt gtgttaccgt caaactagtt gatgttgaag aattaggtta ttttgctaaa	1500
aacaaccaag gtgaagtttg gatcacaggt gccaatgtca cgcctgaata ttataagaat	1560
gaggaagaaa cttctcaagc ttttaacaagc gatggttgggt tcaagaccgg tgacatcggg	1620
gaatgggaag caaatggcca tttgaaaata attgacagga agaaaaactt ggtcaaaaca	1680
atgaacgggt aatatatcgc actcgagaaa ttagagtccg tttacagatc taacgaatat	1740
gttgctaaca tttgtgttta tgccgaccaa tctaagacta agccagttgg tattattgta	1800
ccaaatcatg ctccattaac gaagcttgct aaaaagttgg gaattatgga acaaaaagac	1860
agttcaatta atatcgaata ttatttggag gatgcaaaat tgattaaagc tgttttattct	1920
gatcttttga agacaggtaa agaccaaggt ttggttggca ttgaattact agcaggcata	1980
gtgttctttg acggcgaatg gactccacaa aacggttttg ttacgtccgc tcagaaattg	2040
aaaagaaaag acattttgaa tgctgtcaaa gataaagttg acgccgttta tagttcgtct	2100
taa	2103

<210> 192
 <211> 700
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 192

Met Val Ala Gln Tyr Thr Val Pro Val Gly Lys Ala Ala Asn Glu His
1 5 10 15

Glu Thr Ala Pro Arg Arg Asn Tyr Gln Cys Arg Glu Lys Pro Leu Val
20 25 30

Arg Pro Pro Asn Thr Lys Cys Ser Thr Val Tyr Glu Phe Val Leu Glu
35 40 45

Cys Phe Gln Lys Asn Lys Asn Ser Asn Ala Met Gly Trp Arg Asp Val
50 55 60

Lys Glu Ile His Glu Glu Ser Lys Ser Val Met Lys Lys Val Asp Gly
65 70 75 80

Lys Glu Thr Ser Val Glu Lys Lys Trp Met Tyr Tyr Glu Leu Ser His
85 90 95

Tyr His Tyr Asn Ser Phe Asp Gln Leu Thr Asp Ile Met His Glu Ile
100 105 110

Gly Arg Gly Leu Val Lys Ile Gly Leu Lys Pro Asn Asp Asp Asp Lys
115 120 125

Leu His Leu Tyr Ala Ala Thr Ser His Lys Trp Met Lys Met Phe Leu
130 135 140

Gly Ala Gln Ser Gln Gly Ile Pro Val Val Thr Ala Tyr Asp Thr Leu
145 150 155 160

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

Ile Phe Thr Asp Asn Ser Leu Leu Pro Ser Leu Ile Lys Pro Val Gln
180 185 190

Ala Ala Gln Asp Val Lys Tyr Ile Ile His Phe Asp Ser Ile Ser Ser
195 200 205

Glu Asp Arg Arg Gln Ser Gly Lys Ile Tyr Gln Ser Ala His Asp Ala
210 215 220

Ile Asn Arg Ile Lys Glu Val Arg Pro Asp Ile Lys Thr Phe Ser Phe
225 230 235 240

Asp Asp Ile Leu Lys Leu Gly Lys Glu Ser Cys Asn Glu Ile Asp Val
245 250 255

His Pro Pro Gly Lys Asp Asp Leu Cys Cys Ile Met Tyr Thr Ser Gly
260 265 270

Ser Thr Gly Glu Pro Lys Gly Val Val Leu Lys His Ser Asn Val Val
275 280 285

Ala Gly Val Gly Gly Ala Ser Leu Asn Val Leu Lys Phe Val Gly Asn
290 295 300

Thr Asp Arg Val Ile Cys Phe Leu Pro Leu Ala His Ile Phe Glu Leu
305 310 315 320

Val Phe Glu Leu Leu Ser Phe Tyr Trp Gly Ala Cys Ile Gly Tyr Ala
325 330 335

Thr Val Lys Thr Leu Thr Ser Ser Ser Val Arg Asn Cys Gln Gly Asp
340 345 350

Leu Gln Glu Phe Lys Pro Thr Ile Met Val Gly Val Ala Ala Val Trp
355 360 365

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

Leu Thr Lys Lys Ile Phe Trp Thr Ala Tyr Asn Thr Lys Leu Asn Met
385 390 395 400

Gln Arg Leu His Ile Pro Gly Gly Gly Ala Leu Gly Asn Leu Val Phe
405 410 415

Lys Lys Ile Arg Thr Ala Thr Gly Gly Gln Leu Arg Tyr Leu Leu Asn

420

425

430

Gly Gly Ser Pro Ile Ser Arg Asp Ala Gln Glu Phe Ile Thr Asn Leu
 435 440 445

Ile Cys Pro Met Leu Ile Gly Tyr Gly Leu Thr Glu Thr Cys Ala Ser
 450 455 460

Thr Thr Ile Leu Asp Pro Ala Asn Phe Glu Leu Gly Val Ala Gly Asp
 465 470 475 480

Leu Thr Gly Cys Val Thr Val Lys Leu Val Asp Val Glu Glu Leu Gly
 485 490 495

Tyr Phe Ala Lys Asn Asn Gln Gly Glu Val Trp Ile Thr Gly Ala Asn
 500 505 510

Val Thr Pro Glu Tyr Tyr Lys Asn Glu Glu Glu Thr Ser Gln Ala Leu
 515 520 525

Thr Ser Asp Gly Trp Phe Lys Thr Gly Asp Ile Gly Glu Trp Glu Ala
 530 535 540

Asn Gly His Leu Lys Ile Ile Asp Arg Lys Lys Asn Leu Val Lys Thr
 545 550 555 560

Met Asn Gly Glu Tyr Ile Ala Leu Glu Lys Leu Glu Ser Val Tyr Arg
 565 570 575

Ser Asn Glu Tyr Val Ala Asn Ile Cys Val Tyr Ala Asp Gln Ser Lys
 580 585 590

Thr Lys Pro Val Gly Ile Ile Val Pro Asn His Ala Pro Leu Thr Lys
 595 600 605

Leu Ala Lys Lys Leu Gly Ile Met Glu Gln Lys Asp Ser Ser Ile Asn
 610 615 620

Ile Glu Asn Tyr Leu Glu Asp Ala Lys Leu Ile Lys Ala Val Tyr Ser
 625 630 635 640

Asp Leu Leu Lys Thr Gly Lys Asp Gln Gly Leu Val Gly Ile Glu Leu
645 650 655

Leu Ala Gly Ile Val Phe Phe Asp Gly Glu Trp Thr Pro Gln Asn Gly
660 665 670

Phe Val Thr Ser Ala Gln Lys Leu Lys Arg Lys Asp Ile Leu Asn Ala
675 680 685

Val Lys Asp Lys Val Asp Ala Val Tyr Ser Ser Ser
690 695 700

<210> 193
<211> 2226
<212> DNA
<213> Artificial Sequence

<220>
<223> Truncated medium chain fatty acyl-CoA synthetase Sc_FAA2_Ctrunc

<400> 193
atggcgcgtc cagattatgc acttaccgat ttaattgaat cggatcctcg tttcgaaagt 60
ttgaagacaa gattagccgg ttacaccaa ggctctgatg aatatattga agagctatac 120
tctcaattac cactgaccag ctaccccagg tacaaaacat ttttaaagaa acaggcggtt 180
gccatttcga atccggataa tgaagctggg tttagctcga tttataggag ttctctttct 240
tctgaaaatc tagtgagctg tgtggataaa aacttaagaa ctgcatacga tcacttcatg 300
ttttctgcaa ggagatggcc tcaacgtgac tgtttaggtt caaggccaat tgataaagcc 360
acaggcacct gggaggaaac attccgtttc gagtcgtact ccacggtatc taaaagatgt 420
cataatatcg gaagtgggat attgtctttg gtaaacacga aaaggaaacg tcctttggaa 480
gccaatgatt ttgttgttgc tatcttatca cacaacaacc ctgaatggat cctaacagat 540
ttggcctgtc aggctattc tctaactaac acggctttgt acgaaacatt aggtccaaac 600
acctccgagt acatattgaa ttttaaccgag gccccattc tgatttttgc aaaatcaaat 660
atgtatcatg tattgaagat ggtgcctgat atgaaatttg ttaatacttt ggtttgtatg 720
gatgaattaa ctcatgacga gctccgatg ctaaatgaat cgttgctacc cgttaagtgc 780
aactctctca atgaaaaaat cacatttttt tcattggagc aggtagaaca agttggttgc 840

tttaacaaaa	ttcctgcaat	tccacctacc	ccagattcct	tgtatactat	ttcgtttact	900
tctggtacta	caggtttacc	taaaggtgtg	gaaatgtctc	acagaaacat	tgcgctctggg	960
atagcatttg	ctttttctac	cttcagaata	ccgccagata	aaagaaacca	acagttatat	1020
gatatgtgtt	ttttgccatt	ggctcatatt	tttgaaagaa	tggttattgc	gtatgatcta	1080
gccatcgggt	ttggaatagg	cttcttacat	aaaccagacc	caactgtatt	ggtagaggat	1140
ttgaagattt	tgaaacctta	cgcggttgcc	ctggttccta	gaatattaac	acggtttgaa	1200
gccggtataa	aaaatgcttt	ggataaatcg	actgtccaga	ggaacgtagc	aaatactata	1260
ttggattcta	aatcggccag	atttaccgca	agaggtggtc	cagataaatc	gattatgaat	1320
tttctagttt	atcatcgcg	attgattgat	aaaatcagag	actctttagg	tttgtccaat	1380
aactcgttta	taattaccgg	atcagctccc	atatctaaag	ataccttact	atttttaaga	1440
agcgccttgg	atattgggat	aagacagggc	tacggcttaa	ctgaaacttt	tgctggtgtc	1500
tgtttaagcg	aaccgtttga	aaaagatgtc	ggatcttgtg	gtgccatagg	tatttctgca	1560
gaatgtagat	tgaagtctgt	tccagaaatg	ggttaccatg	ccgacaagga	tttaaaaggt	1620
gaactgcaaa	ttcgtggccc	acaggttttt	gaaagatatt	ttaaaaatcc	gaatgaaact	1680
tcaaaagccg	ttgaccaaga	tggttggttt	tccacgggag	atgttgcat	tatcgatgca	1740
aaaggtcgca	tcagcgtcat	tgatcgagtc	aagaactttt	tcaagctagc	acatggtgaa	1800
tatattgctc	cagagaaaat	cgaaaatatt	tatttatcat	catgccccta	tatcacgcaa	1860
atatttgtct	ttggagatcc	tttgaagaca	tttttagttg	gcatcgttgg	tgttgatgtt	1920
gatgcagcgc	aaccgatttt	agctgcaaag	caccagagg	tgaaaacgtg	gactaaggaa	1980
gtgctagtag	aaaacttaaa	tcgtaataaa	aagctaagga	aggaattttt	aaacaaaatt	2040
aataaatgca	tcgatgggct	acaaggattt	gaaaaattgc	acaacatcaa	agtcggactt	2100
gagcctttga	ctctcgagga	tgatgttgtg	acgccaaactt	ttaaaataaa	gcgtgccaaa	2160
gcatcaaaaat	tcttcaaaga	tacattagac	caactatacg	ccgaaggttc	actagtcaag	2220
acatag						2226

<210> 194
 <211> 741
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Truncated medium chain fatty acyl-CoA synthetase Sc_FAA2_Ctrunc

<400> 194

Met Ala Ala Pro Asp Tyr Ala Leu Thr Asp Leu Ile Glu Ser Asp Pro
1 5 10 15

Arg Phe Glu Ser Leu Lys Thr Arg Leu Ala Gly Tyr Thr Lys Gly Ser
20 25 30

Asp Glu Tyr Ile Glu Glu Leu Tyr Ser Gln Leu Pro Leu Thr Ser Tyr
35 40 45

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

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

Ser Glu Asn Leu Val Ser Cys Val Asp Lys Asn Leu Arg Thr Ala Tyr
85 90 95

Asp His Phe Met Phe Ser Ala Arg Arg Trp Pro Gln Arg Asp Cys Leu
100 105 110

Gly Ser Arg Pro Ile Asp Lys Ala Thr Gly Thr Trp Glu Glu Thr Phe
115 120 125

Arg Phe Glu Ser Tyr Ser Thr Val Ser Lys Arg Cys His Asn Ile Gly
130 135 140

Ser Gly Ile Leu Ser Leu Val Asn Thr Lys Arg Lys Arg Pro Leu Glu
145 150 155 160

Ala Asn Asp Phe Val Val Ala Ile Leu Ser His Asn Asn Pro Glu Trp
165 170 175

Ile Leu Thr Asp Leu Ala Cys Gln Ala Tyr Ser Leu Thr Asn Thr Ala
180 185 190

Leu Tyr Glu Thr Leu Gly Pro Asn Thr Ser Glu Tyr Ile Leu Asn Leu

195

200

205

Thr Glu Ala Pro Ile Leu Ile Phe Ala Lys Ser Asn Met Tyr His Val
 210 215 220

Leu Lys Met Val Pro Asp Met Lys Phe Val Asn Thr Leu Val Cys Met
 225 230 235 240

Asp Glu Leu Thr His Asp Glu Leu Arg Met Leu Asn Glu Ser Leu Leu
 245 250 255

Pro Val Lys Cys Asn Ser Leu Asn Glu Lys Ile Thr Phe Phe Ser Leu
 260 265 270

Glu Gln Val Glu Gln Val Gly Cys Phe Asn Lys Ile Pro Ala Ile Pro
 275 280 285

Pro Thr Pro Asp Ser Leu Tyr Thr Ile Ser Phe Thr Ser Gly Thr Thr
 290 295 300

Gly Leu Pro Lys Gly Val Glu Met Ser His Arg Asn Ile Ala Ser Gly
 305 310 315 320

Ile Ala Phe Ala Phe Ser Thr Phe Arg Ile Pro Pro Asp Lys Arg Asn
 325 330 335

Gln Gln Leu Tyr Asp Met Cys Phe Leu Pro Leu Ala His Ile Phe Glu
 340 345 350

Arg Met Val Ile Ala Tyr Asp Leu Ala Ile Gly Phe Gly Ile Gly Phe
 355 360 365

Leu His Lys Pro Asp Pro Thr Val Leu Val Glu Asp Leu Lys Ile Leu
 370 375 380

Lys Pro Tyr Ala Val Ala Leu Val Pro Arg Ile Leu Thr Arg Phe Glu
 385 390 395 400

Ala Gly Ile Lys Asn Ala Leu Asp Lys Ser Thr Val Gln Arg Asn Val
 405 410 415

Ala Asn Thr Ile Leu Asp Ser Lys Ser Ala Arg Phe Thr Ala Arg Gly
420 425 430

Gly Pro Asp Lys Ser Ile Met Asn Phe Leu Val Tyr His Arg Val Leu
435 440 445

Ile Asp Lys Ile Arg Asp Ser Leu Gly Leu Ser Asn Asn Ser Phe Ile
450 455 460

Ile Thr Gly Ser Ala Pro Ile Ser Lys Asp Thr Leu Leu Phe Leu Arg
465 470 475 480

Ser Ala Leu Asp Ile Gly Ile Arg Gln Gly Tyr Gly Leu Thr Glu Thr
485 490 495

Phe Ala Gly Val Cys Leu Ser Glu Pro Phe Glu Lys Asp Val Gly Ser
500 505 510

Cys Gly Ala Ile Gly Ile Ser Ala Glu Cys Arg Leu Lys Ser Val Pro
515 520 525

Glu Met Gly Tyr His Ala Asp Lys Asp Leu Lys Gly Glu Leu Gln Ile
530 535 540

Arg Gly Pro Gln Val Phe Glu Arg Tyr Phe Lys Asn Pro Asn Glu Thr
545 550 555 560

Ser Lys Ala Val Asp Gln Asp Gly Trp Phe Ser Thr Gly Asp Val Ala
565 570 575

Phe Ile Asp Ala Lys Gly Arg Ile Ser Val Ile Asp Arg Val Lys Asn
580 585 590

Phe Phe Lys Leu Ala His Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu
595 600 605

Asn Ile Tyr Leu Ser Ser Cys Pro Tyr Ile Thr Gln Ile Phe Val Phe
610 615 620

Gly Asp Pro Leu Lys Thr Phe Leu Val Gly Ile Val Gly Val Asp Val

625		630		635		640									
Asp	Ala	Ala	Gln	Pro	Ile	Leu	Ala	Ala	Lys	His	Pro	Glu	Val	Lys	Thr
			645						650					655	
Trp	Thr	Lys	Glu	Val	Leu	Val	Glu	Asn	Leu	Asn	Arg	Asn	Lys	Lys	Leu
			660					665					670		
Arg	Lys	Glu	Phe	Leu	Asn	Lys	Ile	Asn	Lys	Cys	Ile	Asp	Gly	Leu	Gln
		675					680					685			
Gly	Phe	Glu	Lys	Leu	His	Asn	Ile	Lys	Val	Gly	Leu	Glu	Pro	Leu	Thr
	690					695					700				
Leu	Glu	Asp	Asp	Val	Val	Thr	Pro	Thr	Phe	Lys	Ile	Lys	Arg	Ala	Lys
705					710					715					720
Ala	Ser	Lys	Phe	Phe	Lys	Asp	Thr	Leu	Asp	Gln	Leu	Tyr	Ala	Glu	Gly
			725						730					735	
Ser	Leu	Val	Lys	Thr											
			740												

<210> 195
 <211> 2238
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mutated medium chain fatty acyl-CoA synthetase Sc_FAA2_Cmut

<400> 195	
atggccgctc cagattatgc acttaccgat ttaattgaat cggatcctcg tttcgaaagt	60
ttgaagacaa gattagccgg ttacaccaa ggctctgatg aatatattga agagctatac	120
tctcaattac cactgaccag ctaccccagg tacaaaacat ttttaaagaa acaggcggtt	180
gccatttcga atccggataa tgaagctggg tttagctcga tttataggag ttctctttct	240
tctgaaaatc tagtgagctg tgtggataaa aacttaagaa ctgcatacga tcacttcatg	300
ttttctgcaa ggagatggcc tcaacgtgac tgtttaggtt caaggccaat tgataaagcc	360
acaggcacct gggaggaaac attccgtttc gagtcgtact ccacggtatc taaaagatgt	420

cataatatcg gaagtggat attgtctttg gtaaacacga aaaggaaacg tcctttggaa	480
gccaatgatt ttgttgttgc tatcttatca cacaacaacc ctgaatggat cctaacagat	540
ttggcctgtc aggctattc tctaactaac acggctttgt acgaaacatt aggtccaaac	600
acctccgagt acatattgaa ttttaaccgag gccccattc tgatttttgc aaaatcaaat	660
atgtatcatg tattgaagat ggtgcctgat atgaaatttg ttaatacttt ggtttgtatg	720
gatgaattaa ctcatgacga gctccgatg ctaaataaat cgttgctacc cgttaagtgc	780
aactctctca atgaaaaaat cacatTTTTT tcattggagc aggtagaaca agttggttgc	840
tttaacaaaa ttcttgcaat tccacctacc ccagattcct tgtatactat ttcgtttact	900
tctggtacta caggtttacc taaagggtg gaaatgtctc acagaaacat tgcgtctggg	960
atagcatttg ctttttctac cttcagaata ccgccagata aaagaaacca acagttatat	1020
gatatgtgtt ttttgccatt ggctcatatt tttgaaagaa tggttattgc gtatgatcta	1080
gccatcgggt ttggaatagg cttcttacat aaaccagacc caactgtatt ggtagaggat	1140
ttgaagattt tgaaacctta cgcggttgcc ctggttccta gaatattaac acggtttgaa	1200
gccggtataa aaaatgcttt ggataaatcg actgtccaga ggaacgtagc aaatactata	1260
ttggattcta aatcggccag atttaccgca agagggtggtc cagataaatc gattatgaat	1320
tttctagttt atcatcgcgt attgattgat aaaatcagag actctttagg tttgtccaat	1380
aactcgttta taattaccgg atcagctccc atatctaaag ataccttact atttttaaga	1440
agcgccttgg atattggat aagacagggc tacggcttaa ctgaaacttt tgctggtgtc	1500
tgtttaagcg aaccgtttga aaaagatgtc ggatcttgtg gtgccatagg tatttctgca	1560
gaatgtagat tgaagtctgt tccagaaatg ggttaccatg ccgacaagga tttaaaaggt	1620
gaactgcaaa ttcgtggccc acaggttttt gaaagatatt ttaaaaatcc gaatgaaact	1680
tcaaaagccg ttgaccaaga tggttggttt tccacgggag atgttgcat ttcgatgca	1740
aaaggctgca tcagcgtcat tgatcgagtc aagaactttt tcaagctagc acatggtgaa	1800
tatattgctc cagagaaaat cgaaaatatt tatttatcat catgccccta tatcacgcaa	1860
atatttgtct ttggagatcc tttgaagaca tttttagttg gcatcgttgg tgttgatgtt	1920
gatgcagcgc aaccgatttt agctgcaaag caccagagg tgaaaacgtg gactaaggaa	1980
gtgctagtag aaaacttaaa tcgtaataaa aagctaagga aggaattttt aaacaaaatt	2040

aataaatgca tcgatgggct acaaggattt gaaaaattgc acaacatcaa agtcggactt	2100
gagcctttga ctctcgagga tgatgttgtg acgccaactt ttaaaataaa gcgtgccaaa	2160
gcatcaaaat tcttcaaaga tacattagac caactatacg ccgaaggttc actagtcaag	2220
acagaaaagc ttaaatag	2238

<210> 196
 <211> 745
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutated medium chain fatty acyl-CoA synthetase Sc_FAA2_Cmut

<400> 196

Met	Ala	Ala	Pro	Asp	Tyr	Ala	Leu	Thr	Asp	Leu	Ile	Glu	Ser	Asp	Pro
1				5					10					15	

Arg	Phe	Glu	Ser	Leu	Lys	Thr	Arg	Leu	Ala	Gly	Tyr	Thr	Lys	Gly	Ser
			20					25					30		

Asp	Glu	Tyr	Ile	Glu	Glu	Leu	Tyr	Ser	Gln	Leu	Pro	Leu	Thr	Ser	Tyr
		35					40					45			

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

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

Ser	Glu	Asn	Leu	Val	Ser	Cys	Val	Asp	Lys	Asn	Leu	Arg	Thr	Ala	Tyr
			85						90					95	

Asp	His	Phe	Met	Phe	Ser	Ala	Arg	Arg	Trp	Pro	Gln	Arg	Asp	Cys	Leu
			100					105					110		

Gly	Ser	Arg	Pro	Ile	Asp	Lys	Ala	Thr	Gly	Thr	Trp	Glu	Glu	Thr	Phe
		115					120					125			

Arg	Phe	Glu	Ser	Tyr	Ser	Thr	Val	Ser	Lys	Arg	Cys	His	Asn	Ile	Gly
	130						135				140				

Ser Gly Ile Leu Ser Leu Val Asn Thr Lys Arg Lys Arg Pro Leu Glu
145 150 155 160

Ala Asn Asp Phe Val Val Ala Ile Leu Ser His Asn Asn Pro Glu Trp
165 170 175

Ile Leu Thr Asp Leu Ala Cys Gln Ala Tyr Ser Leu Thr Asn Thr Ala
180 185 190

Leu Tyr Glu Thr Leu Gly Pro Asn Thr Ser Glu Tyr Ile Leu Asn Leu
195 200 205

Thr Glu Ala Pro Ile Leu Ile Phe Ala Lys Ser Asn Met Tyr His Val
210 215 220

Leu Lys Met Val Pro Asp Met Lys Phe Val Asn Thr Leu Val Cys Met
225 230 235 240

Asp Glu Leu Thr His Asp Glu Leu Arg Met Leu Asn Glu Ser Leu Leu
245 250 255

Pro Val Lys Cys Asn Ser Leu Asn Glu Lys Ile Thr Phe Phe Ser Leu
260 265 270

Glu Gln Val Glu Gln Val Gly Cys Phe Asn Lys Ile Pro Ala Ile Pro
275 280 285

Pro Thr Pro Asp Ser Leu Tyr Thr Ile Ser Phe Thr Ser Gly Thr Thr
290 295 300

Gly Leu Pro Lys Gly Val Glu Met Ser His Arg Asn Ile Ala Ser Gly
305 310 315 320

Ile Ala Phe Ala Phe Ser Thr Phe Arg Ile Pro Pro Asp Lys Arg Asn
325 330 335

Gln Gln Leu Tyr Asp Met Cys Phe Leu Pro Leu Ala His Ile Phe Glu
340 345 350

Arg Met Val Ile Ala Tyr Asp Leu Ala Ile Gly Phe Gly Ile Gly Phe

355

360

365

Leu His Lys Pro Asp Pro Thr Val Leu Val Glu Asp Leu Lys Ile Leu
 370 375 380

Lys Pro Tyr Ala Val Ala Leu Val Pro Arg Ile Leu Thr Arg Phe Glu
 385 390 395 400

Ala Gly Ile Lys Asn Ala Leu Asp Lys Ser Thr Val Gln Arg Asn Val
 405 410 415

Ala Asn Thr Ile Leu Asp Ser Lys Ser Ala Arg Phe Thr Ala Arg Gly
 420 425 430

Gly Pro Asp Lys Ser Ile Met Asn Phe Leu Val Tyr His Arg Val Leu
 435 440 445

Ile Asp Lys Ile Arg Asp Ser Leu Gly Leu Ser Asn Asn Ser Phe Ile
 450 455 460

Ile Thr Gly Ser Ala Pro Ile Ser Lys Asp Thr Leu Leu Phe Leu Arg
 465 470 475 480

Ser Ala Leu Asp Ile Gly Ile Arg Gln Gly Tyr Gly Leu Thr Glu Thr
 485 490 495

Phe Ala Gly Val Cys Leu Ser Glu Pro Phe Glu Lys Asp Val Gly Ser
 500 505 510

Cys Gly Ala Ile Gly Ile Ser Ala Glu Cys Arg Leu Lys Ser Val Pro
 515 520 525

Glu Met Gly Tyr His Ala Asp Lys Asp Leu Lys Gly Glu Leu Gln Ile
 530 535 540

Arg Gly Pro Gln Val Phe Glu Arg Tyr Phe Lys Asn Pro Asn Glu Thr
 545 550 555 560

Ser Lys Ala Val Asp Gln Asp Gly Trp Phe Ser Thr Gly Asp Val Ala
 565 570 575

Phe Ile Asp Ala Lys Gly Arg Ile Ser Val Ile Asp Arg Val Lys Asn
580 585 590

Phe Phe Lys Leu Ala His Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu
595 600 605

Asn Ile Tyr Leu Ser Ser Cys Pro Tyr Ile Thr Gln Ile Phe Val Phe
610 615 620

Gly Asp Pro Leu Lys Thr Phe Leu Val Gly Ile Val Gly Val Asp Val
625 630 635 640

Asp Ala Ala Gln Pro Ile Leu Ala Ala Lys His Pro Glu Val Lys Thr
645 650 655

Trp Thr Lys Glu Val Leu Val Glu Asn Leu Asn Arg Asn Lys Lys Leu
660 665 670

Arg Lys Glu Phe Leu Asn Lys Ile Asn Lys Cys Ile Asp Gly Leu Gln
675 680 685

Gly Phe Glu Lys Leu His Asn Ile Lys Val Gly Leu Glu Pro Leu Thr
690 695 700

Leu Glu Asp Asp Val Val Thr Pro Thr Phe Lys Ile Lys Arg Ala Lys
705 710 715 720

Ala Ser Lys Phe Phe Lys Asp Thr Leu Asp Gln Leu Tyr Ala Glu Gly
725 730 735

Ser Leu Val Lys Thr Glu Lys Leu Lys
740 745

<210> 197
<211> 2085
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 197
atgtccgaac aacactctgt cgcagtcggt aaagctgcta atgagcacga gactgccct 60
aggagaaatg ttagagtcaa gaagcggccc ttaattagac cattgaactc gtcagcatct 120

acgctgtatg aatttgcct agagtgtttc aacaagggtg gaaaacgaga tggatatggct	180
tggagagatg tcatcgagat tcatgagaca aagaaaacca ttgtgagaaa ggtagacggc	240
aaggataaat ctatagaaaa gacatggctg tattatgaaa tgtcaccata taaaatgatg	300
acctaccagg aactgatctg ggtgatgcac gatatgggcc gtgggctggc aaaaataggc	360
atcaagccca atggagaaca caaattccac atcttcgcat ctacttcca taaatggatg	420
aagattttcc ttggttgcat atcccagggt atccccgtag taaccgcgta tgatactttg	480
ggtgagagcg gtttgattca ctccatgggt gaaaccgagt ctgctgctat tttcactgat	540
aatcaattat tggctaaaaat gatagtgcct ttgcaatctg ctaaagatat caaatttctt	600
atccataacg aacctatcga cccaatgac agaagacaaa acggcaaact ttacaaggct	660
gctaaggatg ccattaataa gatcagagaa gttaggccag acataaaaaat ttatagtttt	720
gaagaagttg tcaagatagg taaaaaaagt aaagatgagg tcaaacttca tccacctgag	780
ccaaaagatt tggcttgtat catgtacacc tcgggctcga tcagtgcacc aaaaggtgta	840
gtattgactc attataatat tgtttcgggt atcgtcgggt taggtcacaa cgtctttgga	900
tggatcggct ctacagaccg tgttttgtcg ttcttgccat tggctcatat ttttgaactg	960
gtctttgaat tcgaagcctt ttactggaac ggtattcttg ggtacggtag tgттаagact	1020
ttgactaata cttcgactcg taattgtaag ggtgacctgg ttgagtttaa gcctactatt	1080
atgatcgggtg tggctgccgt ttgggaaact gtgagaaaag ctattttgga aaagatcagc	1140
gatttaactc ccgtactcca aaagattttt tggctctgcct atagtatgaa agaaaagagt	1200
gtaccatgca ccgggttttt aagtcgtatg gtcttcaaga aagtcagaca agccaccgt	1260
ggtcatctta agtatattat gaacggtggg tctgcgatca gtattgatgc tcagaaattc	1320
ttttctatcg tcctgtgtcc tatgattatc ggttacggcc ttactgaaac agttgcgaat	1380
gcttggtgtt tggagcctga tcatttcgaa tatggtatag ttggtgatct tgttggatcg	1440
gtcactgcca aattggtgga tgттаaggac ctaggttatt atgcaaaaaa caatcaaggt	1500
gaattgcttc taaagggtgc gccggtctgt tctgaatatt ataagaatcc aatagaaacg	1560
gcggtctctt tcacttacga tggatggttt cgtactgggt atattgttga atggactccc	1620
aagggacaac ttaaaattat tgatagaaga aagaatttgg ttaaaaccct aaatggtgaa	1680
tatattgcat tagaaaagtt agaatctgtt tacagggtcaa actcctatgt gaaaaatatc	1740

tgtgtttatg ccgatgaaag taggggttaa ccggtgggta ttgtggtacc caaccagga	1800
cccctatcta aatttgctgt caaattgcgt attatgaaaa aggggtgaaga catcgaaaac	1860
tatatccatg acaaagcatt acgaaatgct gttttcaaag agatgatcgc aacagccaaa	1920
tctcaagggtt tggttggtat tgaactatta tgtggtattg ttttctttga tgaagaatgg	1980
acacctgaaa atggctttgt cacatctgct caaaaattaa agagaagaga aatcttagcc	2040
gctgttaa at cagaagtcga aagggtttac aaagaaaatt cttag	2085

<210> 198
 <211> 694
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 198

Met	Ser	Glu	Gln	His	Ser	Val	Ala	Val	Gly	Lys	Ala	Ala	Asn	Glu	His
1				5					10					15	

Glu	Thr	Ala	Pro	Arg	Arg	Asn	Val	Arg	Val	Lys	Lys	Arg	Pro	Leu	Ile
			20					25					30		

Arg	Pro	Leu	Asn	Ser	Ser	Ala	Ser	Thr	Leu	Tyr	Glu	Phe	Ala	Leu	Glu
		35					40					45			

Cys	Phe	Asn	Lys	Gly	Gly	Lys	Arg	Asp	Gly	Met	Ala	Trp	Arg	Asp	Val
	50					55					60				

Ile	Glu	Ile	His	Glu	Thr	Lys	Lys	Thr	Ile	Val	Arg	Lys	Val	Asp	Gly
65					70					75				80	

Lys	Asp	Lys	Ser	Ile	Glu	Lys	Thr	Trp	Leu	Tyr	Tyr	Glu	Met	Ser	Pro
				85					90					95	

Tyr	Lys	Met	Met	Thr	Tyr	Gln	Glu	Leu	Ile	Trp	Val	Met	His	Asp	Met
			100					105					110		

Gly	Arg	Gly	Leu	Ala	Lys	Ile	Gly	Ile	Lys	Pro	Asn	Gly	Glu	His	Lys
		115					120					125			

Phe His Ile Phe Ala Ser Thr Ser His Lys Trp Met Lys Ile Phe Leu

130

135

140

Gly Cys Ile Ser Gln Gly Ile Pro Val Val Thr Ala Tyr Asp Thr Leu
 145 150 155 160

Gly Glu Ser Gly Leu Ile His Ser Met Val Glu Thr Glu Ser Ala Ala
 165 170 175

Ile Phe Thr Asp Asn Gln Leu Leu Ala Lys Met Ile Val Pro Leu Gln
 180 185 190

Ser Ala Lys Asp Ile Lys Phe Leu Ile His Asn Glu Pro Ile Asp Pro
 195 200 205

Asn Asp Arg Arg Gln Asn Gly Lys Leu Tyr Lys Ala Ala Lys Asp Ala
 210 215 220

Ile Asn Lys Ile Arg Glu Val Arg Pro Asp Ile Lys Ile Tyr Ser Phe
 225 230 235 240

Glu Glu Val Val Lys Ile Gly Lys Lys Ser Lys Asp Glu Val Lys Leu
 245 250 255

His Pro Pro Glu Pro Lys Asp Leu Ala Cys Ile Met Tyr Thr Ser Gly
 260 265 270

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

Ser Gly Ile Ala Gly Val Gly His Asn Val Phe Gly Trp Ile Gly Ser
 290 295 300

Thr Asp Arg Val Leu Ser Phe Leu Pro Leu Ala His Ile Phe Glu Leu
 305 310 315 320

Val Phe Glu Phe Glu Ala Phe Tyr Trp Asn Gly Ile Leu Gly Tyr Gly
 325 330 335

Ser Val Lys Thr Leu Thr Asn Thr Ser Thr Arg Asn Cys Lys Gly Asp
 340 345 350

Leu Val Glu Phe Lys Pro Thr Ile Met Ile Gly Val Ala Ala Val Trp
355 360 365

Glu Thr Val Arg Lys Ala Ile Leu Glu Lys Ile Ser Asp Leu Thr Pro
370 375 380

Val Leu Gln Lys Ile Phe Trp Ser Ala Tyr Ser Met Lys Glu Lys Ser
385 390 395 400

Val Pro Cys Thr Gly Phe Leu Ser Arg Met Val Phe Lys Lys Val Arg
405 410 415

Gln Ala Thr Gly Gly His Leu Lys Tyr Ile Met Asn Gly Gly Ser Ala
420 425 430

Ile Ser Ile Asp Ala Gln Lys Phe Phe Ser Ile Val Leu Cys Pro Met
435 440 445

Ile Ile Gly Tyr Gly Leu Thr Glu Thr Val Ala Asn Ala Cys Val Leu
450 455 460

Glu Pro Asp His Phe Glu Tyr Gly Ile Val Gly Asp Leu Val Gly Ser
465 470 475 480

Val Thr Ala Lys Leu Val Asp Val Lys Asp Leu Gly Tyr Tyr Ala Lys
485 490 495

Asn Asn Gln Gly Glu Leu Leu Leu Lys Gly Ala Pro Val Cys Ser Glu
500 505 510

Tyr Tyr Lys Asn Pro Ile Glu Thr Ala Val Ser Phe Thr Tyr Asp Gly
515 520 525

Trp Phe Arg Thr Gly Asp Ile Val Glu Trp Thr Pro Lys Gly Gln Leu
530 535 540

Lys Ile Ile Asp Arg Arg Lys Asn Leu Val Lys Thr Leu Asn Gly Glu
545 550 555 560

Tyr Ile Ala Leu Glu Lys Leu Glu Ser Val Tyr Arg Ser Asn Ser Tyr

565

570

575

Val Lys Asn Ile Cys Val Tyr Ala Asp Glu Ser Arg Val Lys Pro Val
580 585 590

Gly Ile Val Val Pro Asn Pro Gly Pro Leu Ser Lys Phe Ala Val Lys
595 600 605

Leu Arg Ile Met Lys Lys Gly Glu Asp Ile Glu Asn Tyr Ile His Asp
610 615 620

Lys Ala Leu Arg Asn Ala Val Phe Lys Glu Met Ile Ala Thr Ala Lys
625 630 635 640

Ser Gln Gly Leu Val Gly Ile Glu Leu Leu Cys Gly Ile Val Phe Phe
645 650 655

Asp Glu Glu Trp Thr Pro Glu Asn Gly Phe Val Thr Ser Ala Gln Lys
660 665 670

Leu Lys Arg Arg Glu Ile Leu Ala Ala Val Lys Ser Glu Val Glu Arg
675 680 685

Val Tyr Lys Glu Asn Ser
690

<210> 199
<211> 2085
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 199
atgaccgaac aatattccgt tgcagttggc gaagccgaca atgagcatga aaccgctcca 60
agaagaaata tcagggttaa agacaagcct ttgattagac ccataaactc ctcagcatct 120
aactgtacg aattcgccct ggaatgtttt accaaagggtg gtaagagaga cggatatggca 180
tggagagata ttatagatat acatgagacg aaaaaacca tagtcaagag ggtggatggt 240
aaggataagc ccatcgaaaa aacatgggtg tactacgaac tgactcccta cataaccatg 300
acatacgagg agatgatctg cgtaatgcac gacattggac gtgggctgat aaagattggt 360
gttaaacctt acggtgagaa caagttccac atctttgcct ctacatctca caagtggatg 420

aaaacttttc ttggttgcac gtcacaaggt attcctgtgg tcaccgcgta cgacactttg	480
ggtgagagcg gtttgattca ctccatggtg gaaacggatt ccgtcgccat tttcacggac	540
aaccagctgt tgtccaaatt agcagttcct ttgaaaaccg ccaagaacgt aaaattcgtc	600
attcacaacg aacccatcga tccaagtacg aaaagacaaa atggtaagct ttacaaggct	660
gccaaggatg ctgttgacaa aatcaaggaa gttagaccgg acataaaaaat ctacagtttc	720
gatgaaatta ttgagatagg taaaaaggcc aaggacgagg ttgaattgca tttccccaag	780
cctgaagatc cagcttgtat catgtacact tctggttcca ctggtacacc aaagggtgtg	840
gtattgacac attacaacat tgtagctggt attggtggtg tgggccataa cgttatcgga	900
tggattggcc caacagaccg tattatcgca ttcttgccat tggctcatat ttttgaatta	960
atctttgaat tcgaagcggt ctactggaat ggtatcctag ggtacgccac tgtcaagact	1020
ttaaccccaa cttctacacg taattgccaa ggtgacctga tggagtttaa acctaccgta	1080
atggtaggtg ttgccgcagt ttgggaaaca gtgagaaaag gtatcctggc caagatcaac	1140
gaattgcccg gttggtctca aacgcttttc tggactgtct atgctttgaa agagagaaat	1200
ataccatgca gcggcttgct gagtgggttg atcttcaaga gaatcagaga agcaaccggt	1260
ggaaacttaa ggtttattct gaacggtggg tctgcaatca gcatagacgc caaaaattc	1320
ctctccaacc ttctatgtcc tatgctcatt ggatatgggc taactgaggg tgtggctaata	1380
gcctgtgtcc tggagcctga acattttgat tacggtattg ctggtgacct tgtcggaact	1440
attacagcta aattggtgga tgtcgaagat ttgggctatt ttgccaagaa taaccaaggt	1500
gaattgctgt taaagggtgc acccatctgt tctgaatact ataagaatcc tgaagaaact	1560
gctgcggcct ttaccgatga tggctggttc cgtaccggtg atatcgctga atggaccccc	1620
aagggacaaa ttaagatcat tgatagaaag aaaaatttgg tcaagacctt aaacggtgag	1680
tacattgcat tggaataatt agaattcatt tacagatcaa atccttacgt ccaaacatc	1740
tgtgtctacg ctgatgaaaa caaagttaag cctgtcggtg ttgtggtccc taacttagga	1800
cacttgtcta agctggctat cgaattaggt ataatggtac caggtgaaga tgtcgaaagc	1860
tatatccatg aaaagaagct acaggatgcc gtttgcaaag atatgctgtc aactgccaaa	1920
tctcaaggct tgaatggtat tgaattatta tgtggcattg ttttctttga agaagaatgg	1980
actccagaaa acggtcttgt tacatccgcc caaaaattaa agagaagaga tattctagcg	2040

gctgtcaagc cagatgtgga aagagtttat aaagaaaaca cttaa

2085

<210> 200

<211> 694

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 200

Met Thr Glu Gln Tyr Ser Val Ala Val Gly Glu Ala Asp Asn Glu His
1 5 10 15

Glu Thr Ala Pro Arg Arg Asn Ile Arg Val Lys Asp Lys Pro Leu Ile
20 25 30

Arg Pro Ile Asn Ser Ser Ala Ser Thr Leu Tyr Glu Phe Ala Leu Glu
35 40 45

Cys Phe Thr Lys Gly Gly Lys Arg Asp Gly Met Ala Trp Arg Asp Ile
50 55 60

Ile Asp Ile His Glu Thr Lys Lys Thr Ile Val Lys Arg Val Asp Gly
65 70 75 80

Lys Asp Lys Pro Ile Glu Lys Thr Trp Leu Tyr Tyr Glu Leu Thr Pro
85 90 95

Tyr Ile Thr Met Thr Tyr Glu Glu Met Ile Cys Val Met His Asp Ile
100 105 110

Gly Arg Gly Leu Ile Lys Ile Gly Val Lys Pro Asn Gly Glu Asn Lys
115 120 125

Phe His Ile Phe Ala Ser Thr Ser His Lys Trp Met Lys Thr Phe Leu
130 135 140

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

Gly Glu Ser Gly Leu Ile His Ser Met Val Glu Thr Asp Ser Val Ala
165 170 175

Ile Phe Thr Asp Asn Gln Leu Leu Ser Lys Leu Ala Val Pro Leu Lys
180 185 190

Thr Ala Lys Asn Val Lys Phe Val Ile His Asn Glu Pro Ile Asp Pro
195 200 205

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

Val Asp Lys Ile Lys Glu Val Arg Pro Asp Ile Lys Ile Tyr Ser Phe
225 230 235 240

Asp Glu Ile Ile Glu Ile Gly Lys Lys Ala Lys Asp Glu Val Glu Leu
245 250 255

His Phe Pro Lys Pro Glu Asp Pro Ala Cys Ile Met Tyr Thr Ser Gly
260 265 270

Ser Thr Gly Thr Pro Lys Gly Val Val Leu Thr His Tyr Asn Ile Val
275 280 285

Ala Gly Ile Gly Gly Val Gly His Asn Val Ile Gly Trp Ile Gly Pro
290 295 300

Thr Asp Arg Ile Ile Ala Phe Leu Pro Leu Ala His Ile Phe Glu Leu
305 310 315 320

Ile Phe Glu Phe Glu Ala Phe Tyr Trp Asn Gly Ile Leu Gly Tyr Ala
325 330 335

Thr Val Lys Thr Leu Thr Pro Thr Ser Thr Arg Asn Cys Gln Gly Asp
340 345 350

Leu Met Glu Phe Lys Pro Thr Val Met Val Gly Val Ala Ala Val Trp
355 360 365

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

Trp Ser Gln Thr Leu Phe Trp Thr Val Tyr Ala Leu Lys Glu Arg Asn

385		390		395		400									
Ile	Pro	Cys	Ser	Gly	Leu	Leu	Ser	Gly	Leu	Ile	Phe	Lys	Arg	Ile	Arg
				405					410					415	
Glu	Ala	Thr	Gly	Gly	Asn	Leu	Arg	Phe	Ile	Leu	Asn	Gly	Gly	Ser	Ala
			420					425					430		
Ile	Ser	Ile	Asp	Ala	Gln	Lys	Phe	Leu	Ser	Asn	Leu	Leu	Cys	Pro	Met
		435					440					445			
Leu	Ile	Gly	Tyr	Gly	Leu	Thr	Glu	Gly	Val	Ala	Asn	Ala	Cys	Val	Leu
	450					455					460				
Glu	Pro	Glu	His	Phe	Asp	Tyr	Gly	Ile	Ala	Gly	Asp	Leu	Val	Gly	Thr
465					470					475					480
Ile	Thr	Ala	Lys	Leu	Val	Asp	Val	Glu	Asp	Leu	Gly	Tyr	Phe	Ala	Lys
			485						490					495	
Asn	Asn	Gln	Gly	Glu	Leu	Leu	Leu	Lys	Gly	Ala	Pro	Ile	Cys	Ser	Glu
			500					505					510		
Tyr	Tyr	Lys	Asn	Pro	Glu	Glu	Thr	Ala	Ala	Ala	Phe	Thr	Asp	Asp	Gly
		515					520					525			
Trp	Phe	Arg	Thr	Gly	Asp	Ile	Ala	Glu	Trp	Thr	Pro	Lys	Gly	Gln	Ile
	530					535					540				
Lys	Ile	Ile	Asp	Arg	Lys	Lys	Asn	Leu	Val	Lys	Thr	Leu	Asn	Gly	Glu
545					550					555					560
Tyr	Ile	Ala	Leu	Glu	Lys	Leu	Glu	Ser	Ile	Tyr	Arg	Ser	Asn	Pro	Tyr
			565						570					575	
Val	Gln	Asn	Ile	Cys	Val	Tyr	Ala	Asp	Glu	Asn	Lys	Val	Lys	Pro	Val
			580					585					590		
Gly	Ile	Val	Val	Pro	Asn	Leu	Gly	His	Leu	Ser	Lys	Leu	Ala	Ile	Glu
		595					600					605			

Leu Gly Ile Met Val Pro Gly Glu Asp Val Glu Ser Tyr Ile His Glu
610 615 620

Lys Lys Leu Gln Asp Ala Val Cys Lys Asp Met Leu Ser Thr Ala Lys
625 630 635 640

Ser Gln Gly Leu Asn Gly Ile Glu Leu Leu Cys Gly Ile Val Phe Phe
645 650 655

Glu Glu Glu Trp Thr Pro Glu Asn Gly Leu Val Thr Ser Ala Gln Lys
660 665 670

Leu Lys Arg Arg Asp Ile Leu Ala Ala Val Lys Pro Asp Val Glu Arg
675 680 685

Val Tyr Lys Glu Asn Thr
690

<210> 201
<211> 6702
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutated acetyl-CoA carboxylase (ACC1) (S659A, S1157A)

<400> 201
atgagcgaag aaagcttatt cgagtcttct ccacagaaga tggagtacga aattacaaac 60
tactcagaaa gacatacaga acttccaggt catttcattg gcctcaatac agtagataaa 120
ctagaggagt ccccgttaag ggactttgtt aagagtcacg gtgggtcacac ggtcatatcc 180
aagatcctga tagcaaataa tggatttgcc gccgtgaaag aaattagatc cgtcagaaaa 240
tgggcatacg agacgttcgg cgatgacaga accgtccaat tcgtcgccat ggccacccca 300
gaagatctgg aggccaacgc agaatatatc cgtatggccg atcaatacat tgaagtgcc 360
ggtggtacta ataataacaa ctacgctaac gtagacttga tcgtagacat cgccgaaaga 420
gcagacgtag acgccgtatg ggctggctgg ggtcacgcct ccgagaatcc actattgcct 480
gaaaaattgt cccagtctaa gaggaaagtc atctttattg ggccctccagg taacgccatg 540
aggtctttag gtgataaaat ctcctctacc attgtcgctc aaagtgctaa agtcccatgt 600

attccatggt ctggtaccgg tgttgacacc gttcacgtgg acgagaaaac cggctctggtc	660
tctgtcgacg atgacatcta tcaaaagggt tgttgtagct ctcctgaaga tggttttacaa	720
aaggccaagc gtattggttt tcctgtcatg attaaaggcat ccgaagggtg tggtggtaaa	780
ggtatcagac aagttgaacg tgaagaagat ttcatcgctt tataccacca ggcagccaac	840
gaaattccag gctcccccat tttcatcatg aagttggccg gtagagcgcg tcacttgga	900
gttcaactgc tagcagatca gtacggtaca aatatttcct tgttcggtag agactgttcc	960
gttcagagac gtcatcaaaa aattatcgaa gaagcaccag ttacaattgc caaggctgaa	1020
acatttcacg agatggaaaa ggctgccgtc agactgggga aactagtcgg ttatgtctct	1080
gccggtaccg tggagtatct atattctcat gatgatggaa aattctactt tttagaattg	1140
aaccaagat tacaagtcga gcatccaaca acggaaatgg tctccggtgt taacttacct	1200
gcagctcaat taaaaatcg tatgggtatc cctatgcata gaataagtga cattagaact	1260
ttatatggta tgaatcctca ttctgcctca gaaatcgatt tcgaattcaa aactcaagat	1320
gccaccaaga aacaaagaag acctattcca aagggtcatt gtaccgcttg tcgtatcaca	1380
tcagaagatc caaacgatgg attcaagcca tcgggtggta ctttgcatga actaaacttc	1440
cgttcttcct ctaatgtttg gggttacttc tccgtgggta acaatggtaa tattcactcc	1500
ttttcggact ctcagttcgg ccatatTTTT gcttttggtg aaaatagaca agcttccagg	1560
aaacacatgg ttgttgccct gaaggaattg tccattaggg gtgatttcag aactactgtg	1620
gaatacttga tcaaactttt ggaaactgaa gatttcgagg ataacactat taccaccggt	1680
tggttggacg atttgattac tcataaaatg accgctgaaa agcctgatcc aactcttgcc	1740
gtcatttgcg gtgccgtac aaaggctttc ttagcatctg aagaagcccg ccacaagtat	1800
atcgaatcct taaaaaggg acaagttcta tctaaagacc tactgcaaac tatgttccct	1860
gtagatttta tccatgaggg taaaagatac aagttcaccg tagctaaatc cggtaatgac	1920
cgttacacat tatttatcaa tggttctaaa tgtgatatca tactgcgtca actatctgat	1980
ggtggtcttt tgattgcat aggcggtaaa tcgcatacca tctattggaa agaagaagtt	2040
gctgtacaa gattatccgt tgactctatg actactttgt tggaagttga aaacgatcca	2100
accagttgc gtactccatc ccctggtaaa ttggttaaat tcttggtgga aaatggtgaa	2160
cacattatca aggccaacc atatgcagaa attgaagtta tgaaaatgca aatgcctttg	2220

gtttctcaag aaaatggtat cgtccagtta ttaaagcaac ctggttctac cattgttgca	2280
ggtgatataca tggctattat gactcttgac gatccatcca aggtcaagca cgctctacca	2340
tttgaaggta tgctgccaga ttttggttct ccagttatcg aaggaaccaa acctgcctat	2400
aaattcaagt cattagtgtc tacttttgaa aacattttga agggttatga caaccaagtt	2460
attatgaacg cttccttgca acaattgata gaggttttga gaaatccaaa actgccttac	2520
tcagaatgga aactacacat ctctgcttta cattcaagat tgcctgctaa gctagatgaa	2580
caaatggaag agttagttgc acgttctttg agacgtggtg ctgttttccc agctagacaa	2640
ttaagtaa at tgattgatata ggccgtgaag aatcctgaat acaaccccga caaattgctg	2700
ggcgccgtcg tggaaccatt ggcggtatatt gtcataagt actctaacgg gttagaagcc	2760
catgaacatt ctatatttgt ccatttcttg gaagaatatt acgaagttga aaagttattc	2820
aatggtccaa atgttcgtga ggaaaatatc attctgaaat tgcgtgatga aaaccctaaa	2880
gatctagata aagttgcgct aactgttttg tctcattcga aagtttcagc gaagaataac	2940
ctgatcctag ctatcttgaa acattatcaa ccattgtgca agttatcttc taaagtttct	3000
gccattttct ctactcctct acaacatatt gttgaactag aatctaaggc taccgctaag	3060
gtcgctctac aagcaagaga aattttgatt caaggcgctt taccttcggt caaggaaaga	3120
actgaacaaa ttgaacatat cttaaaatcc tctgttgtga aggttgcccta tggctcatcc	3180
aatccaaagc gctctgaacc agatttgaat atcttgaagg acttgatcga ttctaattac	3240
gttgtgttcg atgttttact tcaattccta acccatcaag acccagttgt gactgctgca	3300
gctgctcaag tctatattcg tcgtgcttat cgtgcttaca ccataggaga tattagagtt	3360
cacgaagggtg tcacagttcc aattgttgaa tggaaattcc aactaccttc agctgcgttc	3420
tccacctttc caactgttaa atctaaaatg ggtatgaaca gggctgtttc tgtttcagat	3480
ttgtcatatg ttgcaaacag tcagtcattc ccgttaagag aaggtatttt gatggctgtg	3540
gatcatttag atgatgttga tgaaattttg tcacaaagtt tggaagttat tcctcgtcac	3600
caatcttctt ctaacggacc tgctcctgat cgttctggta gctccgcac gttgagtaat	3660
gttgcta atg tttgtgttgc ttctacagaa ggtttcgaat ctgaagagga aatttttgta	3720
aggttgagag aaatttttga tttgaataag caggaattaa tcaatgcttc tatccgtcgt	3780
atcacattta tgttcggttt taaagatggg tcttatccaa agtattatac ttttaacggt	3840

ccaaattata acgaaaatga aacaattcgt cacattgagc cggctttggc cttccaactg	3900
gaattaggaa gattgtccaa cttcaacatt aaaccaattt tcaactgataa tagaaacatc	3960
catgtctacg aagctgttag taagacttct ccattggata agagattctt tacaagaggt	4020
attattagaa cgggtcatat ccgtgatgac atttctattc aagaatatct gacttctgaa	4080
gctaacagat tgatgagtga tatattggat aatttagaag tcaccgacac ttcaaattct	4140
gatttgaatc atatcttcat caacttcatt gcggtgtttg atatctctcc agaagatgtc	4200
gaagccgcct tcggtggttt cttagaaaga tttggtaaga gattgttgag attgcgtgtt	4260
tcttctgccg aaattagaat catcatcaaa gatcctcaaa caggtgcccc agtaccattg	4320
cgtgccttga tcaataacgt ttctggttat gttatcaaaa cagaaatgta caccgaagtc	4380
aagaacgcaa aaggtgaatg ggtatttaag tctttgggta aacctggatc catgcattta	4440
agacctattg ctactcctta ccctgttaag gaatggttgc aaccaaacg ttataaggca	4500
cacttgatgg gtaccacata tgtctatgac ttcccagaat tattccgcca agcatcgtca	4560
tccaatgga aaaatttctc tgcagatgtt aagttaacag atgatttctt tatttccaac	4620
gagttgattg aagatgaaaa cggcgaatta actgaggtgg aaagagaacc tggtgccaac	4680
gctattggta tggttgctt taagattact gtaaagactc ctgaatatcc aagaggccgt	4740
caatttgttg ttgttgctaa cgatatcaca ttcaagatcg gttcctttgg tccacaagaa	4800
gacgaattct tcaataaggt tactgaatat gctagaaagc gtggtatccc aagaatttac	4860
ttggctgcaa actcaggtgc cagaattgggt atggctgaag agattgttcc actatttcaa	4920
gttgcattgga atgatgctgc caatccggac aagggtctcc aatacttata cttacaagt	4980
gaaggatatg aaactttaaa gaaatttgac aaagaaaatt ctgttctcac tgaacgtact	5040
gttataaacg gtgaagaaag atttgtcatc aagacaatta ttggttctga agatgggtta	5100
ggtgtcgaat gtctacgtgg atctggttta attgctggtg caacgtcaag ggcttaccac	5160
gatatttca ctatcacctt agtcacttgt agatccgtcg gtatcgggtc ttatttggtt	5220
cgtttgggtc aaagagctat tcaggtcgaa ggccagccaa ttattttaac tggtgctcct	5280
gcaatcaaca aaatgctggg tagagaagtt tatacttcta acttacaatt ggggtgtact	5340
caaatcatgt ataacaacgg tgtttcacat ttgactgctg ttgacgattt agctggtgta	5400
gagaagattg ttgaatggat gtcttatgtt ccagccaagc gtaatatgcc agttcctatc	5460

ttggaaacta aagacacatg ggatagacca gttgatttca ctccaactaa tgatgaaact	5520
tacgatgtaa gatggatgat tgaaggtcgt gagactgaaa gtggatttga atatggtttg	5580
tttgataaag ggtcttttctt tgaaactttg tcaggatggg ccaaaggtgt tgtcgttggt	5640
agagcccgtc ttggtggtat tccactgggt gttatttggtg ttgaaacaag aactgtcgag	5700
aacttgattc ctgctgatcc agctaatacca aatagtgtg aaacattaat tcaagaacct	5760
ggtcaagttt ggcacccaaa ctccgccttc aagactgctc aagctatcaa tgactttaac	5820
aacggtgaac aattgccaat gatgattttg gccaaactgga gaggtttctc tgggtggtcaa	5880
cgtgatatgt tcaacgaagt cttgaagtat ggttcgttta ttgttgacgc attggtggat	5940
tacaaacaac caattattat ctatatccca cctaccggtg aactaagagg tggttcatgg	6000
gttgttgtcg atccaactat caacgctgac caaatggaaa tgtatgccga cgtcaacgct	6060
agagctgggtg ttttgaacc acaaggtatg gttggtatca agttccgtag agaaaaattg	6120
ctggacacca tgaacagatt ggatgacaag tacagagaat tgagatctca attatccaac	6180
aagagtttgg ctccagaagt acatcagcaa atatccaagc aattagctga tcgtgagaga	6240
gaactattgc caatttacgg acaaatcagt cttcaatttg ctgatttgca cgataggtct	6300
tcacgtatgg tggccaaggg tggtatttct aaggaactgg aatggaccga ggcacgtcgt	6360
ttcttcttct ggagattgag aagaagattg aacgaagaat atttgattaa aaggttgagc	6420
catcaggtag gcgaagcatc aagattagaa aagatcgcaa gaattagatc gtggtaccct	6480
gcttcagtgg accatgaaga tgataggcaa gtcgcaacat ggattgaaga aaactacaaa	6540
actttggacg ataaactaaa gggtttgaaa ttagagtcac tcgctcaaga cttagctaaa	6600
aagatcagaa gcgacatga caatgctatt gatggattat ctgaagttat caagatgtta	6660
tctaccgatg ataaagaaaa attgttgaag actttgaaat aa	6702

<210> 202

<211> 894

<212> DNA

<213> Artificial Sequence

<220>

<223> Truncated geranylgeranyl pyrophosphate synthase Ag_GPPS_Ntrunc

<400> 202

atgtcttttg acttcaataa gtatatggat tctaaggcta tgaccgtcaa cgaggctttg	60
---	----

aataaagcca tcccattgcg ttaccacaaa aagatctacg aatctatgag atattctttg 120
ttagctgggtg gtaagagagt ccgtccagtt ttgtgtatcg ccgcttgtga attagtcggt 180
ggtactgagg agttagctat tccaaccgcc tgtgccatcg aaatgatcca caccatgtct 240
ttgatgcacg atgatttgcc atgtatcgac aacgatgact tgagacgtgg taaacctacc 300
aatcataaga ttttcggtga agatactgct gttactgccg gtaacgcttt acactcttac 360
gccttcgaac atattgctgt ttctacttcc aagactgttg gtgctgatag aattttgaga 420
atggtttctg aattaggtcg tgctactggg tccgaagggtg ttatgggtgg tcaaattggtc 480
gatattgctt ctgaagggtga cccttcatt gatttgcaaa ctttagaatg gatccacatc 540
cacaagactg ctatgttatt agaattgttct gttgtctgtg gtgccatcat cgggtggtgct 600
tctgaaattg ttattgagag agccagacgt tatgctcgtt gtgtcgggtt attgtttcaa 660
gttgttgacg acattttaga tgttacaaa tcttctgacg aattgggtaa aactgctggt 720
aaagatttaa tctccgataa agccacctac cctaagttga tgggtttgga gaaggccaaa 780
gagttttccg atgaattatt aaacagagct aaaggtgaat tgtcttgctt cgatccagtt 840
aaggctgccc cattgttagg tttggctgac tacgttgcct tcagacaaaa ctaa 894

<210> 203
<211> 297
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated geranylgeranyl pyrophosphate synthase Ag_GPPS_Ntrunc
<400> 203

Met Ser Phe Asp Phe Asn Lys Tyr Met Asp Ser Lys Ala Met Thr Val
1 5 10 15

Asn Glu Ala Leu Asn Lys Ala Ile Pro Leu Arg Tyr Pro Gln Lys Ile
20 25 30

Tyr Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val Arg
35 40 45

Pro Val Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Thr Glu Glu
50 55 60

Leu Ala Ile Pro Thr Ala Cys Ala Ile Glu Met Ile His Thr Met Ser
65 70 75 80

Leu Met His Asp Asp Leu Pro Cys Ile Asp Asn Asp Asp Leu Arg Arg
85 90 95

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

Ala Gly Asn Ala Leu His Ser Tyr Ala Phe Glu His Ile Ala Val Ser
115 120 125

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

Leu Gly Arg Ala Thr Gly Ser Glu Gly Val Met Gly Gly Gln Met Val
145 150 155 160

Asp Ile Ala Ser Glu Gly Asp Pro Ser Ile Asp Leu Gln Thr Leu Glu
165 170 175

Trp Ile His Ile His Lys Thr Ala Met Leu Leu Glu Cys Ser Val Val
180 185 190

Cys Gly Ala Ile Ile Gly Gly Ala Ser Glu Ile Val Ile Glu Arg Ala
195 200 205

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

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

Lys Asp Leu Ile Ser Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu
245 250 255

Glu Lys Ala Lys Glu Phe Ser Asp Glu Leu Leu Asn Arg Ala Lys Gly
260 265 270

Glu Leu Ser Cys Phe Asp Pro Val Lys Ala Ala Pro Leu Leu Gly Leu

275

280

285

Ala Asp Tyr Val Ala Phe Arg Gln Asn
290 295

<210> 204

<211> 1356

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 204

ttatttatca agataagttt ccggatcttt ttctttccta acaccccagt cagcctgagt	60
tacatccagc cattgaacct tagaaaatct tttgtcatca gcggtttgag ccctaagatc	120
aacatcttgc ttagcaatca ctgcaatggc gtcataacca ccagcaccag gtattaagca	180
agtaagaact ctttttaagg tctggcaatc atccaataag ctagtttgta cgggagggttc	240
gatatcggca ccagattctt tagttatttt tctaaaggaa cgtctaattg tggcaactgc	300
atctctaact tctgtgatct caggatactt ttgacaggta cagtcattcc tctcaagaga	360
ctcaaataatc tgatcgctgt aatcgatcatg agtctcgtgt aagcgatcta gtttagatag	420
tccatccata aatctagaat ttgcatgcat gagttctgta tatattttca agctttccgg	480
catatgcgaa tcataccaat tttttacctt ctggaccagt tttactgttt ctgaaccatt	540
cttaatatcg cccatccata aagttaatcc cgaaggtaaa tggttacttt taatcgttat	600
attccagtct tcttcattaa ccaaatacgc cagtttactg ccgtaagtag cacttccaat	660
atctggcaaa ttagagatta atgcgggttg gaatcttcta tatctgatag atccatatgc	720
tgccgccgct acatcaaacc cgcttccaat tttaccctga gcttgacaat gagcaacttg	780
tgataaatta tgaataactt ctctatatat gtctacatta ttttccaggc ccgatacaaa	840
aaaggaggcc aaagctgtag ttaaaactgt gactaaacct gccgaggagc ccagccctgt	900
tttgggaact tcttcaattc tgtgcgaatg aaaactcaat cttctgttgc cacgatgttc	960
ggtaacgctg tcctcctgag aatggtaggc atcatcagag aaaatatcaa taacgaacaa	1020
gtttctattg cagtagtcgt ccatgttagg cttaaagtag ctaaatacgt tagcgataac	1080
tttttcaatg aaagggttct tagatccgcc tatcgaaaca ggaatgaagc cagttttagg	1140
acttatatgg tacagccact ccccatcttt aaattgttta cttttcacac gcacttcaaa	1200
cttatcagac tcttgcaatg aaccgtaagg atgggctaca gcatgcattc ttgccgataa	1260

tccgactaca aatgcttcat atttcggatc taaaactaaa tatccaccag ctagtaacgc 1320

tttccctggg gcactgaagg ctctcaactc tgacat 1356

<210> 205

<211> 451

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 205

Met Ser Glu Leu Arg Ala Phe Ser Ala Pro Gly Lys Ala Leu Leu Ala
1 5 10 15

Gly Gly Tyr Leu Val Leu Asp Pro Lys Tyr Glu Ala Phe Val Val Gly
20 25 30

Leu Ser Ala Arg Met His Ala Val Ala His Pro Tyr Gly Ser Leu Gln
35 40 45

Glu Ser Asp Lys Phe Glu Val Arg Val Lys Ser Lys Gln Phe Lys Asp
50 55 60

Gly Glu Trp Leu Tyr His Ile Ser Pro Lys Thr Gly Phe Ile Pro Val
65 70 75 80

Ser Ile Gly Gly Ser Lys Asn Pro Phe Ile Glu Lys Val Ile Ala Asn
85 90 95

Val Phe Ser Tyr Phe Lys Pro Asn Met Asp Asp Tyr Cys Asn Arg Asn
100 105 110

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

Asp Ser Val Thr Glu His Arg Gly Asn Arg Arg Leu Ser Phe His Ser
130 135 140

His Arg Ile Glu Glu Val Pro Lys Thr Gly Leu Gly Ser Ser Ala Gly
145 150 155 160

Leu Val Thr Val Leu Thr Thr Ala Leu Ala Ser Phe Phe Val Ser Asp

165

170

175

Leu Glu Asn Asn Val Asp Lys Tyr Arg Glu Val Ile His Asn Leu Ser
 180 185 190

Gln Val Ala His Cys Gln Ala Gln Gly Lys Ile Gly Ser Gly Phe Asp
 195 200 205

Val Ala Ala Ala Ala Tyr Gly Ser Ile Arg Tyr Arg Arg Phe Pro Pro
 210 215 220

Ala Leu Ile Ser Asn Leu Pro Asp Ile Gly Ser Ala Thr Tyr Gly Ser
 225 230 235 240

Lys Leu Ala His Leu Val Asn Glu Glu Asp Trp Asn Ile Thr Ile Lys
 245 250 255

Ser Asn His Leu Pro Ser Gly Leu Thr Leu Trp Met Gly Asp Ile Lys
 260 265 270

Asn Gly Ser Glu Thr Val Lys Leu Val Gln Lys Val Lys Asn Trp Tyr
 275 280 285

Asp Ser His Met Pro Glu Ser Leu Lys Ile Tyr Thr Glu Leu Asp His
 290 295 300

Ala Asn Ser Arg Phe Met Asp Gly Leu Ser Lys Leu Asp Arg Leu His
 305 310 315 320

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

Asn Asp Cys Thr Cys Gln Lys Tyr Pro Glu Ile Thr Glu Val Arg Asp
 340 345 350

Ala Val Ala Thr Ile Arg Arg Ser Phe Arg Lys Ile Thr Lys Glu Ser
 355 360 365

Gly Ala Asp Ile Glu Pro Pro Val Gln Thr Ser Leu Leu Asp Asp Cys
 370 375 380

Gln Thr Leu Lys Gly Val Leu Thr Cys Leu Ile Pro Gly Ala Gly Gly
 385 390 395 400

Tyr Asp Ala Ile Ala Val Ile Ala Lys Gln Asp Val Asp Leu Arg Ala
 405 410 415

Gln Thr Ala Asp Asp Lys Arg Phe Ser Lys Val Gln Trp Leu Asp Val
 420 425 430

Thr Gln Ala Asp Trp Gly Val Arg Lys Glu Lys Asp Pro Glu Thr Tyr
 435 440 445

Leu Asp Lys
 450

<210> 206
 <211> 1332
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 206
 atgtcattac cgttcttaac ttctgcaccg ggaaagggtta ttatTTTTTgg tgaacactct 60
 gctgtgtaca acaagcctgc cgtcgtgct agtgtgtctg cgttgagaac ctacctgcta 120
 ataagcgagt catctgcacc agatactatt gaattggact tcccggacat tagctttaat 180
 cataagtggc ccatcaatga tttcaatgcc atcaccgagg atcaagtaaa ctccccaaaa 240
 ttggccaagg ctcaacaagc caccgatggc ttgtctcagg aactcgttag tcttttggat 300
 ccgttgtag ctcaactatc cgaatcctt cactaccatg cagcgTTTTg tttcctgtat 360
 atgtttgttt gcctatgccc ccatgccaag aatattaagt tttctttaaa gtctacttta 420
 cccatcgggtg ctgggttggg ctcaagcgcc tctatttctg tatcactggc cttagctatg 480
 gcctacttgg gggggttaat aggatctaag gacttggaag agctgtcaga aaacgataag 540
 catatagtga atcaatgggc cttcataggt gaaaagtgtt ttcacggtag cccttcagga 600
 atagataacg ctgtggccac ttatggtaat gccctgctat ttgaaaaaga ctacataat 660
 ggaacaataa acacaaacaa ttttaagttc ttagatgatt tcccagccat tccaatgatc 720
 ctaacctata ctagaattcc aaggtctaca aaagatcttg ttgctcgcgt tcgtgtgttg 780
 gtcaccgaga aatttcctga agttatgaag ccaattctag atgcatggg tgaatgtgcc 840

ctacaaggct tagagatcat gactaagtta agtaaagtta aaggcaccga tgacgaggct 900
 gtagaaacta ataatgaact gtatgaacaa ctattggaat tgataagaat aaatcatgga 960
 ctgcttgtct caatcgggtgt ttctcatcct ggattagaac ttattaaaaa tctgagcgat 1020
 gatttgagaa ttggctccac aaaacttacc ggtgctggtg gcggcggttg ctctttgact 1080
 ttgttacgaa gagacattac tcaagagcaa attgacagtt tcaaaaagaa attgcaagat 1140
 gattttagtt acgagacatt tgaaacagac ttgggtggga ctggctgctg tttgttaagc 1200
 gcaaaaaatt tgaataaaga tcttaaaatc aaatccctag tattccaatt atttgaaaat 1260
 aaaactacca caaagcaaca aattgacgat ctattattgc caggaaacac gaatttacca 1320
 tggacttcat aa 1332

<210> 207
 <211> 2233
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutated acetyl-CoA carboxylase (ACC1) (S659A, S1157A)
 <400> 207

Met Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr
 1 5 10 15

Glu Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe
 20 25 30

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

Phe Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile
 50 55 60

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

Trp Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala
 85 90 95

Met Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met
100 105 110

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

Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp
130 135 140

Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro
145 150 155 160

Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro
165 170 175

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

Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val
195 200 205

Asp Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp
210 215 220

Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln
225 230 235 240

Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly
245 250 255

Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile
260 265 270

Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe
275 280 285

Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu
290 295 300

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

Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile
325 330 335

Ala Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu
340 345 350

Gly Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr
355 360 365

Ser His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu
370 375 380

Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro
385 390 395 400

Ala Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser
405 410 415

Asp Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile
420 425 430

Asp Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro
435 440 445

Ile Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro
450 455 460

Asn Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe
465 470 475 480

Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly
485 490 495

Asn Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe
500 505 510

Gly Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys
515 520 525

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile
530 535 540

Lys Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly
545 550 555 560

Trp Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp
565 570 575

Pro Thr Leu Ala Val Ile Cys Gly Ala Ala Thr Lys Ala Phe Leu Ala
580 585 590

Ser Glu Glu Ala Arg His Lys Tyr Ile Glu Ser Leu Gln Lys Gly Gln
595 600 605

Val Leu Ser Lys Asp Leu Leu Gln Thr Met Phe Pro Val Asp Phe Ile
610 615 620

His Glu Gly Lys Arg Tyr Lys Phe Thr Val Ala Lys Ser Gly Asn Asp
625 630 635 640

Arg Tyr Thr Leu Phe Ile Asn Gly Ser Lys Cys Asp Ile Ile Leu Arg
645 650 655

Gln Leu Ser Asp Gly Gly Leu Leu Ile Ala Ile Gly Gly Lys Ser His
660 665 670

Thr Ile Tyr Trp Lys Glu Glu Val Ala Ala Thr Arg Leu Ser Val Asp
675 680 685

Ser Met Thr Thr Leu Leu Glu Val Glu Asn Asp Pro Thr Gln Leu Arg
690 695 700

Thr Pro Ser Pro Gly Lys Leu Val Lys Phe Leu Val Glu Asn Gly Glu
705 710 715 720

His Ile Ile Lys Gly Gln Pro Tyr Ala Glu Ile Glu Val Met Lys Met
725 730 735

Gln Met Pro Leu Val Ser Gln Glu Asn Gly Ile Val Gln Leu Leu Lys
740 745 750

Gln Pro Gly Ser Thr Ile Val Ala Gly Asp Ile Met Ala Ile Met Thr
755 760 765

Leu Asp Asp Pro Ser Lys Val Lys His Ala Leu Pro Phe Glu Gly Met
770 775 780

Leu Pro Asp Phe Gly Ser Pro Val Ile Glu Gly Thr Lys Pro Ala Tyr
785 790 795 800

Lys Phe Lys Ser Leu Val Ser Thr Leu Glu Asn Ile Leu Lys Gly Tyr
805 810 815

Asp Asn Gln Val Ile Met Asn Ala Ser Leu Gln Gln Leu Ile Glu Val
820 825 830

Leu Arg Asn Pro Lys Leu Pro Tyr Ser Glu Trp Lys Leu His Ile Ser
835 840 845

Ala Leu His Ser Arg Leu Pro Ala Lys Leu Asp Glu Gln Met Glu Glu
850 855 860

Leu Val Ala Arg Ser Leu Arg Arg Gly Ala Val Phe Pro Ala Arg Gln
865 870 875 880

Leu Ser Lys Leu Ile Asp Met Ala Val Lys Asn Pro Glu Tyr Asn Pro
885 890 895

Asp Lys Leu Leu Gly Ala Val Val Glu Pro Leu Ala Asp Ile Ala His
900 905 910

Lys Tyr Ser Asn Gly Leu Glu Ala His Glu His Ser Ile Phe Val His
915 920 925

Phe Leu Glu Glu Tyr Tyr Glu Val Glu Lys Leu Phe Asn Gly Pro Asn
930 935 940

Val Arg Glu Glu Asn Ile Ile Leu Lys Leu Arg Asp Glu Asn Pro Lys
945 950 955 960

Asp Leu Asp Lys Val Ala Leu Thr Val Leu Ser His Ser Lys Val Ser
965 970 975

Ala Lys Asn Asn Leu Ile Leu Ala Ile Leu Lys His Tyr Gln Pro Leu
980 985 990

Cys Lys Leu Ser Ser Lys Val Ser Ala Ile Phe Ser Thr Pro Leu Gln
995 1000 1005

His Ile Val Glu Leu Glu Ser Lys Ala Thr Ala Lys Val Ala Leu
1010 1015 1020

Gln Ala Arg Glu Ile Leu Ile Gln Gly Ala Leu Pro Ser Val Lys
1025 1030 1035

Glu Arg Thr Glu Gln Ile Glu His Ile Leu Lys Ser Ser Val Val
1040 1045 1050

Lys Val Ala Tyr Gly Ser Ser Asn Pro Lys Arg Ser Glu Pro Asp
1055 1060 1065

Leu Asn Ile Leu Lys Asp Leu Ile Asp Ser Asn Tyr Val Val Phe
1070 1075 1080

Asp Val Leu Leu Gln Phe Leu Thr His Gln Asp Pro Val Val Thr
1085 1090 1095

Ala Ala Ala Ala Gln Val Tyr Ile Arg Arg Ala Tyr Arg Ala Tyr
1100 1105 1110

Thr Ile Gly Asp Ile Arg Val His Glu Gly Val Thr Val Pro Ile
1115 1120 1125

Val Glu Trp Lys Phe Gln Leu Pro Ser Ala Ala Phe Ser Thr Phe
1130 1135 1140

Pro Thr Val Lys Ser Lys Met Gly Met Asn Arg Ala Val Ser Val
1145 1150 1155

Ser Asp Leu Ser Tyr Val Ala Asn Ser Gln Ser Ser Pro Leu Arg
1160 1165 1170

Glu Gly Ile Leu Met Ala Val Asp His Leu Asp Asp Val Asp Glu
1175 1180 1185

Ile Leu Ser Gln Ser Leu Glu Val Ile Pro Arg His Gln Ser Ser
1190 1195 1200

Ser Asn Gly Pro Ala Pro Asp Arg Ser Gly Ser Ser Ala Ser Leu
1205 1210 1215

Ser Asn Val Ala Asn Val Cys Val Ala Ser Thr Glu Gly Phe Glu
1220 1225 1230

Ser Glu Glu Glu Ile Leu Val Arg Leu Arg Glu Ile Leu Asp Leu
1235 1240 1245

Asn Lys Gln Glu Leu Ile Asn Ala Ser Ile Arg Arg Ile Thr Phe
1250 1255 1260

Met Phe Gly Phe Lys Asp Gly Ser Tyr Pro Lys Tyr Tyr Thr Phe
1265 1270 1275

Asn Gly Pro Asn Tyr Asn Glu Asn Glu Thr Ile Arg His Ile Glu
1280 1285 1290

Pro Ala Leu Ala Phe Gln Leu Glu Leu Gly Arg Leu Ser Asn Phe
1295 1300 1305

Asn Ile Lys Pro Ile Phe Thr Asp Asn Arg Asn Ile His Val Tyr
1310 1315 1320

Glu Ala Val Ser Lys Thr Ser Pro Leu Asp Lys Arg Phe Phe Thr
1325 1330 1335

Arg Gly Ile Ile Arg Thr Gly His Ile Arg Asp Asp Ile Ser Ile
1340 1345 1350

Gln Glu Tyr Leu Thr Ser Glu Ala Asn Arg Leu Met Ser Asp Ile
1355 1360 1365

Leu	Asp	Asn	Leu	Glu	Val	Thr	Asp	Thr	Ser	Asn	Ser	Asp	Leu	Asn
	1370					1375					1380			
His	Ile	Phe	Ile	Asn	Phe	Ile	Ala	Val	Phe	Asp	Ile	Ser	Pro	Glu
	1385					1390					1395			
Asp	Val	Glu	Ala	Ala	Phe	Gly	Gly	Phe	Leu	Glu	Arg	Phe	Gly	Lys
	1400					1405					1410			
Arg	Leu	Leu	Arg	Leu	Arg	Val	Ser	Ser	Ala	Glu	Ile	Arg	Ile	Ile
	1415					1420					1425			
Ile	Lys	Asp	Pro	Gln	Thr	Gly	Ala	Pro	Val	Pro	Leu	Arg	Ala	Leu
	1430					1435					1440			
Ile	Asn	Asn	Val	Ser	Gly	Tyr	Val	Ile	Lys	Thr	Glu	Met	Tyr	Thr
	1445					1450					1455			
Glu	Val	Lys	Asn	Ala	Lys	Gly	Glu	Trp	Val	Phe	Lys	Ser	Leu	Gly
	1460					1465					1470			
Lys	Pro	Gly	Ser	Met	His	Leu	Arg	Pro	Ile	Ala	Thr	Pro	Tyr	Pro
	1475					1480					1485			
Val	Lys	Glu	Trp	Leu	Gln	Pro	Lys	Arg	Tyr	Lys	Ala	His	Leu	Met
	1490					1495					1500			
Gly	Thr	Thr	Tyr	Val	Tyr	Asp	Phe	Pro	Glu	Leu	Phe	Arg	Gln	Ala
	1505					1510					1515			
Ser	Ser	Ser	Gln	Trp	Lys	Asn	Phe	Ser	Ala	Asp	Val	Lys	Leu	Thr
	1520					1525					1530			
Asp	Asp	Phe	Phe	Ile	Ser	Asn	Glu	Leu	Ile	Glu	Asp	Glu	Asn	Gly
	1535					1540					1545			
Glu	Leu	Thr	Glu	Val	Glu	Arg	Glu	Pro	Gly	Ala	Asn	Ala	Ile	Gly
	1550					1555					1560			
Met	Val	Ala	Phe	Lys	Ile	Thr	Val	Lys	Thr	Pro	Glu	Tyr	Pro	Arg
	1565					1570					1575			

Gly Arg Gln Phe Val Val Val Ala Asn Asp Ile Thr Phe Lys Ile
1580 1585 1590

Gly Ser Phe Gly Pro Gln Glu Asp Glu Phe Phe Asn Lys Val Thr
1595 1600 1605

Glu Tyr Ala Arg Lys Arg Gly Ile Pro Arg Ile Tyr Leu Ala Ala
1610 1615 1620

Asn Ser Gly Ala Arg Ile Gly Met Ala Glu Glu Ile Val Pro Leu
1625 1630 1635

Phe Gln Val Ala Trp Asn Asp Ala Ala Asn Pro Asp Lys Gly Phe
1640 1645 1650

Gln Tyr Leu Tyr Leu Thr Ser Glu Gly Met Glu Thr Leu Lys Lys
1655 1660 1665

Phe Asp Lys Glu Asn Ser Val Leu Thr Glu Arg Thr Val Ile Asn
1670 1675 1680

Gly Glu Glu Arg Phe Val Ile Lys Thr Ile Ile Gly Ser Glu Asp
1685 1690 1695

Gly Leu Gly Val Glu Cys Leu Arg Gly Ser Gly Leu Ile Ala Gly
1700 1705 1710

Ala Thr Ser Arg Ala Tyr His Asp Ile Phe Thr Ile Thr Leu Val
1715 1720 1725

Thr Cys Arg Ser Val Gly Ile Gly Ala Tyr Leu Val Arg Leu Gly
1730 1735 1740

Gln Arg Ala Ile Gln Val Glu Gly Gln Pro Ile Ile Leu Thr Gly
1745 1750 1755

Ala Pro Ala Ile Asn Lys Met Leu Gly Arg Glu Val Tyr Thr Ser
1760 1765 1770

Asn Leu Gln Leu Gly Gly Thr Gln Ile Met Tyr Asn Asn Gly Val
1775 1780 1785

Ser His Leu Thr Ala Val Asp Asp Leu Ala Gly Val Glu Lys Ile
1790 1795 1800

Val Glu Trp Met Ser Tyr Val Pro Ala Lys Arg Asn Met Pro Val
1805 1810 1815

Pro Ile Leu Glu Thr Lys Asp Thr Trp Asp Arg Pro Val Asp Phe
1820 1825 1830

Thr Pro Thr Asn Asp Glu Thr Tyr Asp Val Arg Trp Met Ile Glu
1835 1840 1845

Gly Arg Glu Thr Glu Ser Gly Phe Glu Tyr Gly Leu Phe Asp Lys
1850 1855 1860

Gly Ser Phe Phe Glu Thr Leu Ser Gly Trp Ala Lys Gly Val Val
1865 1870 1875

Val Gly Arg Ala Arg Leu Gly Gly Ile Pro Leu Gly Val Ile Gly
1880 1885 1890

Val Glu Thr Arg Thr Val Glu Asn Leu Ile Pro Ala Asp Pro Ala
1895 1900 1905

Asn Pro Asn Ser Ala Glu Thr Leu Ile Gln Glu Pro Gly Gln Val
1910 1915 1920

Trp His Pro Asn Ser Ala Phe Lys Thr Ala Gln Ala Ile Asn Asp
1925 1930 1935

Phe Asn Asn Gly Glu Gln Leu Pro Met Met Ile Leu Ala Asn Trp
1940 1945 1950

Arg Gly Phe Ser Gly Gly Gln Arg Asp Met Phe Asn Glu Val Leu
1955 1960 1965

Lys Tyr Gly Ser Phe Ile Val Asp Ala Leu Val Asp Tyr Lys Gln
1970 1975 1980

Pro 1985	Ile	Ile	Ile	Tyr	Ile	Pro 1990	Pro	Thr	Gly	Glu	Leu 1995	Arg	Gly	Gly
Ser 2000	Trp	Val	Val	Val	Asp	Pro 2005	Thr	Ile	Asn	Ala	Asp 2010	Gln	Met	Glu
Met 2015	Tyr	Ala	Asp	Val	Asn	Ala 2020	Arg	Ala	Gly	Val	Leu 2025	Glu	Pro	Gln
Gly 2030	Met	Val	Gly	Ile	Lys	Phe 2035	Arg	Arg	Glu	Lys	Leu 2040	Leu	Asp	Thr
Met 2045	Asn	Arg	Leu	Asp	Asp	Lys 2050	Tyr	Arg	Glu	Leu	Arg 2055	Ser	Gln	Leu
Ser 2060	Asn	Lys	Ser	Leu	Ala	Pro 2065	Glu	Val	His	Gln	Gln 2070	Ile	Ser	Lys
Gln 2075	Leu	Ala	Asp	Arg	Glu	Arg 2080	Glu	Leu	Leu	Pro	Ile 2085	Tyr	Gly	Gln
Ile 2090	Ser	Leu	Gln	Phe	Ala	Asp 2095	Leu	His	Asp	Arg	Ser 2100	Ser	Arg	Met
Val 2105	Ala	Lys	Gly	Val	Ile	Ser 2110	Lys	Glu	Leu	Glu	Trp 2115	Thr	Glu	Ala
Arg 2120	Arg	Phe	Phe	Phe	Trp	Arg 2125	Leu	Arg	Arg	Arg	Leu 2130	Asn	Glu	Glu
Tyr 2135	Leu	Ile	Lys	Arg	Leu	Ser 2140	His	Gln	Val	Gly	Glu 2145	Ala	Ser	Arg
Leu 2150	Glu	Lys	Ile	Ala	Arg	Ile 2155	Arg	Ser	Trp	Tyr	Pro 2160	Ala	Ser	Val
Asp 2165	His	Glu	Asp	Asp	Arg	Gln 2170	Val	Ala	Thr	Trp	Ile 2175	Glu	Glu	Asn

Tyr Lys Thr Leu Asp Asp Lys Leu Lys Gly Leu Lys Leu Glu Ser
2180 2185 2190

Phe Ala Gln Asp Leu Ala Lys Lys Ile Arg Ser Asp His Asp Asn
2195 2200 2205

Ala Ile Asp Gly Leu Ser Glu Val Ile Lys Met Leu Ser Thr Asp
2210 2215 2220

Asp Lys Glu Lys Leu Leu Lys Thr Leu Lys
2225 2230

<210> 208
<211> 524
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated 3-hydroxy-3-methyl-glutaryl-CoA reductase (Sc_tHMG1)

<400> 208

Met Gln Leu Val Lys Thr Glu Val Thr Lys Lys Ser Phe Thr Ala Pro
1 5 10 15

Val Gln Lys Ala Ser Thr Pro Val Leu Thr Asn Lys Thr Val Ile Ser
20 25 30

Gly Ser Lys Val Lys Ser Leu Ser Ser Ala Gln Ser Ser Ser Ser Gly
35 40 45

Pro Ser Ser Ser Ser Glu Glu Asp Asp Ser Arg Asp Ile Glu Ser Leu
50 55 60

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

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

His Gly Lys Leu Pro Leu Tyr Ala Leu Glu Lys Lys Leu Gly Asp Thr
100 105 110

Thr Arg Ala Val Ala Val Arg Arg Lys Ala Leu Ser Ile Leu Ala Glu
115 120 125

Ala Pro Val Leu Ala Ser Asp Arg Leu Pro Tyr Lys Asn Tyr Asp Tyr
130 135 140

Asp Arg Val Phe Gly Ala Cys Cys Glu Asn Val Ile Gly Tyr Met Pro
145 150 155 160

Leu Pro Val Gly Val Ile Gly Pro Leu Val Ile Asp Gly Thr Ser Tyr
165 170 175

His Ile Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Ala Met
180 185 190

Arg Gly Cys Lys Ala Ile Asn Ala Gly Gly Gly Ala Thr Thr Val Leu
195 200 205

Thr Lys Asp Gly Met Thr Arg Gly Pro Val Val Arg Phe Pro Thr Leu
210 215 220

Lys Arg Ser Gly Ala Cys Lys Ile Trp Leu Asp Ser Glu Glu Gly Gln
225 230 235 240

Asn Ala Ile Lys Lys Ala Phe Asn Ser Thr Ser Arg Phe Ala Arg Leu
245 250 255

Gln His Ile Gln Thr Cys Leu Ala Gly Asp Leu Leu Phe Met Arg Phe
260 265 270

Arg Thr Thr Thr Gly Asp Ala Met Gly Met Asn Met Ile Ser Lys Gly
275 280 285

Val Glu Tyr Ser Leu Lys Gln Met Val Glu Glu Tyr Gly Trp Glu Asp
290 295 300

Met Glu Val Val Ser Val Ser Gly Asn Tyr Cys Thr Asp Lys Lys Pro
305 310 315 320

Ala Ala Ile Asn Trp Ile Glu Gly Arg Gly Lys Ser Val Val Ala Glu
325 330 335

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

Ser Ala Leu Val Glu Leu Asn Ile Ala Lys Asn Leu Val Gly Ser Ala
355 360 365

Met Ala Gly Ser Val Gly Gly Phe Asn Ala His Ala Ala Asn Leu Val
370 375 380

Thr Ala Val Phe Leu Ala Leu Gly Gln Asp Pro Ala Gln Asn Val Glu
385 390 395 400

Ser Ser Asn Cys Ile Thr Leu Met Lys Glu Val Asp Gly Asp Leu Arg
405 410 415

Ile Ser Val Ser Met Pro Ser Ile Glu Val Gly Thr Ile Gly Gly Gly
420 425 430

Thr Val Leu Glu Pro Gln Gly Ala Met Leu Asp Leu Leu Gly Val Arg
435 440 445

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

Ile Val Ala Cys Ala Val Leu Ala Gly Glu Leu Ser Leu Cys Ala Ala
465 470 475 480

Leu Ala Ala Gly His Leu Val Gln Ser His Met Thr His Asn Arg Lys
485 490 495

Pro Ala Glu Pro Thr Lys Pro Asn Asn Leu Asp Ala Thr Asp Ile Asn
500 505 510

Arg Leu Lys Asp Gly Ser Val Thr Cys Ile Lys Ser
515 520

<210> 209
<211> 1197
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 209
atgtctcaga acgtttacat tgtatcgact gccagaaccc caattgggttc attccagggt 60
tctctatcct ccaagacagc agtggaattg ggtgctgttg ctttaaaagg cgccttggct 120
aaggttccag aattggatgc atccaaggat tttgacgaaa ttatTTTTtg taacgttctt 180
tctgccaatt tgggccaagc tccggccaga caagttgctt tggctgccgg tttgagtaat 240
catatcgttg caagcacagt taacaaggtc tgtgcatccg ctatgaaggc aatcattttg 300
ggtgctcaat ccatcaaagtg tggtaatgct gatgttgtcg tagctgggtg ttgtgaatct 360
atgactaacg caccatacta catgccagca gcccgTgcgg gtgccaaatt tggccaaact 420
gttcttgttg atggtgtcga aagagatggg ttgaacgatg cgtacgatgg tctagccatg 480
ggtgtacacg cagaaaagtg tgcccgtgat tgggatatta ctagagaaca acaagacaat 540
tttgccatcg aatcctacca aaaatctcaa aaatctcaaa aggaaggtaa attcgacaat 600
gaaattgtac ctgttaccat taagggattt agaggtaagc ctgatactca agtcacgaag 660
gacgaggaac ctgctagatt acacgttgaa aaattgagat ctgcaaggac tgTTTTccaa 720
aaagaaaacg gtactgttac tgccgctaac gcttctccaa tcaacgatgg tgctgcagcc 780
gtcatcttgg tttccgaaaa agttttgaag gaaaagaatt tgaagccttt ggctattatc 840
aaaggttggg gtgaggccgc tcatcaacca gctgatttta catgggctcc atctcttgca 900
gttccaaagg ctttgaaaca tgctggcatc gaagacatca attctgttga ttactttgaa 960
ttcaatgaag ctttttcggt tgtcggtttg gtgaacacta agattttgaa gctagaccga 1020
tctaaggtta atgtatatgg tgggtgctgtt gctctaggtc acccattggg ttgttctggt 1080
gctagagtgg ttgttacact gctatccatc ttacagcaag aaggaggtaa gatcggtgtt 1140
gccgccattt gtaatggtgg tgggtggtgct tcctctattg tcattgaaaa gatatga 1197

<210> 210
<211> 867
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial truncated geranyl pyrophosphate olivetolic acid
geranyltransferase CsPT4_t112

<400> 210
atgtcttacg ttgtcaaggg tatgatctct attgcttgtg gtttgttcgg tagagaattg 60

tttaacaaca gacacttggt ctcttggggg ttgatgtgga aagctttctt cgctttggtc	120
ccaatthttgt ctttcaatth cttcgccgcc atcatgaacc aaatctacga tgttgatata	180
gaccgtatca acaagccaga cttaccttta gtttccgggtg aaatgtccat tgaaactgct	240
tggatcttgt ctatcattgt tgccttgact ggtttaattg ttactattaa gttgaagtcc	300
gctccattgt ttgtcttcat ctacatcttc ggtatcttcg ctggtttcgc ttactccgtc	360
ccacctatta gatggaaaca atatccttht accaatthct tgatcactat ttccttcat	420
gttggtttgg ctttcacttc ttactctgcc accacttctg ctttaggttt gcctthcggt	480
tggcgtcctg ccttctctth cattattgct ttcatgactg tcatgggtat gactattgcc	540
tttgctaaag acatthctga tatcgaaggt gatgctaagt acggtgtctc taccgttgct	600
accaagttag gtgctagaaa tatgacttht gttgtthctg gtgtcttatt gttgaactac	660
ttggthtcta tctctattgg tatcatttgg ccacaagtht tcaagtctaa cattatgata	720
ttgtctcatg ctatthtggc thtctgtthg atctthcaaa ctcgtgaatt agccttagcc	780
aattatgcct ctgccccatc ccgtcaatth ttcgaattca tctggthgtt atactatgcc	840
gaatacttcg thtacgtctt catttaa	867

<210> 211
 <211> 288
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Truncated geranyl pyrophosphate olivetolic acid
 geranyltransferase CsPT4_t112

<400> 211

Met	Ser	Tyr	Val	Val	Lys	Gly	Met	Ile	Ser	Ile	Ala	Cys	Gly	Leu	Phe
1				5				10						15	

Gly	Arg	Glu	Leu	Phe	Asn	Asn	Arg	His	Leu	Phe	Ser	Trp	Gly	Leu	Met
		20					25					30			

Trp	Lys	Ala	Phe	Phe	Ala	Leu	Val	Pro	Ile	Leu	Ser	Phe	Asn	Phe	Phe
		35				40					45				

Ala	Ala	Ile	Met	Asn	Gln	Ile	Tyr	Asp	Val	Asp	Ile	Asp	Arg	Ile	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50

55

60

Lys Pro Asp Leu Pro Leu Val Ser Gly Glu Met Ser Ile Glu Thr Ala
 65 70 75 80

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

Lys Leu Lys Ser Ala Pro Leu Phe Val Phe Ile Tyr Ile Phe Gly Ile
 100 105 110

Phe Ala Gly Phe Ala Tyr Ser Val Pro Pro Ile Arg Trp Lys Gln Tyr
 115 120 125

Pro Phe Thr Asn Phe Leu Ile Thr Ile Ser Ser His Val Gly Leu Ala
 130 135 140

Phe Thr Ser Tyr Ser Ala Thr Thr Ser Ala Leu Gly Leu Pro Phe Val
 145 150 155 160

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

Met Thr Ile Ala Phe Ala Lys Asp Ile Ser Asp Ile Glu Gly Asp Ala
 180 185 190

Lys Tyr Gly Val Ser Thr Val Ala Thr Lys Leu Gly Ala Arg Asn Met
 195 200 205

Thr Phe Val Val Ser Gly Val Leu Leu Leu Asn Tyr Leu Val Ser Ile
 210 215 220

Ser Ile Gly Ile Ile Trp Pro Gln Val Phe Lys Ser Asn Ile Met Ile
 225 230 235 240

Leu Ser His Ala Ile Leu Ala Phe Cys Leu Ile Phe Gln Thr Arg Glu
 245 250 255

Leu Ala Leu Ala Asn Tyr Ala Ser Ala Pro Ser Arg Gln Phe Phe Glu
 260 265 270

Phe	Ile	Trp	Leu	Leu	Tyr	Tyr	Ala	Glu	Tyr	Phe	Val	Tyr	Val	Phe	Ile
		275					280				285				

<210> 212
 <211> 810
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial truncated geranyl pyrophosphate olivetolic acid
 geranyltransferase CsPT4_t131 nucleotide sequence

<400> 212
 atgtctaaca acagacactt gttctcttgg ggtttgatgt ggaaagcttt cttcgctttg 60
 gtcccaattt tgtctttcaa tttcttcgcc gccatcatga accaaatcta cgatgttgat 120
 atcgaccgta tcaacaagcc agacttacct ttagtttccg gtgaaatgtc cattgaaact 180
 gcttggatct tgtctatcat tgttgccttg actggtttaa ttgttactat taagttgaag 240
 tccgctccat tgtttgtctt catctacatc ttcggtatct tcgctggttt cgcttactcc 300
 gtcccaccta ttagatggaa acaatatcct tttaccaatt tcttgatcac tatttcctct 360
 catgttgggtt tggctttcac ttcttactct gccaccactt ctgctttagg tttgcctttc 420
 gtttggcgtc ctgccttctc tttcattatt gctttcatga ctgtcatggg tatgactatt 480
 gcctttgcta aagacatttc tgatatcgaa ggtgatgcta agtacgggtgt ctctaccgtt 540
 gttaccaagt taggtgctag aaatatgact tttgttggtt ctggtgtctt attgttgaac 600
 tacttgggtt ctatctctat tgggtatcatt tggccacaag ttttcaagtc taacattatg 660
 atcttgtctc atgctatctt ggctttctgt ttgatctttc aaactcgtga attagcctta 720
 gccaatatg cctctgcccc atcccgtaa tttttcgaat tcatctgggt gttatactat 780
 gccgaatact tcgtttacgt cttcatttaa 810

<210> 213
 <211> 269
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Truncated geranyl pyrophosphate olivetolic acid
 geranyltransferase CsPT4_t131

<400> 213

Met Ser Asn Asn Arg His Leu Phe Ser Trp Gly Leu Met Trp Lys Ala
1 5 10 15

Phe Phe Ala Leu Val Pro Ile Leu Ser Phe Asn Phe Phe Ala Ala Ile
20 25 30

Met Asn Gln Ile Tyr Asp Val Asp Ile Asp Arg Ile Asn Lys Pro Asp
35 40 45

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

Ser Ile Ile Val Ala Leu Thr Gly Leu Ile Val Thr Ile Lys Leu Lys
65 70 75 80

Ser Ala Pro Leu Phe Val Phe Ile Tyr Ile Phe Gly Ile Phe Ala Gly
85 90 95

Phe Ala Tyr Ser Val Pro Pro Ile Arg Trp Lys Gln Tyr Pro Phe Thr
100 105 110

Asn Phe Leu Ile Thr Ile Ser Ser His Val Gly Leu Ala Phe Thr Ser
115 120 125

Tyr Ser Ala Thr Thr Ser Ala Leu Gly Leu Pro Phe Val Trp Arg Pro
130 135 140

Ala Phe Ser Phe Ile Ile Ala Phe Met Thr Val Met Gly Met Thr Ile
145 150 155 160

Ala Phe Ala Lys Asp Ile Ser Asp Ile Glu Gly Asp Ala Lys Tyr Gly
165 170 175

Val Ser Thr Val Ala Thr Lys Leu Gly Ala Arg Asn Met Thr Phe Val
180 185 190

Val Ser Gly Val Leu Leu Leu Asn Tyr Leu Val Ser Ile Ser Ile Gly
195 200 205

Ile Ile Trp Pro Gln Val Phe Lys Ser Asn Ile Met Ile Leu Ser His

210

215

220

Ala Ile Leu Ala Phe Cys Leu Ile Phe Gln Thr Arg Glu Leu Ala Leu
 225 230 235 240

Ala Asn Tyr Ala Ser Ala Pro Ser Arg Gln Phe Phe Glu Phe Ile Trp
 245 250 255

Leu Leu Tyr Tyr Ala Glu Tyr Phe Val Tyr Val Phe Ile
 260 265

<210> 214

<211> 777

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial truncated geranyl pyrophosphate olivetolic acid
 geranyltransferase CsPT4_t142 nucleotide sequence

<400> 214

atgtcttgga aagctttctt cgctttggtc ccaattttgt ctttcaattt cttcgccgcc 60
 atcatgaacc aaatctacga tgttgatata gaccgtatca acaagccaga cttaccttta 120
 gtttccggtg aaatgtccat tgaaactgct tggatcttgt ctatcattgt tgccttgact 180
 ggtttaattg ttactattaa gttgaagtcc gctccattgt ttgtcttcat ctacatcttc 240
 ggtatcttcg ctggtttcgc ttactccgtc ccacctatta gatggaaaca atatcctttt 300
 accaatttct tgatcactat ttcctctcat gttggtttgg ctttcacttc ttactctgcc 360
 accacttctg ctttaggttt gcctttcgtt tggcgtcctg ctttctcttt cattattgct 420
 ttcattgactg tcatgggtat gactattgcc tttgctaaag acatttctga tatcgaaggt 480
 gatgctaagt acgggtgtctc taccgttgct accaagttag gtgctagaaa tatgactttt 540
 gttgtttctg gtgtcttatt gttgaactac ttggtttcta tctctattgg tatcatttgg 600
 ccacaagttt tcaagtctaa cattatgatc ttgtctcatg ctattttggc tttctgtttg 660
 atctttcaaa ctcgtgaatt agccttagcc aattatgcct ctgccccatc ccgtcaattt 720
 ttcgaattca tctggttggt atactatgcc gaatacttcg tttacgtctt catttaa 777

<210> 215

<211> 258

<212> PRT
<213> Artificial Sequence

<220>

<223> Truncated geranyl pyrophosphate olivetolic acid
geranyltransferase CsPT4_t142

<400> 215

Met Ser Trp Lys Ala Phe Phe Ala Leu Val Pro Ile Leu Ser Phe Asn
1 5 10 15

Phe Phe Ala Ala Ile Met Asn Gln Ile Tyr Asp Val Asp Ile Asp Arg
20 25 30

Ile Asn Lys Pro Asp Leu Pro Leu Val Ser Gly Glu Met Ser Ile Glu
35 40 45

Thr Ala Trp Ile Leu Ser Ile Ile Val Ala Leu Thr Gly Leu Ile Val
50 55 60

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

Gly Ile Phe Ala Gly Phe Ala Tyr Ser Val Pro Pro Ile Arg Trp Lys
85 90 95

Gln Tyr Pro Phe Thr Asn Phe Leu Ile Thr Ile Ser Ser His Val Gly
100 105 110

Leu Ala Phe Thr Ser Tyr Ser Ala Thr Thr Ser Ala Leu Gly Leu Pro
115 120 125

Phe Val Trp Arg Pro Ala Phe Ser Phe Ile Ile Ala Phe Met Thr Val
130 135 140

Met Gly Met Thr Ile Ala Phe Ala Lys Asp Ile Ser Asp Ile Glu Gly
145 150 155 160

Asp Ala Lys Tyr Gly Val Ser Thr Val Ala Thr Lys Leu Gly Ala Arg
165 170 175

Asn Met Thr Phe Val Val Ser Gly Val Leu Leu Leu Asn Tyr Leu Val

180

185

190

Ser Ile Ser Ile Gly Ile Ile Trp Pro Gln Val Phe Lys Ser Asn Ile
 195 200 205

Met Ile Leu Ser His Ala Ile Leu Ala Phe Cys Leu Ile Phe Gln Thr
 210 215 220

Arg Glu Leu Ala Leu Ala Asn Tyr Ala Ser Ala Pro Ser Arg Gln Phe
 225 230 235 240

Phe Glu Phe Ile Trp Leu Leu Tyr Tyr Ala Glu Tyr Phe Val Tyr Val
 245 250 255

Phe Ile

<210> 216
 <211> 705
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial truncated geranyl pyrophosphate olivetolic acid
 geranyltransferase CsPT4_t166 nucleotide sequence

<400> 216
 atgtctgatg ttgatatcga ccgtatcaac aagccagact tacctttagt ttccggtgaa 60
 atgtccattg aaactgcttg gatcttgtct atcattgttg ccttgactgg ttttaattggt 120
 actattaagt tgaagtccgc tccattgttt gtcttcatct acatcttcgg tatcttcgct 180
 ggtttcgctt actccgtccc acctattaga tggaacaat atccttttac caatttcttg 240
 atcactatct cctctcatgt tggtttggct ttcacttctt actctgccac cacttctgct 300
 ttaggtttgc ctttcgttg gcgtcctgcc ttctctttca ttattgcttt catgactgtc 360
 atgggtatga ctattgcctt tgctaaagac atttctgata tcgaaggatga tgctaagtac 420
 ggtgtctcta ccgttgctac caagttaggt gctagaaata tgacttttgt tgtttctggt 480
 gtcttattgt tgaactactt ggtttctatc tctattggta tcatttggcc acaagttttc 540
 aagtctaaca ttatgatctt gtctcatgct attttggctt tctgtttgat ctttcaaact 600
 cgtgaattag ccttagccaa ttatgcctct gccccatccc gtcaattttt cgaattcatc 660

tggttggttat actatgccga atacttcgtt tacgtcttca tttaa

705

<210> 217

<211> 234

<212> PRT

<213> Artificial Sequence

<220>

<223> Truncated geranyl pyrophosphate olivetolic acid
geranyltransferase CsPT4_t166

<400> 217

Met Ser Asp Val Asp Ile Asp Arg Ile Asn Lys Pro Asp Leu Pro Leu
1 5 10 15

Val Ser Gly Glu Met Ser Ile Glu Thr Ala Trp Ile Leu Ser Ile Ile
20 25 30

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

Leu Phe Val Phe Ile Tyr Ile Phe Gly Ile Phe Ala Gly Phe Ala Tyr
50 55 60

Ser Val Pro Pro Ile Arg Trp Lys Gln Tyr Pro Phe Thr Asn Phe Leu
65 70 75 80

Ile Thr Ile Ser Ser His Val Gly Leu Ala Phe Thr Ser Tyr Ser Ala
85 90 95

Thr Thr Ser Ala Leu Gly Leu Pro Phe Val Trp Arg Pro Ala Phe Ser
100 105 110

Phe Ile Ile Ala Phe Met Thr Val Met Gly Met Thr Ile Ala Phe Ala
115 120 125

Lys Asp Ile Ser Asp Ile Glu Gly Asp Ala Lys Tyr Gly Val Ser Thr
130 135 140

Val Ala Thr Lys Leu Gly Ala Arg Asn Met Thr Phe Val Val Ser Gly
145 150 155 160

Val Leu Leu Leu Asn Tyr Leu Val Ser Ile Ser Ile Gly Ile Ile Trp
165 170 175

Pro Gln Val Phe Lys Ser Asn Ile Met Ile Leu Ser His Ala Ile Leu
180 185 190

Ala Phe Cys Leu Ile Phe Gln Thr Arg Glu Leu Ala Leu Ala Asn Tyr
195 200 205

Ala Ser Ala Pro Ser Arg Gln Phe Phe Glu Phe Ile Trp Leu Leu Tyr
210 215 220

Tyr Ala Glu Tyr Phe Val Tyr Val Phe Ile
225 230

<210> 218
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial truncated geranyl pyrophosphate olivetolic acid
geranyltransferase CsPT4_t186 nucleotide sequence

<400> 218
atgtctattg aaactgcttg gatcttgtct atcattgttg ccttgactgg ttttaattggt 60
actattaagt tgaagtccgc tccattgttt gtcttcatct acatcttcgg tatcttcgct 120
ggtttcgctt actccgtccc acctattaga tggaacaat atccttttac caatttcttg 180
atcactatth cctctcatgt tggtttggct ttcacttctt actctgccac cacttctgct 240
ttaggtttgc ctttcgtttg gcgtcctgcc ttctctttca ttattgcttt catgactgtc 300
atgggtatga ctattgcctt tgctaaagac atttctgata tcgaaggtga tgctaagtac 360
ggtgtctcta ccgttgctac caagttaggt gctagaaata tgacttttgt tgtttctggt 420
gtcttattgt tgaactactt ggtttctatc tctattggta tcatttggcc acaagttttc 480
aagtctaaca ttatgatctt gtctcatgct attttggctt tctgtttgat ctttcaaact 540
cgtgaattag ccttagccaa ttatgcctct gccccatccc gtcaatthtt cgaattcatc 600
tggttggtat actatgccga atacttcggt tacgtcttca tttaa 645

<210> 219
<211> 214
<212> PRT
<213> Artificial Sequence

<220>

<223> Truncated geranyl pyrophosphate olivetolic acid
geranyltransferase CsPT4_t186

<400> 219

Met Ser Ile Glu Thr Ala Trp Ile Leu Ser Ile Ile Val Ala Leu Thr
1 5 10 15

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

Ile Tyr Ile Phe Gly Ile Phe Ala Gly Phe Ala Tyr Ser Val Pro Pro
35 40 45

Ile Arg Trp Lys Gln Tyr Pro Phe Thr Asn Phe Leu Ile Thr Ile Ser
50 55 60

Ser His Val Gly Leu Ala Phe Thr Ser Tyr Ser Ala Thr Thr Ser Ala
65 70 75 80

Leu Gly Leu Pro Phe Val Trp Arg Pro Ala Phe Ser Phe Ile Ile Ala
85 90 95

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

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

Leu Gly Ala Arg Asn Met Thr Phe Val Val Ser Gly Val Leu Leu Leu
130 135 140

Asn Tyr Leu Val Ser Ile Ser Ile Gly Ile Ile Trp Pro Gln Val Phe
145 150 155 160

Lys Ser Asn Ile Met Ile Leu Ser His Ala Ile Leu Ala Phe Cys Leu
165 170 175

Ile Phe Gln Thr Arg Glu Leu Ala Leu Ala Asn Tyr Ala Ser Ala Pro
180 185 190

Ser Arg Gln Phe Phe Glu Phe Ile Trp Leu Leu Tyr Tyr Ala Glu Tyr
195 200 205

Phe Val Tyr Val Phe Ile
210

<210> 220
<211> 1188
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial geranyl pyrophosphate olivetolic acid
geranyltransferase CsGOT (CsPT1) nucleotide sequence

<400> 220
atggggtttat cttccgtttg tacttttttct ttccaaacta actaccacac tttgttaaatt 60
ccacacaaca acaaccctaa aacctccttg ttatgtttaca gacacccaaa gacccttatt 120
aaatactcct acaacaactt cccatccaaa cactgctcca ctaagtcctt tcacttgcaa 180
aacaagtgtt ctgaatcctt gtccattgcc aagaactcta ttcgtgccgc tactactaac 240
caaactgagc cacctgaatc cgataaccac tccgtcgcca ccaagatcctt gaatttttgg 300
aaagcttgct ggaaattgca aagaccatac actattattg ctttcacttc ctgtgcttgt 360
ggttttattcg gtaaggaatt attgcataac accaacttga tttcttggtc cttaatgttc 420
aaagccttct tcttttttagt tgccatttta tgtattgctt ctttcactac tactattaat 480
caaatttacg atttgacat tgacagaatc aataagcctg acttgccatt agcttccggt 540
gaaatttctg ttaacactgc ttggatcatg tccatcattg tcgctttgtt cggtttaatt 600
atcaccatca aaatgaaggg tggtcctttg tacatcttcg gttattgctt cggtattttc 660
ggtggtattg tctactctgt cccaccattc agatggaagc aaaacccatc cactgccttt 720
ttgttgaatt tcttggtca catcattacc aattttactt tctactatgc ctcccgtgct 780
gctttagggtt tgccttttga gttacgtcca tccttcactt ttttattggc ttttatgaag 840
tccatgggtt ctgcttttagc cttaattaag gacgcctctg acgttgaagg tgatactaag 900
ttcggtatct ctacttttagc ctctaagtac ggttctcgta acttgacctt gttctgttct 960

ggattgtct tgtgtctta cgtcgccgct attttggccg gtatcatctg gccacaagct	1020
ttcaactcta acgttatggt gttgtctcat gctatcttag ctttctgggt gatcttacia	1080
accagagact tcgctttgac taactacgac ccagaagccg gtcgtagatt ctacgaattc	1140
atgtggaaat tgtactacgc cgagtacttg gtctacgttt tcatttag	1188

<210> 221
 <211> 972
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial truncated geranyl pyrophosphate olivetolic acid
 geranyltransferase CsPT4t nucleotide sequence

<400> 221	
atgtctgctg gctctgacca aattgaaggt tccccgcatac acgaatcaga taatagtatt	60
gccacaaaga tcttaaaactt tgggcataca tgttggaat tacaaaggcc ctacgtcgtc	120
aaaggaatga taagcatcgc ttgcggtctg ttcggaaggg aattatttaa caataggcat	180
ctattcagct ggggggtaat gtggaaagct ttcttcgcgt tagtgccaat cctaagcttt	240
aactttttcg ccgcatcat gaaccagatt tatgatgttg atatcgacag gataaataag	300
ccagatcttc cattggatc cggtgaaatg tcaatagaaa ctgcatggat attatctatt	360
atcgttgcgc tgaccggact gatagtaaca atcaaattga aatctgcacc cctgtttgtt	420
tttatatata tatttggtat tttcgctgga ttcgcttact cagtgccacc tatcaggtgg	480
aagcagtacc cattcacgaa ttttctgatc acgatctcta gccacgtcgg gttagcgttc	540
acatcttact ctgcaaccac gtagtccttg gggcttcctt tcgtctggcg tccagctttt	600
agttttatca ttgcctttat gaccgtaatg ggaatgacga tcgcattcgc aaaggacatt	660
tctgacatag aggggggatgc aaaatacggg gtctccactg tggcgacaaa attaggagct	720
aggaatatga ctttcgtggt gtccggtgta ttattactaa attatctggt atctataagt	780
atcggcacat tatggccgca agtgttttaa tccaacatta tgatactgag tcatgctatt	840
ttggcttttt gtctgatttt tcagacgcgt gagttggcgc ttgcaaaacta tgcctctgcg	900
cccagcaggc agttttttga attcatatgg ttattgtact atgccgagta tttcgtctac	960
gtatttattt aa	972

<210> 222
<211> 969
<212> DNA
<213> Artificial Sequence

<220>

<223> Artificial truncated geranyl pyrophosphate olivetolic acid
geranyltransferase CsGOT_t75 (CsPT1_t75) nucleotide sequence

<400> 222
atgtctgccg ctactactaa ccaaactgag ccacctgaat ccgataacca ctccgtcgcc 60
accaagatct tgaatthttgg taaagcttgc tggaaattgc aaagaccata cactattatt 120
gctttcactt cctgtgcttg tggthttattc ggtaaggaat tattgcataa caccaacttg 180
atttcttggt ccttaatgtht caaagccttc thtthtttag ttgccatttht atgtattgct 240
thtthtacta ctactattaa tcaaatttht gattthgcaca ttgacagaat caataagcct 300
gacttgccat tagctthccgg tgaattthtct gthtaactg cthtgatcat gtccatcatt 360
gtcgctthtg thcggtthaat tatcaccatc aaatgaagg gtggtccttht gtacatcttc 420
ggttattgct thcggtatttht cggtggtatt gtctactctg thccaccatt cagatggaag 480
caaaacccat ccactgcctt thtgttgaat thtctggctc acatcattac caattthtact 540
thtctactatg cthccccgtgc thgctthtaggt thgcctthttg agthtacgtcc atcctthtact 600
thtthtattgg cththtatgaa gtccatgggt thtgctthtag cthtaattaa ggacgcctct 660
gacgttgaag gtgatactaa gthtcggtatc thtactthtag cthtctaagta cggtthtctgt 720
aacttgacct thgtthgttc thggtattgtc thgtthgtctt acgtcgccgc thtthttggcc 780
ggtatcatct ggccacaagc thtcaactct aacgttatgt thgtthgtctca thgtatctta 840
gctthtctgggt thgatcttaca aaccagagac thtcgctthga thtaactacga cccagaagcc 900
ggtcgtagat thtacgaatt catgtggaaa thgtactacg ccgagtactt ggtctacgtt 960
thcatttag 969

<210> 223
<211> 322
<212> PRT
<213> Artificial Sequence

<220>

<223> Truncated geranyl pyrophosphate olivetolic acid
geranyltransferase CsGOT_t75 (CsPT1_t75)

<400> 223

Met Ser Ala Ala Thr Thr Asn Gln Thr Glu Pro Pro Glu Ser Asp Asn
1 5 10 15

His Ser Val Ala Thr Lys Ile Leu Asn Phe Gly Lys Ala Cys Trp Lys
20 25 30

Leu Gln Arg Pro Tyr Thr Ile Ile Ala Phe Thr Ser Cys Ala Cys Gly
35 40 45

Leu Phe Gly Lys Glu Leu Leu His Asn Thr Asn Leu Ile Ser Trp Ser
50 55 60

Leu Met Phe Lys Ala Phe Phe Phe Leu Val Ala Ile Leu Cys Ile Ala
65 70 75 80

Ser Phe Thr Thr Thr Ile Asn Gln Ile Tyr Asp Leu His Ile Asp Arg
85 90 95

Ile Asn Lys Pro Asp Leu Pro Leu Ala Ser Gly Glu Ile Ser Val Asn
100 105 110

Thr Ala Trp Ile Met Ser Ile Ile Val Ala Leu Phe Gly Leu Ile Ile
115 120 125

Thr Ile Lys Met Lys Gly Gly Pro Leu Tyr Ile Phe Gly Tyr Cys Phe
130 135 140

Gly Ile Phe Gly Gly Ile Val Tyr Ser Val Pro Pro Phe Arg Trp Lys
145 150 155 160

Gln Asn Pro Ser Thr Ala Phe Leu Leu Asn Phe Leu Ala His Ile Ile
165 170 175

Thr Asn Phe Thr Phe Tyr Tyr Ala Ser Arg Ala Ala Leu Gly Leu Pro
180 185 190

Phe Glu Leu Arg Pro Ser Phe Thr Phe Leu Leu Ala Phe Met Lys Ser
195 200 205

Met Gly Ser Ala Leu Ala Leu Ile Lys Asp Ala Ser Asp Val Glu Gly
210 215 220

Asp Thr Lys Phe Gly Ile Ser Thr Leu Ala Ser Lys Tyr Gly Ser Arg
225 230 235 240

Asn Leu Thr Leu Phe Cys Ser Gly Ile Val Leu Leu Ser Tyr Val Ala
245 250 255

Ala Ile Leu Ala Gly Ile Ile Trp Pro Gln Ala Phe Asn Ser Asn Val
260 265 270

Met Leu Leu Ser His Ala Ile Leu Ala Phe Trp Leu Ile Leu Gln Thr
275 280 285

Arg Asp Phe Ala Leu Thr Asn Tyr Asp Pro Glu Ala Gly Arg Arg Phe
290 295 300

Tyr Glu Phe Met Trp Lys Leu Tyr Tyr Ala Glu Tyr Leu Val Tyr Val
305 310 315 320

Phe Ile

<210> 224
<211> 972
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial truncated geranyl pyrophosphate olivetolic acid
geranyltransferase CsPT4_t76 (CsPT4t) nucleotide sequence

<400> 224
atgtccgccg gttctgatca aatcgaaggt tcccctcatc atgagtccga taactccatt 60
gctactaaaa ttttaaattt cggtcatact tgttggaagt tgcaacgtcc ttacgttgtc 120
aagggtatga tctctattgc ttgtggtttg ttcggtagag aattgtttta caacagacac 180
ttgttctctt ggggtttgat gtggaaagct ttcttcgctt tgggtccaat tttgtctttc 240
aatcttctcg ccgcatcat gaaccaaadc tacgatgttg atatcgaccg tatcaacaag 300
ccagacttac ctttagtttc cggtgaaatg tccattgaaa ctgcttggat cttgtctatc 360

attgttgcct tgactggttt aattgttact attaagttga agtccgctcc attgtttgtc	420
ttcatctaca tcttcggtat cttcgctggt ttcgcttact ccgtcccacc tattagatgg	480
aaacaatatc cttttaccaa tttcttgatc actatttcct ctcatgttgg tttggctttc	540
acttcttact ctgccaccac ttctgcttta ggtttgcctt tcgtttggcg tcctgccttc	600
tctttcatta ttgctttcat gactgtcatg ggtatgacta ttgcctttgc taaagacatt	660
tctgatatcg aagggtgatgc taagtacggt gtctctaccg ttgctaccaa gttaggtgct	720
agaaatatga cttttgttgt tttcggtgtc ttattgttga actacttggg ttctatctct	780
attggtatca tttggccaca agttttcaag tctaacatta tgatcttgtc tcatgctatt	840
ttggctttct gtttgatctt tcaaactcgt gaattagcct tagccaatta tgcctctgcc	900
ccatcccgtc aatttttcga attcatctgg ttgttatact atgccgaata cttcgtttac	960
gtcttcattt aa	972

<210> 225
 <211> 1197
 <212> DNA
 <213> Cannabis sativa

<400> 225	
atgggactct cattagtttg taccttttca tttcaaacta attatcatac tttattaaac	60
cctcataata agaatcccaa aaactcatta ttatcttatac aacaccccaa aacaccaata	120
attaaatcct cttatgataa ttttccctct aaatattgct taaccaagaa ctttcattta	180
cttggactca attcacacaa cagaataagc tcacaatcaa ggtccattag ggcaggtagc	240
gatcaaattg aaggttctcc tcatcatgaa tctgataatt caatagcaac taaaatttta	300
aattttggac atacttgttg gaaacttcaa agaccatatg tagtaaaagg gatgatttca	360
atcgcttggt gtttgtttgg gagagagttg ttcaataaca gacatttatt cagttggggg	420
ttgatgtgga aggcattctt tgctttggtg cctatatattg ctttcaattt ctttgcagca	480
atcatgaatc aaatttacga tgtggacatc gacaggataa acaagcctga tctaccacta	540
gtttcagggg aaatgtcaat tgaaacagct tggattttga gcataattgt ggcactaact	600
gggttgatag taactataaa attgaaatct gcaccacttt ttgttttcat ttacattttt	660
ggtatatattg ctgggtttgc ctattctgtt ccaccaatta gatggaagca atatcctttt	720

accaattttc taattaccat atcgagtcac gtgggcttag ctttcacatc atattctgca	780
accacatcag ctcttggttt accatttgtg tggaggcctg cttttagttt catcatagca	840
ttcatgacag ttatgggtat gactattgct tttgccaaag atatttcaga tattgaaggc	900
gacgccaaat atgggggtatc aactgttgca accaaattag gtgctaggaa catgacattt	960
gttgtttctg gagttcttct tctaaactac ttggtttcta tatctattgg gataatttgg	1020
cctcagggtt tcaagagtaa cataatgata ctttctcatg caatcttagc attttgctta	1080
atcttccaga ctcgtgagct tgctctagca aattacgcct cggcgccaag cagacaattc	1140
ttcgagtta tctgggttgct atattatgct gaatactttg tatatgtatt tatataa	1197